2013

Molecular Evolution of Hominoid Seminal Plasma Genes

Sarah Jean Carnahan Craig

MOLECULAR EVOLUTION OF HOMINOID SEMINAL PLASMA GENES

A Dissertation

Submitted to the Bayer School of Natural and Environmental Sciences

Duquesne University

In partial fulfillment of the requirements for

the degree of Doctor of Philosophy

By

Sarah Jean Carnahan Craig

December 2013

MOLECULAR EVOLUTION OF HOMINOID SEMINAL PLASMA GENES

By

Sarah Jean Carnahan Craig

Approved August 22, 2013

Michael I. Jensen-Seaman, Ph.D. Associate Professor of Biological Sciences (Committee Chair)	Philip E. Auron, Ph.D. Professor of Biological Sciences (Committee Member)
Brady Porter, Ph.D. Associate Professor of Biological Sciences (Committee Member)	Kateryna D. Makova, Ph.D. Professor of Biology Pennsylvania State University (Committee Member)
Philip Paul Reeder, Ph.D. Dean and Professor Bayer School of Natural and Environmental Sciences	Joseph R. McCormick, Ph.D. Associate Professor of Biology Chair, Biological Sciences

ABSTRACT

MOLECULAR EVOLUTION OF HOMINOID SEMINAL PLASMA GENES

By

Sarah Jean Carnahan Craig

December 2013

Dissertation supervised by Dr. Michael I. Jensen-Seaman

When asking the question of what underlying genetic changes drive species to be different, it is debated whether protein coding or non-coding mutations are more important. The hominoids (humans, great apes, and gibbons) are a group of closely related species, yet vary widely in their mating system behaviors and predicted levels of sperm competition. In species where females mate with multiple males, sperm competition is hypothesized to increase the rate of adaptive evolution of proteins expressed in male reproductive tissues through recurrent selective sweeps (positive selection). Previous studies have shown this to be true for individual male reproductive genes. In a comprehensive study of over six hundred proteins expressed in ejaculated semen, however, the same trend was not observed. Although, parsing the data based on their different functional and expression properties identifies a subset of proteins that are likely targets for adaptive evolution driven by sexual selection. Two of these rapidly

evolving proteins are the duplicated, primate specific semenogelins, SEMG1 and SEMG2. An *in vitro* expression system was used to test if selection was acting similarly on the non-coding regions, but no effect of mating system on the expression was observed. However, the two genes are expressed differently within each hominoid species. One model for divergence after gene duplication is duplication-divergence-complementation. This model was used in conjunction with phylogenetic footprinting to identify potential regulatory elements that may be important for expression level differences between the two genes.

DEDICATION

To my family and friends,

For believing in me when I didn't believe in myself.

For picking me up when I was down.

For celebrating in my successes.

For never letting me give up.

ACKNOWLEDGEMENT

I would first like to express my very great appreciation to my advisor, Dr. Michael Jensen-Seaman, for without his endless patience, encouragement, guidance, and pushing me to the best of my abilities this project would not have been possible and I would not be the scientist I am today. I would also like to thank my committee members, Dr. Brady Porter, Dr. Philip Auron, and Dr. Kateryna Makova, for your insightful and helpful comments; my dissertation is certainly better because of them. I want to acknowledge the Seaman lab members both past and present, but specifically Scott Hergenrother, Amanda Colvin, Ranajit Das, Kathryn Hooper-Boyd, Alicia Martinez, Amanda Lekse, Matthew Kučmanić, and Jason Hehr for helping me with my research and for all the camaraderie; you've made the Seaman lab an enjoyable and special place to work for the past eight-and-half years. A special thank you goes to the faculty of the Bayer School of Natural and Environmental Sciences – you've taught me everything I know. I also want to thank the staffs of the Biology Department office (especially Judy Quinque and Pamela Ferchak) and Dean's office (especially Heather Costello) for keeping everything so organized and helping me to make sure all my i's are dotted and t's are crossed. Furthermore, a huge thank you to all the people who gave assistance with sequencing (Renee Veltri, Carlos Guerrero, TJ Firneno, and Nick Bongio), cloning (Dr. Joseph McCormick and McCormick lab members, especially Allen Kotun), and tissue culture/expression assays (Dr. Philip Auron, Auron lab members, Dr. Kyle Selcer, Heidi DiFrancesca, PhD, and Natasha Dias). I am particularly grateful for my fellow graduate students, especially Allen Kotun, Metis Hasipek, Kellie Rosiek, Andrew Bishop,

Sumedha Sethi, Beth Surlow, Maria Wheeler, Tiffaney Czapski, Ruth Leehacharoenkul, and Chris Fonner for being a wonderful support system, technical support group, and some of my best friends. Another very special thank you to my lifelong friends (Audrey Tierney, Julia Schillinger, and Donna Tinkey) and feels-like-I've-known-you-a-lifetime friends (Bess Krahn and all the friends throughout the many years at Duquesne); for always being there, always being understanding, and always keeping me grounded. Finally I would like to thank my family and my husband for the years of endless support, unquestioning understanding, unyielding patience, and unwavering love, you are my rock.

TABLE OF CONTENTS

Page

ABSTRACT iv

DEDICATION vii

ACKNOWLEDGEMENT viii

LIST OF TABLES xv

LIST OF FIGURES xvii

Chapter 1: Introduction 1

Living primates of today 1

Sexual selection 4

Mating system classification and sexual selection in hominoids 11

Gene Duplication 20

REFERENCES 25

Chapter 2: Rates of evolution of hominoid seminal proteins are correlated with function and expression, rather than mating system 29

Introduction 29

Methods 33

Sequence data 33

Maximum likelihood estimates 34

Expression 35

Gene Ontology 36

Statistical Analysis 36

Results 37

Compilation of data sets....37
Seminal plasma genes evolve under evolutionary constraint....37
Seminal genes' tissue specificity correlates with rate of protein evolution....40
Seminal plasma genes involved in reproduction, immune system processes, metabolic processes, and responses to stimuli evolve more rapidly....44
Discussion....45
Quality of the datasets....45
Overall evolution of reproductive genes....47
Tempo of evolution related to function and expression....49
References....51

CHAPTER 3: Optimization of an *in vitro* system to study the evolution of transcriptional regulation -AND- *TGM4* trial and error: death by unrepeatability. 59

INTRODUCTION....59
Why study regulatory evolution?....59
Studying regulatory evolution....61
TGM4....63
METHODS....66
in vitro analysis....66
Luciferase expression assays....70
TGM4 expression experiments....72
RESULTS....73
Luciferase optimization....73
TGM4 expression....80
DISCUSSION....81
Optimal transfection conditions and the use of an internal control....81

Expression of *TGM4* 82
REFERENCES 84

Chapter 4: Evolution in the expression of the duplicated primate semenogelin genes 87

Introduction 87
Evolution of duplicated *cis*-regulatory sequences 88
Characterization and function of the semenogelins 90
Expression and regulation of the semenogelins 94
The evolution of *SEMG1* and *SEMG2* in primates 95
Using semenogelin as a model for transcriptional divergence post gene duplication 99
Methods 101
in vitro analysis 101
in silico analysis 104
Results 107
Mating system does not have an effect on transcriptional regulation of the semenogelins. 107
SEMG2 proximal promoter drives expression higher than *SEMG1* 109
Androgen does not affect the transcriptional control of the proximal promoter of the semenogelins 110
Reconstruction of ancestral semenogelin sequences 111
Modified phylogenetic footprinting identified candidate transcription factor binding sites that may account for expression differences between *SEMG1* and *SEMG2* 113
Identifying candidate TFBSs to explain expression differences between hominoid *SEMG2* expression and macaque *SEMG2* expression 115
DISCUSSION 116
An uncoupling of non-coding and coding region evolution in the semenogelins 116

Semenogelins: evolution by gene duplication 117

References 119

Chapter 5: Final Thoughts 126

Appendix 1: Custom Perl scripts used in Chapter 1 1333

Script to randomly pick genes from the genome 133

Script to make multi-species alignments 1344

Script to filter alignments based on if non-human sequence had 70% of human length 136

Script used to run PAML with a uniform model and subsequently parse the output 138

Script to run PAML for the free model and subsequently parse the output 139

Script used to run PAML for branch models and subsequently parse the output 143

Script to calculate Tau 145

Script used to calculate average Tau 147

Script used to parse Tau data 148

Appendix 2: Data from chapter 2 150

Seminal uniform estimates of *ω, Ka,* and *Ks* 150

Control estimates of *ω, Ka,* and *Ks* 1566

Seminal estimates of pairwise *ω, Ka,* and *Ks* 162

Control estimates of pairwise *ω, Ka,* and *Ks* 199

Seminal free estimates of *ω, Ka,* and *Ks* 223

Seminal Branch Estimate – LRT 235

Human 235

Chimpanzee 246

Gorilla 257

Orangutan 267

Gibbon 278

Macaque 289
Human-Chimp Ancestor 300
Stem-African Ape 311
Stem-Hominoid 321
Control Branch Estimate – LRT 331
Human 331
Chimpanzee 342
Gorilla 353
Orangutan 363
Gibbon 374
Macaque 385
Human-Chimp Ancestor 396
Stem-African Branch 407
Stem Hominoid 415
Seminal Tau Estimates 425
Control Tau Estimates 436
Tissue of expression 447
Bulbourethral Diverticulum – maximum expression 447
Bulbourethral Diverticulum 448
Bulbourethral Gland – maximum expression 449
Bulbourethral Gland 450
Prostate – maximum expression 452
Prostate 453
Seminal Vesicle – maximum expression 455
Seminal Vesicle 455
Seminal Gene Ontology 456

Control Gene Ontology 466

Appendix 3: Sequence alignments from Chapter 4 475

Sequence alignment of the 5' putative proximal promoter region of the hominoids used in the *in vitro* expression study 475

All species *SEMG1* alignment 478

All species *SEMG2* alignment 481

Ancestral sequences 484

LIST OF TABLES

Page

Table 1.1: Mating systems of the primates 12

Table 2.1: Spearman's correlation coefficients (r) between branch-specific ω and τ 41

Table 2.2: Spearman's correlation coefficients (r) between terminal branch-specific *Ka* and τ 42

Table 3.1: Primers used in screening of TOPO or pGL constructs 68

Table 3.2: Primers used for cloning of *TGM4* proximal promoter region. 72

Table 3.3: Primers used in the creation of additional *TGM4* constructs 73

Table 3.4: Spectrophotometer readings and calculated average concentrations from Bradford assay 79

Table 4.1: Number of repeats of the Ia repeat in primate semenogelins. 97

Table 4.2: Primers used for *SEMG1* 101

Table 4.3: Primers used for *SEMG2* 102

Table 4.4: Vector primers used in screening steps 102

LIST OF FIGURES

Page

Figure 1.1: Phylogenetic relationships between the extant primates 3

Figure 1.2: Schematic of the types of sexual selection. 4

Figure 1.3: Representations of various strategies employed to achieve reproductive success.....6

Figure 1.4: Graph of the measured velocity and force of escape for sperm of four species. 8

Figure 1.5: Graph displaying testes weight versus body weight.....10

Figure 1.6: Hominoid characteristics thought to be influenced by sexual selective forces 16

Figure 1.7: Generic regulatory elements of a eukaryotic promoter. 20

Figure 1.8: Example of a sequence logo of a transcription factor binding site (NFKB1). 20

Figure 1.9: Two ways of the ways in which gene duplications arise. 22

Figure 1.10: The fate of duplicated genes. 24

Figure 2.1: Seminal versus control median estimates of ω. 38

Figure 2.2: *Ka* and *Ks* estimates for seminal vs control.....38

Figure 2.3: Seminal and Control branch estimates of ω.....39

Figure 2.4: Mean tissue specificity index (τ) for seminal control and all genes.....41

Figure 2.5: Branch specific *Ka* vs Tau 42

Figure 2.6: Median ω of genes expressed in different male tissues.....43

Figure 2.7: Gene ontology of seminal genes 45

Figure 3.1: Genomic structure of *TGM4* 65

Figure 3.2: Fugene:DNA ratio optimization experiment.....74
Figure 3.3: Time-post transfection to assay experiment.....75
Figure 3.4: Firefly luciferase effect on *Renilla* luciferase.....76
Figure 3.5: Effitiveness of Stop-N-Glo.....77
Figure 3.6: *Renilla* luciferase effect on firefly luciferase expression.....78
Figure 3.7: Standard Curve for Bradford Assay.....79
Figure 3.8: Protein concentrations of cell lysates.....80
Figure 3.9: Average relative light unit (RLU) of the *TGM4* proximal promoter driven pGL4.10.....81
Figure 4.1: Genomic arrangement of the semenogelin genes.....92
Figure 4.2: Important functional elements in the promoter of *SEMG1*.....95
Figure 4.3: Stop codons in the hominoid semenogelin genes.....98
Figure 4.4: Modified phylogenetic footprinting incorporating DDC.....100
Figure 4.5: Expression of the hominoid semenogelin promoter regions.....108
Figure 4.6: Mating system effect on expression.....109
Figure 4.7: *SEMG1* and *SEMG2* expression.....110
Figure 4.8: Androgen effect on semenogelin expression.....111
Figure 4.9: Phylogenetic tree of the semenogelins.....112
Figure 4.10: Schematic of the method to find unique, conserved TFBSs.....114
Figure 4.11: Unique, conserved *SEMG1* TFBSs.....114
Figure 4.12: Unique, conserved *SEMG2* TFBSs.....115
Figure 4.13: Schematic to find differences in TFBSs between macaque and hominoid *SEMG2*.....115

Figure 4.14: Hominoid unique, conserved TFBSs in *SEMG2*.....116

Chapter 1: Introduction

Living primates of today

The extant primates are grouped with the generalized morphological characters of forward facing eyes (stereoscopic vision), grasping hands and feet (opposable thumbs and big toes), flattened nails instead of claws, a slow reproduction rate in comparison to other mammals of comparable size, single offspring as the norm (even though multiples do occur), and an extended infant/juvenile stage (Fleagle 1999).

The primates are split into two suborders (Perleman et al. 2011; Groves 2001; Fig 1.1). The suborders are Strepsirrhini and Haplorrhini. Some distinguishing features between these two groups are the Strepsirrhini lack a postorbital closure, have grooming claws, and have tapetum lucidum (reflective layer in the eye) (Fleagle 1999). The Strepsirrhini are further split into two infraorders: Lemuriformes (the Madagascar lemurs) and Lorisiformes (lorises and galagos). Haplorrhini primates are also split into two infraorders: Tarsiiformes (tarsiers) and Simiiformes. Simiiformes are further split into two parvorders: Platyrrhini (New World monkeys; characterized by laterally facing/widely spaced nostrils and the use of a vomeronasal organ in scent communication) and Catarhini (Old World monkeys, apes, and humans; characterized by downward facing/close spaced nostrils with no vomeronasal organ). The Platyrrhini parvorder contains the families Ceboidea, Atelidae, and Pitheciidae, which are all arboreal with some species having prehensile tails. Olfactory communication is important but they also use facial expressions, vocalizations, and posture to communicate. These families are split into further subfamilies (Fig 1.1): Cebidea - Callitrichinae (marmosets and tamarins), Aotinae (owl monkeys), Cebinae (capuchins), Saimirinae (squirrel

monkeys); Atelidae – Atelinae (spider monkey and woolly monkey), and Alouattinae (howler monkey); Pitheciidae – Callicebinae (titis) and Pitheciinae (saki and uakari) (Groves 2001). The Catarrhine parvorder is split into two superfamilies: Cercopithecoidea (Old World monkeys) and Hominoidea (apes and humans). Cercopithecoidea has both arboreal and terrestrial forms and females have menstrual cycles often with a sexual swelling at the periovulatory phase (Dixson 2012), which attracts males. Old World monkeys are further split into two subfamilies: Colobinae (langurs, proboscis, African colobus, Asian leaf-monkeys, and snub-nose monkeys) and Cercopithecinae (baboons, geladas, mandrills, and macaques). The Hominoidea superfamily is split into two families: Hylobatidae or lesser apes (gibbon, siamang) and Hominidae (orangutan, gorilla, chimpanzee, and human). And the family Hominidae is split into two subfamilies: Ponginae (orangutan) and Homininae (gorilla, chimpanzee, and human) (Perelman et al. 2011).

The common ancestor to all primates lived approximately 80-90 million years ago (MYA) at the time of the Cretaceous/Paleocene likely in what would be Asia today (Perelman et al. 2011). The radiation of primates began with the split of the Haplorhine and Strepshirhine primates at approximately 87 MYA (Steiper and Young 2006; Perelman et al. 2011). The next split at approximately 43 MYA was the split between the Platyrrhine primates and Catarrhine primates, followed by the split of the Cercopithecoidea and Hominoidea at approximately 32 MYA (Steiper and Young 2006; Perleman et al. 2011). The extant species of the hominoid clade arose at approximately 20 MYA (gibbon), 17 MYA (orangutan), 8 MYA (gorilla), and 6 MYA (human-chimpanzee split) (Jensen-Seaman and Hooper-Boyd 2013).

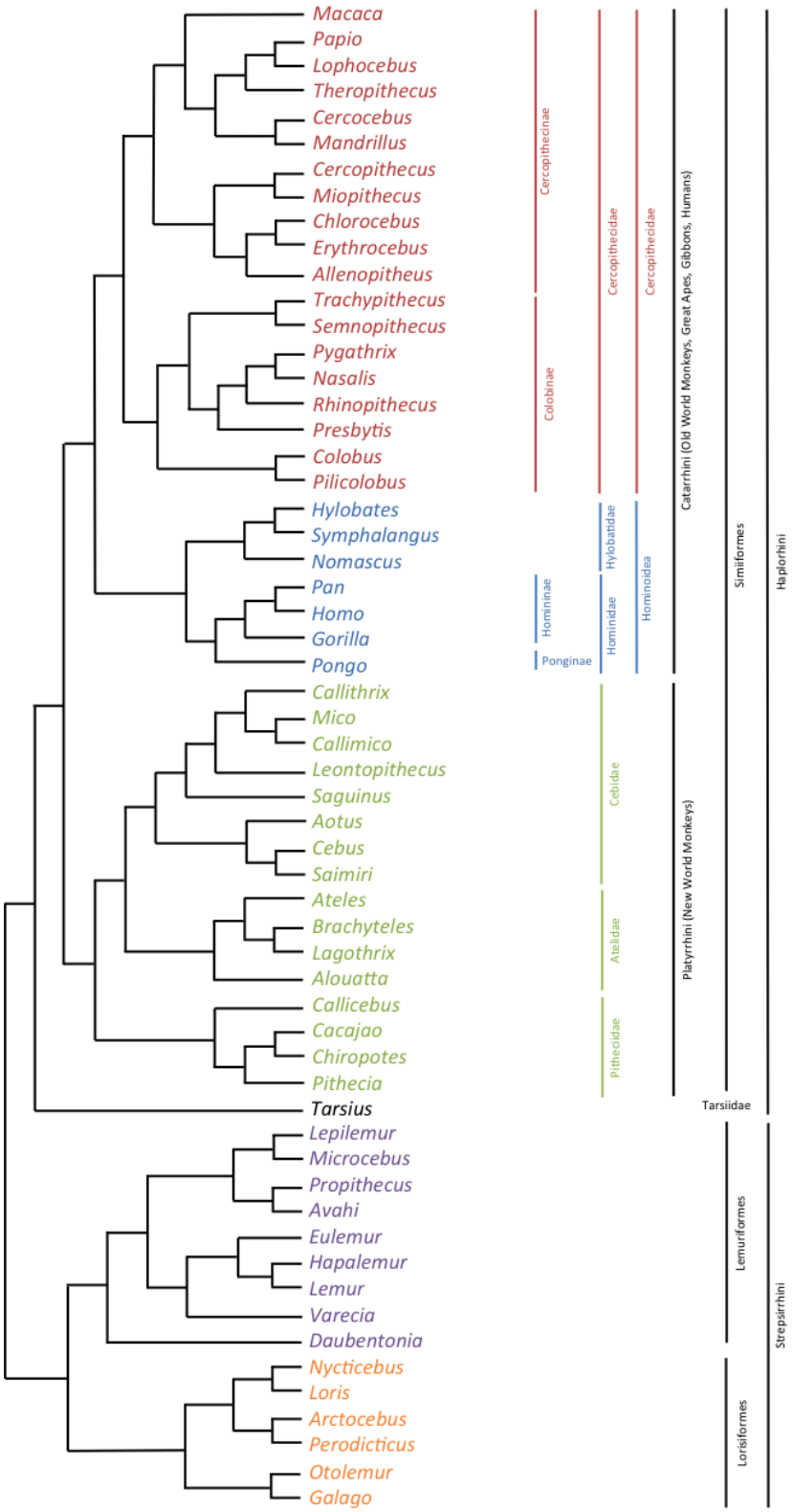

Figure 1.1: Phylogenetic relationships between the extant primates
Topological relationships redrawn from Perleman et al. 2011. Tree was built using maximum likelihood on molecular data and represents the general consensus tree of the relationships between primate species.

Sexual selection

Charles Darwin described the force of sexual selection to explain features that do not help an organism survive, but increase chances of successful mating (Darwin 1871). Sexual selection can take on many forms but can be broken into two main categories: pre-copulatory sexual selection and post-copulatory sexual selection (Fig. 1.2). Within each category are both intrasexual selection forms (between members of the same sex, black arrows in Fig 1.2) and intersexual selection forms (between members of the opposite sex, white arrows in Fig 1.2).

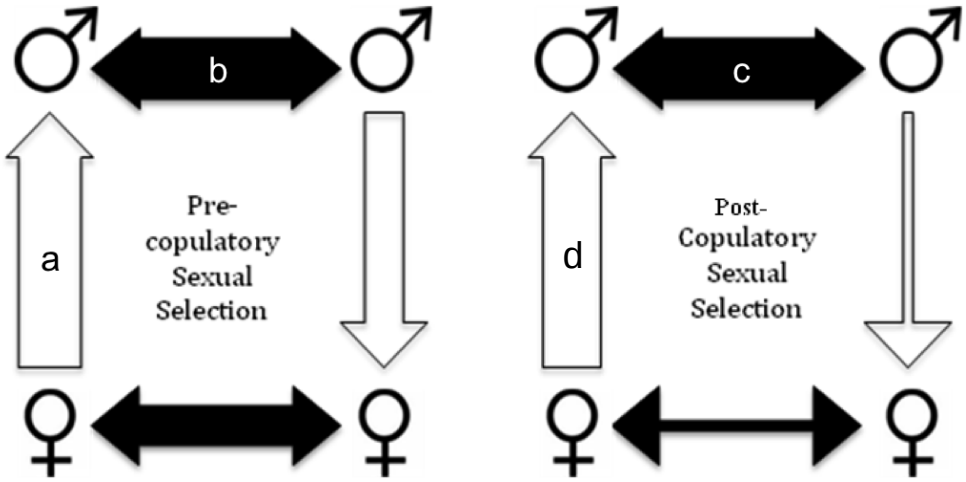

Figure 1.2: Schematic of the types of sexual selection.
Modified from Dixson 2012. Intrasexual selection types are shown by black arrows and intersexual selection types are shown in white arrows. The direction of the arrow shows the direction of the selection and the width of the arrow represents the overall commonness of the type. There are four commonly described modes of selection (labeled a,b,c, and d) and for the purpose of this document will be the focus of explanation.

Female choice is a type of pre-copulatory, intersexual selection (Fig 1.2a). In this type of selection the female will choose a mate based on male characteristics such as a mating ritual or physical displays. These displays can be auditory as in cicadas, crickets, locusts, and grasshoppers (Gould and Gould 1989), or ornamentations like the long, colorful tail-feathers of the peacock (Fig 1.3a). The characteristics that the female bases

her choice on are usually sexually dimorphic traits – the sound producing organs in the above insects are absent in the female and the female peacock has drab coloration. Furthermore, the same characteristics that males use to attract mates can also attract predators, so while they may confer reproductive success, they may not be beneficial for survival. So by having larger more extravagant ornamentation in the face of such adversity, the males can communicate to the female that he is healthy, has good genes, and she should mate with him. This type of 'artificial selection' by the female is hypothesized to potentially lead to runaway selection (Fisher 1915) – as an increase in size/color leads to a selective advantage in males, the females will evolve genes to prefer that trait. This will further propagate that trait in association with reproductive success. If sexual selection were the only force acting on an individual this runaway selection could continue indefinitely with the males' evolving more elaborate ornamentations and the females' preference evolving to prefer the extreme. However, sexual selection is not the only force acting on an individual and so there must be an upper limit to ornamentation/preference that intersects with natural selection and an individual's ability to survive (Pomiankowski and Iwasa 1998).

Male competition is another pre-copulatory type of sexual selection that is intrasexual (male-male, Fig 1.2b). In this type of selection, males battle each other for reproductive access to females and can lead to sexually dimorphic body traits that give males a selective advantage (Gould and Gould 1989). Male honeybees for example have much larger eyes and flight muscles to spot a female further away and fly to her faster than other males (Fig 1.3b). Similarly, male gorillas are much larger than females with well-developed muscles and strong jaws to aid in hand-to-hand combat to protect his

territory and reproductive rights over his harem of females (Fig 1.3c). Another trait used male competition weaponry. These traits can be seen across a wide range of taxa such as leg spurs in roosters (Fig 1.3d), exaggerated claws in male fiddler crabs (Fig 1.3e), horns or enlargement of the mandible of the male beetle, and antlers the moose (Fig 1.3g). While these characters can lead to success as they battle for a mate, they are also costly; the claw of the male fiddler crab can be an impediment to feeding and burrowing for protection. Likewise, large racks in antlered animals are costly to produce and then are very heavy and can impede locomotion.

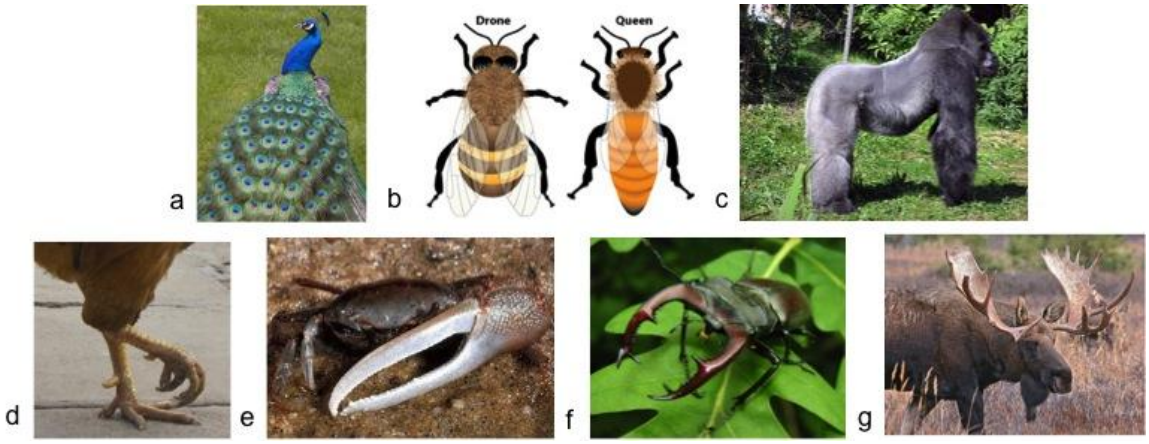

Figure 1.3: Representations of various strategies employed to achieve reproductive success. a) A male peacock displaying for a female b) diagram of the differences between the female queen honey bee and the male drone honey bee (http://www.state.nj.us/dep/parksandforests/forest/bees.html) c) male gorillas use their large, muscular bodies to engage in battle d-g) representations of weaponry d- spurs on the legs of roosters, e- male fiddle crabs fight with their exaggerated claw f- horns/enlarged mandibles in a beetle species, g– massive horns of the male moose used in a fight with another male. All figures except b are copyright free images (copyright for b on-file).

A third form of sexual selection is post-copulatory, intrasexual competition between males known as sperm competition (Fig 1.2c). This is defined as "competition within a single female between the sperm from two or more males for fertilization of the ova" (Parker 1970, page 527). The mechanisms of sperm competition can be seen in modifications to sperm, modifications to male accessory organs, and modifications of the

ejaculate. Sperm morphology is a trait that is responsive to sexual selection. In some species of birds and insects longer sperm is selected for and while the reasons are still unclear, it could be that longer sperm help to block the female reproductive tract (Wigby and Chapman 2004) or other competitive advantages (displacing smaller sperm, swimming faster, or longevity; Snook 2005). In the primates, sperm length, while not correlated with body weight, is correlated with testes size (another indicator of sperm competition discussed below) and therefore thought to be responsive to sexual selection (Dixson 1993). Sperm motility is also an important factor that can influence a male's reproductive potential and believed to be responsive to sperm competition by helping a sperm out-swim competitor sperms (Snook 2005). In primates this has been studied using optical tweezers (Nascimento et al. 2008) and found that multi-partner species had faster, more forcefully swimming sperm than those species in single-partner societies (Fig 1.4) (Nascimento et al. 2008; Shi et al. 2011). Furthermore, midpiece volume (part of the sperm that carries the mitochondria) is also larger in species that have more promiscuous mating systems and in positive correlation with relative testes size (Anderson and Dixson 2002). Midpiece volume is a likely indicator of mitochondrial loading, which has a bearing on flagellar movements and therefore may impact the motility of sperm making it a potential target of sexual selection. In addition to just the amount of mitochondria present, equally important is the activity of those mitochondria. In the great apes, chimpanzees have more metabolically active mitochondria that stay active for longer than other ape species (Anderson et al. 2007), which is in accordance with levels of sexual selection. It has also been hypothesized that sperm dimorphism (presence of alternative types of sperm) may also be a form of sperm competition in which 'kamikaze' sperms

may be present to directly compete with sperms of other ejaculates (Wigby and Chapman 2004). While this is a universal trend in species of Lepidoptera and in some fruit flies it does not seem to have a footing in human sperm competition (Moore et al. 1999).

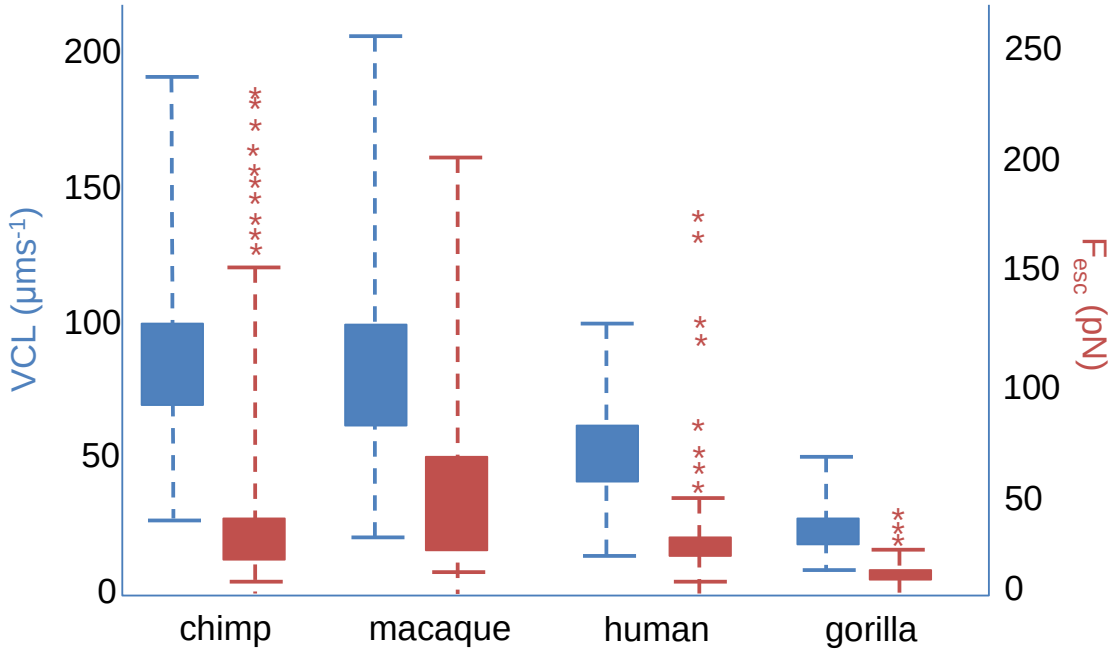

Figure 1.4: Graph of the measured velocity and force of escape for sperm of four species. Graph displaying a comparison of the velocity of sperm (blue) and force with which sperm swim (red). Figure redrawn and modified from Nascimento et al. 2008.

Besides the morphology of the sperm, the amount of sperm produced is equally important. With an increase in sperm count an individual can increase the odds that one of his sperm will be able to fertilize the egg (Birkhead and Møller 1998). This is a trait that is related to the relative size of the testicles – larger number of sperm requires more spermatogonial tissue (Dixson 2012). Sexual selection seems to drive this trend as larger relative testicles is often associated with more promiscuous mating systems (Fig 1.5, Harcourt 1981). This trend is seen in a wide taxonomic sampling including eutherian,

marsupial, and montreme species (reviewed in Dixson 2012), porpoise (Fontaine and Barrette 1997), and primates (Kappeler 1997). In addition to the testes, other male reproductive accessory organs (vas deferens, seminal vesicles, prostate) also seem to be influenced by levels of sperm competition. The vas deferens, the muscular tubular organ which serves as the passage of sperm from the testicles to the urethra, is shorter in species where the females mate with multiple partners and also has different thicknesses of the muscle layers within the vas deferens wall (Anderson, Nyholt, Dixson 2004). This could be a selective advantage because the sperm has less distance to travel from production site to ejaculation and the musculature structure may increase the ability to recover non-ejaculated sperm in order to conserve resources for the next ejaculate. The seminal vesicles, the accessory gland that produces the majority of the seminal fluid (60% total ejaculate volume, Dixson 2012), are significantly larger in species with multi-male mating strategies relative to body weight (Dixson 1998; Anderson and Dixson 2009). Continuing with this trend, the prostate (production of 30% total ejaculate volume, Dixson 2012) is positively correlated with testes size (Ramm et al. 2005; Anderson and Dixson 2009). These observations show that sexual selection via sperm competition is a major factor in the evolution of male secondary sexual organs.

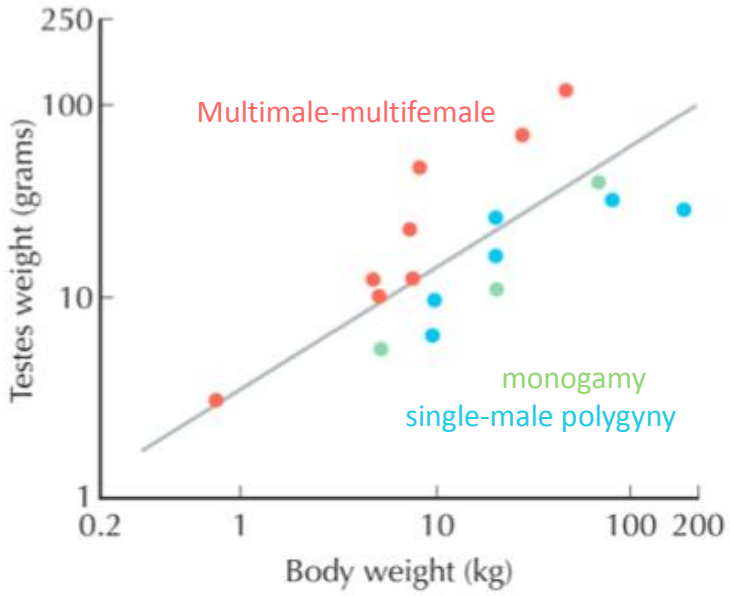

Figure 1.5: Graph displaying testes weight versus body weight.
A positive correlation is seen and species that live in multimale-multifemale mating systems have higher ratios than species in monogamous or single-male polygynous systems. Graph from Barton et al. 2007 and redrawn from Harcourt et al. 1981.

The final way in which sperm competition can influence evolutionary change is through modifications of the seminal fluid. A major variant in the phenotype of seminal fluid is the production of a copulatory plug found in many primates, rodents, and bats. It is a firm rubbery coagulation of semen in the female reproductive tract that occurs when fluids from male accessory glands mix. There are several hypotheses for the function of the plug: sperm positioning, prevention of sperm loss, or a blockade (reviewed in Dixson 2012). The positioning of sperm and prevention of backflow loss is a hypothesis based on evidence that ejaculation occurs in spurts, which cause a layering effect of the ejaculate within the female reproductive tract of which the more sperm rich fractions are close to the cervix (Tauber et al. 1980). The coagulation of the fluid behind this sperm rich fraction may act by facilitating sperm transfer through the cervix by keeping its position and preventing backflow (Dixson 2012). An alternative hypothesis is that coagulation prevents sperm deposition by subsequent males by acting as a chastity belt. This function

is hypothesized for rodents and other mammals, but has not been supported in experimental models (Dewsbury 1985). Additional seminal fluid pathways that are affected by sperm competition are gamete recognition proteins in broadcast spawners (e.g. abalone, Swanson and Vacquier 2002), female modification substances in *Drosophila* **(**Chapman et al 2003**)** and mosquitos (Sirot 2012) that, among other effects, make the female less receptive to subsequent matings or induce ovulation (Eberhard 2009).

The fourth category of sexual selection is described as cryptic female choice. This is a post-copulatory type of sexual selection in which the female will "decide" which sperm to use to fertilize her egg(s). In this type of sexual selection, the female can influence the evolution of male seminal fluids by preferentially keeping only "'superior' seminal products" (Eberhard and Cordero 1995). This selection may be based on a biochemical signal between the seminal fluid proteins and proteins in the female's reproductive tract (e.g. Drosophila spermatheca proteins, Prokupek et al. 2008), mediated by the nuptial gift, which can signify male quality to the female (e.g. in the spider, *Pisaura mirabilis*, Albo et al. 2013), or (as in the case of primates) it could be driving the evolution of more macroscopic features such as genitalia morphology (Dixson and Anderson 2001).

Mating system classification and sexual selection in hominoids

Mammalian socio-sexual behavior is complex and diverse. The behaviors described below do not serve as the rule for the groups but just the trend; just as the systems are diverse between species, there are also exceptions *within* each species. The context as to how primate mating systems are usually described centers around two

important considerations: 1) does a female mate with one male or more than one male during the fertile phase of her ovarian cycle (as well as how many mates will a male have in a given period of time) and 2) are the sexual relationships long-term and exclusive or short-term and non-exclusive. With these considerations in mind there are five mating systems to describe primate sexual behavior and they are summarized in the following table (Dixson 1998).

Table 1.1: Mating systems of the primates (Dixson 2012)

Mating System	**Number of males per periovulatory phase**	**Type of sexual relationship**	**Examples**
Monogamy	One	Long-term, exclusive	Gibbon
Polygyny	One	Long-term, exclusive*	Gorilla
Polyandry	Two or more	Long-term, exclusive	Marmoset, tamarin
Multimale-multifemale	Many	Short-term, not exclusive, gregarious	Macaque, chimpanzee, bonobo
Dispersed	Two or more?	Short-term, not exclusive, nongregarious	Orangutan

*Exclusive from female perspective, a single male will mate with other females in the 'harem' unit

The macaque (not a hominoid, yet used as the Old World monkey outgroup in many of my analyses) lives in large fission-fusion, multimale social groups containing fifty or more individuals (Fleagle 1999). Approaching mating season, males experience a reddening of the sexual swelling and an increase in testes size (associated with an increase in spermatogenesis), which is due to an increase in testosterone levels. Dominance rank within macaque groups also correlate with testicular development with higher ranking males (or sons of high-ranking female) having larger testes than lower ranked individuals. Copulations between males and females often occur as part of a consortship but females may consort with multiple males (up to four) at a time (Dixson 2012).

The gibbon (*Hylobates*), a lesser ape from southeast Asia, is the smallest of the living apes (Fleagle 1999). There are numerous gibbon species, but all are relatively uniform in morphology and behavior. Gibbons are fiercely territorial and both sexes will perform vocal duets to help with intergroup spacing. The socio-sexual behavior is monogamous with the social unit made of a mated pair and up to four dependent offspring (Fleagle 1999).

Orangutan (*Pongo pygmaeus*) stands out among the diurnal primates in that adults are non-gregarious. Orangutans experience extreme sexual dimorphisms with males approximately twice the size of females (Dixson 2012) and exhibiting male bimaturism (subordinate males will suppress secondary sexual traits – cheek flanges, laryngeal sac, and long hair) (van Schiak and van Hooff 1996). Mating between a male and female may occur either in voluntary or involuntary contexts whenever the sexes associate. A receptive female will willingly engage in consortships with adult males and adolescent females will actively seek out relationships with adult males. However, females will strongly resist mating with some males (usually subadults but also certain adults) and are not always successful. During mating a dominant male of the area will essentially guard mating access to the female with subordinate males trailing the mating pair and attempting to mate with the female while the consorting male is distracted (van Schaik and van Hooff 1996).

The gorillas (*Gorilla gorilla* and *G.beringei*) are selective herbivores with extensive home ranges that track seasonal fruit crops (Watts 1996). They live in groups that average between nine and ten individuals with one mature adult male (the 'silverback'), one or more younger males, and several adult (unrelated) females with

offspring (Fleagle 1999, Dixson 2012). The silverback is the leader of the group and has exclusive mating rights to the females. The subordinate males in the group form other relationships with the females consisting of protection, food, and grooming. However, these subordinates often try to 'steal' fertilizations through competition over estrous females, which are often interrupted by the dominant male who may guard the females from these advances (Watts 1996).

The most fluid socio-sexual group of the hominoids belongs to members of the *Pan* family – chimpanzee (*Pan troglodytes*) and bonobo (*Pan paniscus*). The group is described as having a fission-fusion society (Fleagle 1999; White 1996; Dixson 2012) with small foraging groups regularly splitting and rejoining. While the mating system of both the chimpanzee and bonobo is multimale-multifemale there are several reported mating strategies utilized by both species: opportunistic mating, possessiveness, and consortship (Takahata et al. 1996). Copulation rates of chimpanzees and bonobos are approximately equal during periovulatory periods (more than 135 times before each conception– Hasegawa and Hiraiwa-Hasegawa 1990) but the rate of copulation throughout the interbirth interval is much higher in the bonobo.

The most unique primate species is the human (*Homo sapiens*). The human is a bipedal, omnivorous, cosmopolitan species with a large balloon-like cranium and an apparent lack of hair over most of its body. There is no single pattern of social organization among humans, but monogamous families and single-male groups (where females mate with a single male during a periovulatory period) are the most common practices (Fleagle 1999). These single male units are grouped into additional higher-level social structures such as clans and tribes (Chapais 2013). Humans also show dimorphic

characteristics between the sexes – males are larger than females and have facial hair, muscular build, enlarged larynx, and a deepened voice (Dixson 2012).

The mating system of each species affects the type and intensity of sexual selection that it will face (summarized in Fig 1.6). Individuals living in a polygynous mating system – like the gorilla – will have low levels of sperm competition because their main selective pressure is pre-copulatory, male-male combat. This results in traits such as small testes:body weight ratio, liquid ejaculates, slower and less forcefully swimming sperm (Fig 1.4), but very large sexual size dimorphism. On the other hand, species living in promiscuous mating systems (chimpanzee) have very high levels of sperm competition and lower levels of pre-copulatory sexual selection have characteristics such as large testes:body weight ratio, fast and forcefully swimming sperm (Fig 1.4), and firm coagulation of the ejaculate but have small sexual size dimorphism.

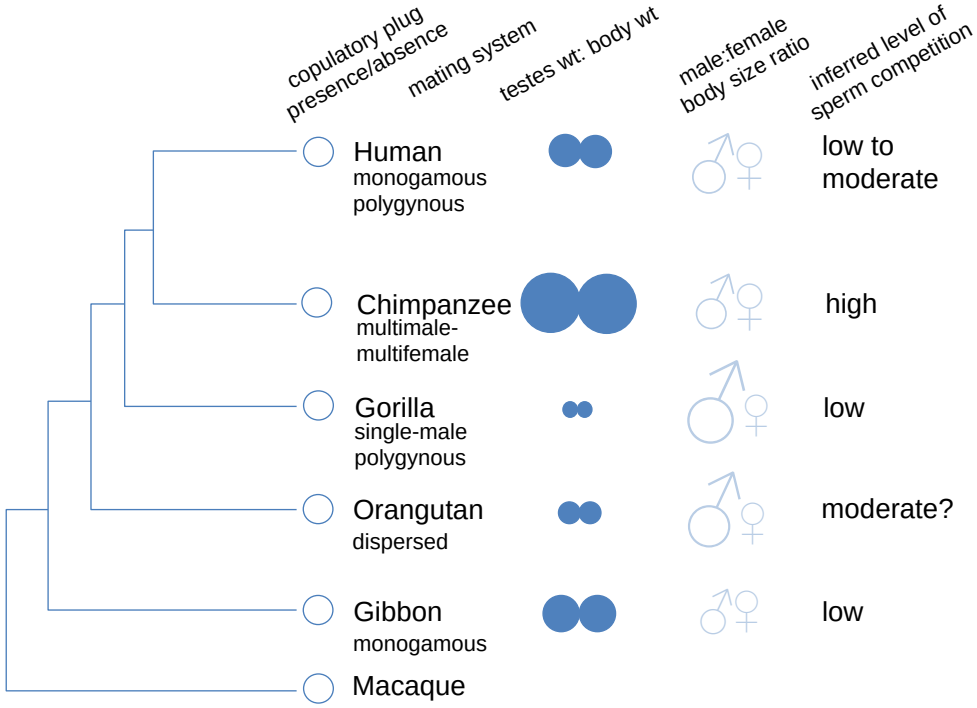

Figure 1.6: Hominoid characteristics thought to be influenced by sexual selective forces
Filled in circles represent presence/absence of the copulatory plug with filled in circles representing plug and open representing no plug. Under testes wt:body wt – the circles represent approximate size with larger circles indicating a larger ratio, Similarly, the male:female body size ratio the symbols represent approximate size ratios.

Eukaryotic gene regulation

Eukaryotic protein coding genes (Class II genes) are transcribed by the enzyme RNA polymerase II. The final end product of gene expression is a protein that has a certain job in the cell and helps to confer a specific phenotype. This complex process has many levels of regulation to get from DNA to protein: gene accessibility, transcriptional initiation, mRNA processing, transport of mRNA, translation, and post-translational modifications. Of these types of regulation, I will be focusing on one, initiation of transcription.

Transcription initiation is mediated through several types of regulatory sequences: promoter regions (core and proximal), distal elements (enhancers, silencers, insulators), and *trans*-acting factors (see Fig 1.7). The promoter region is the sequence upstream from

the transcription start site (with the exception of a few downstream elements like the DPE-downstream promoter element) that typically spans for about a kilobase (Maston et al. 2006). The promoter is typically split into two regions. The first is the core promoter, which serves as a docking station for the basic transcriptional machinery and is the site of the pre-initation complex (PIC = TATA binding protein and associated transcription factors) assembly. The binding of these elements gives the direction of transcription and provides a basal level of transcription. There are three classes of core promoters: tissue specific, housekeeping, and developmental; and they differ based on the different combination of elements within this region, although these are not strict classes as there are exceptions for each class (Lenhard et al. 2012). The second region is the proximal promoter region, which is the sequence upstream of the core promoter. Transcription factors or other DNA binding proteins (collectively known as 'activators') bind in this area to help control transcription by increasing the formation of the PIC by targeting transcriptional machinery to the region, targeting chromatin modifiers to the area, or binding to additional proteins to further refine control. Transcription factors (TFs) bind to specific locations within the proximal promoter region called transcription factor binding sites (TFBSs), which are small (6-12 nucleotides) and are usually degenerate (there is a consensus sequence for specific TFs but there is some room for variation, see Fig 1.8). However, the TFBSs are very important because depending on their sequence they can affect the efficiency of a given TF to bind, binding partners of a TF (TFs can form homo- or hetero- dimers to help achieve specificity), or the structure of the TF (which can affect other factors' ability to recognize it) all of which may affect the overall transcriptional output (Maston et al. 2006). The 'coactivators' (factors that bind to the activators) are not

directed by sequence specificity but are recruited to the promoter region by protein-protein interactions. A common example of a coactivator is a chromatin remodeler enzyme, which can modify the activators ability to suppress (the remodeler will make inactive chromatin) or activate (the remodeler will make active or open chromatin) transcriptional activity (Li et al. 2007).

The second region identified in Fig 1.7 is the distal regulatory elements: insulators, enhancers, and silencers. Insulators are boundary elements that when bound to DNA can block enhancer/silencer/chromatin-remodeling effects at one gene from affecting the environment around a second gene. Enhancer elements regulate transcription *positively* in spatial (tissue or gradient)- and temporal (developmental stage or at a particular stage in a process)- specific manner (Ong and Corces 2011). Enhancers are made of a group of closely spaced TFBSs that act synergistically to modulate activity. Alternatively, silencers work in a similar manner to enhancers only with the opposite effect (they *repress* or shut down transcription). Both enhancers and silencers can be located far from the promoter of which they are acting upon so the distance and orientation of the enhancer relative to the promoter is irrelevant, but the distance and orientation of specific elements in the enhancer is important (Maston et al. 2006). The distal elements and the proximal elements come into contact mediated by chromosome looping. As an example, in the β-globin locus, the hypersensitive sites of the locus control region (group of regulatory elements that regulate an entire locus or gene cluster), which is located about 40-60 kilobases away from active genes, comes into close spatial proximity of these genes by looping out in active genes that lie between these regions in order to only activate the specific globin gene that is appropriate for that particular

developmental stage. This was discovered using 3C (chromosome conformation capture) technology (Tolhuis et al. 2002).

Another interesting factor that can affect transcription initiation are long non-coding RNA (long ncRNA)products. These are products that do not code for protein but can act to regulate neighboring protein-coding genes (Mercer et al. 2009). For instance, the promoter region can be transcribed into a long ncRNA that can recruit RNA binding proteins and integrate them into the transcriptional regulation machinery. These ncRNAs can also influence transcription by acting as a cofactor to other transcription factors to help guide them to the correct location or act as a scaffold to bring different proteins together, to act as a decoy to take proteins away from binding with DNA, interact with the initiation complex to specify promoter usage, interacting with the basal components of the transcription machinery to mediate transcription in 'enhancer'-like ways (e.g. chromosome looping) (Mercer et al. 2009; Rinn and Chang 2012).

The combination of all the different regulatory regions and nature of the regulatory elements (activators, coactivators, enhancer, silencer, etc.) to interact with each other leads to a robustness in the regulatory network that is termed combinatorial control (Maston et al. 2006). The synergistic character of regulatory complexes (the combination of proximal and distal elements) accounts for the robustness of these regions and why with about 25,000 genes and roughly only 1,900 DNA-binding transcription factors there can be coordinated and specific control of transcription (Lemon and Tijan 2000).

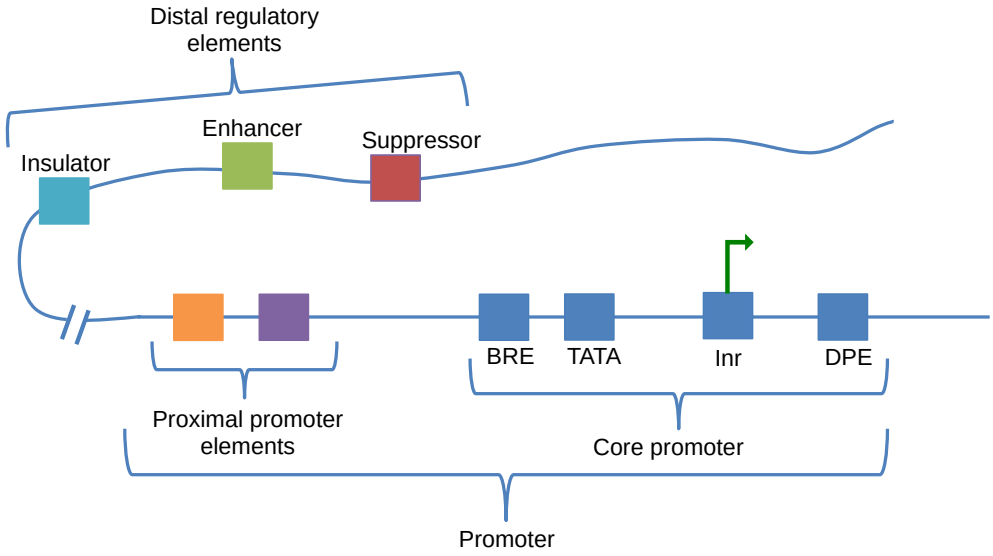

Figure 1.7: Generic regulatory elements of a eukaryotic promoter.
Redrawn and modified from Maston et al. 2006. Trans elements are not represented here. BRE = TFIIB=recognition element; TATA=binding site for TATA binding element; Inr= initiator element; DPE= downstream promoter element. Green arrow indicates the transcription start site.

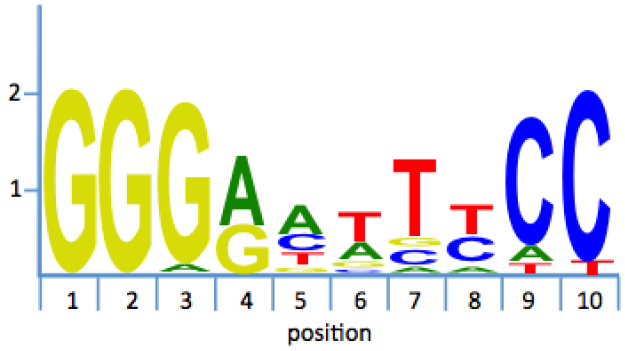

Figure 1.8: Degeneracy of transcription factor binding sites
TFBSs are often visualized using sequence logos. Example of a sequence logo of a transcription factor binding site (NFKB1). The y axis is the approximate preference level of any given position within the binding site (x axis): 1 = no preference, 2 = only one base is used. The height of each nucleotide at each position is approximate to its relative occurrence at that position and sorted with the most common at top (figure adapted from Schneider 1994).

Gene Duplication

Gene duplication occurs in all three domains of life (Zhang 2003) and is the supplier of new raw genetic material upon which natural selection, genetic drift, and mutation may act (Ohno 1970). This is an important process in evolution because it can enhance the plasticity of a genome or organism to allow for adaptation in an ever

changing environment, allow for the evolution of gene networks which can confer sophisticated regulation to control and enhance complex traits, and can contribute to species-specific functions (Zhang 2003). A 2005 study of gene duplications in the human and chimpanzee genomes estimated that 2.7 percent of the genome has been duplicated in one species but not the other, which is greater than the single-base-substitution estimate of 1.2 percent (Cheng). These estimates put a rate of about four to five megabases of genome duplicated per million years since the human-chimpanzee divergence (Cheng 2005).

Gene duplications can happen in a variety of ways (Ohno 1970; Zhang 2003). The first is unequal crossing over during homologous recombination (Fig 1.9a). In this case the duplicated genes are usually located tandemly on a chromosome (or close to each other depending on location of cross over) and the duplicated genes both retain their genomic arrangements – they may be flipped in orientation but will maintain introns, etc. With unequal crossing over it is possible to duplicate more than one gene at a time. The second mechanism is through retrotransposition (Fig 1.9b). In this case the gene is transcribed into messenger RNA, reverse transcribed into cDNA, and then reinserted somewhere in the genome. The new duplicate will be similar to the original gene in the coding sequence but will differ in genomic arrangement; it will have lost the introns, there will be a polyA sequence at the 3' end, and there will be flanking short repeats at either end of the gene. This type of gene duplication will result in the duplication in only one gene. A third type of gene duplication is the result of whole genome or whole chromosome duplication. This is a common process in plants but rarely seen in animals and is the result of nondisjunction during division. The final mechanism of gene

duplication is segmental duplication in which 1000 to >200,000 nucleotides are duplicated at a time. These duplications are not usually in tandem and therefore are not thought to be due to unequal crossing over.

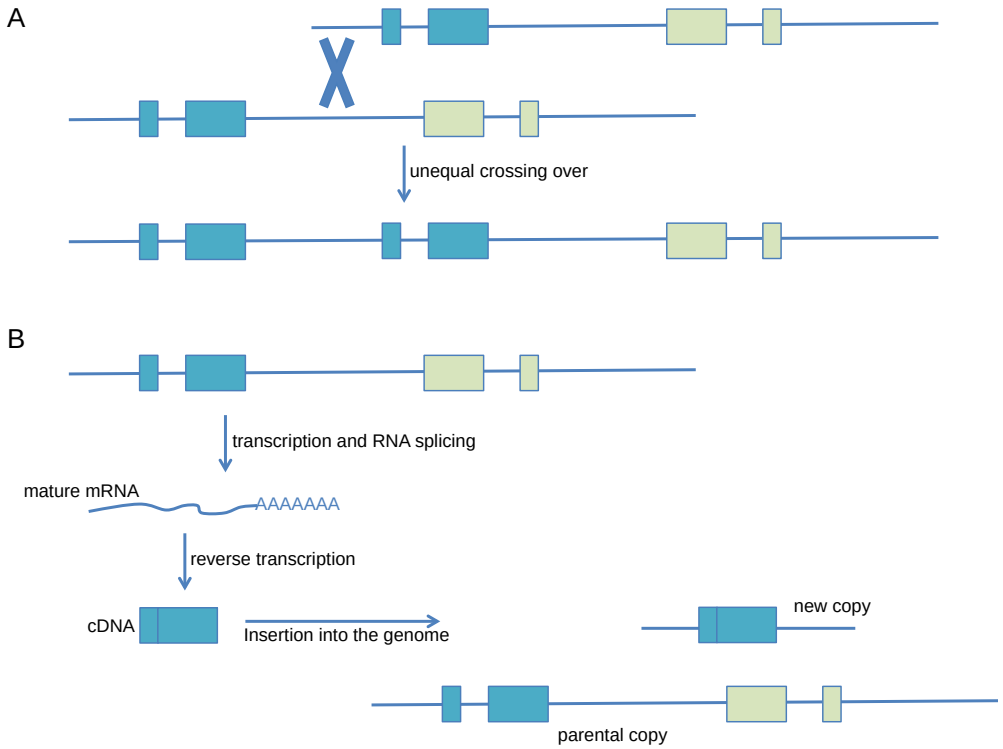

Figure 1.9: Two ways of the ways in which gene duplications arise.
A) Unequal crossing over. A pair of homologous chromosomes may misalign during homologous recombination resulting in unequal crossing over. The result is that on one of the chromosomes there is two copies of the gene. B) Retrotransposition. A gene is transcribed and processed into mRNA, reverse transcribed into cDNA and reinserted into the genome. Modified from Zhang 2003.

After a gene has been duplicated there are several fates that the paralogous genes may have (Fig 1.10; Ohno 1970; Zhang 2003): splitting of function, new function, gene loss, or conservation. Splitting of the parental gene's function between daughter genes is referred to as sub-functionalization. This splitting can be of functional domains of the protein for divergent function, but often the regulatory functions are spilt and diverge to create tissue specific or temporal specific expression of the duplicates. These changes can be driven by relaxed selection under a model of complementary degenerate mutations

(Papp et al. 2003; Zhang 2003) or positive selection. A common example of sub-functionalization is seen in the β-globin genes in human (Gumucio et al. 1992). At this locus there are five functional genes and one pseudogene created by several tandem gene duplications. These genes express at developmentally specific timeponts: in early embryonic life ε-globin is expressed, at 6-8 weeks of gestation the two γ-globin genes become active, and at birth there is a 'switch' to repress expression of these previous globins and to then express the δ- and β- globin genes. The differences in the expression are due to differences in the regulatory region, which are thought to be recognized by the LCR (locus control region) enhancers. Neo-functionalization is the evolution of novel function. This type of selection is often driven by positive selection – a mutation creates a few substitutions to create a new function which later becomes fixed due to an adaptive advantage from this new function. An example of neo-functionalization is in the evolution of the eosinophil-derived neurotoxin (*EDN*) and the eosinophil cationoic protein (*ECP*) which have structural similarities to ribonucleases (Rosenberg 1995) and were duplicated about 31 million years ago (Zhang et al. 1998). After the duplication *ECP* evolved a novel antibacterial property not found for *EDN* due to specific changes in the regulatory regions (Rosenberg 1995; Zhang et al. 1998). The third fate of duplicated genes is pseudogenization or gene loss. This occurs with the accumulation of mutations (either coding or non-coding) to make one a non-functional copy. After a long enough time the paralogs will be unrecognizable because the non-functional copy will not be under any selection and may be freely mutating or it may be deleted from the genome. It's estimated that for every two functional genes in the human genome there is one pseudogene (Zhang 2003). An example of pseudogenization in the human genome is the

loss of function of approximately 50 percent of the olfactory genes (Rouquier et al. 2000), which is the highest pseudogenization rate for primates at this locus and could account for humans reduced ability to discriminate between odor molecules. The final fate of a duplicated gene is conservation. This is a rare fate because it depends on extra amounts of the protein product to beneficial. One case of this in humans is the amylase gene, *AMY1*, (a salivary protein which aids in digestion of starches). It is found that there is a positive correlation between copy number of *AMY1* and the amount of protein product found. The increase in copy number of this gene is human specific and seems to be related to the evolution of diet from frugivorous ancestors to the starch-rich diet of modern humans (Perry et al. 2007).

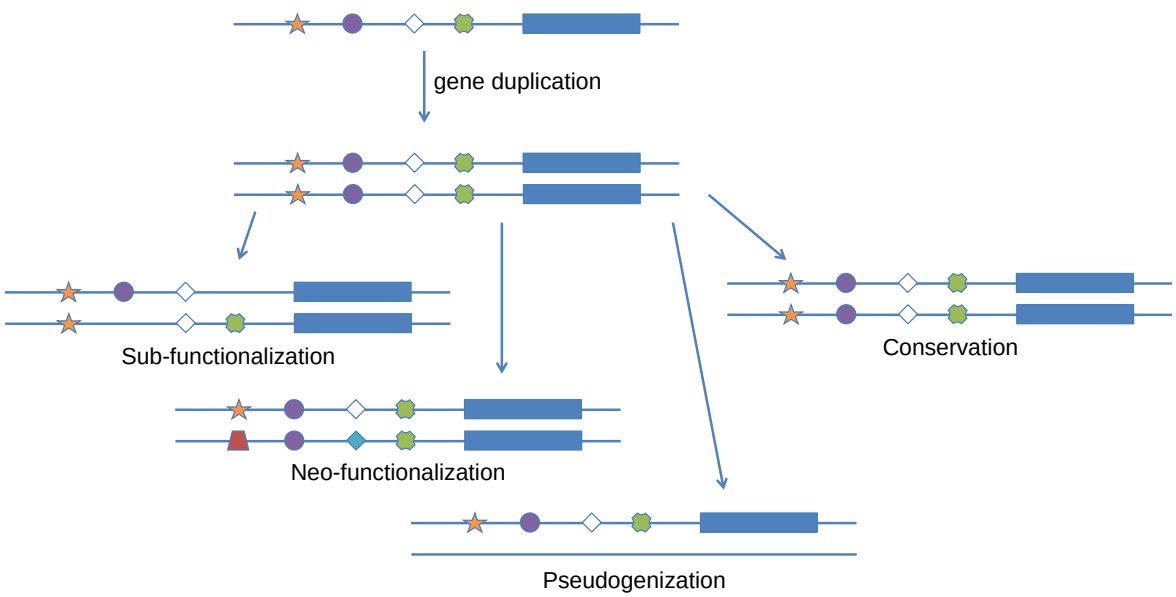

Figure 1.10: The fate of duplicated genes.
After gene duplication there are four possible fates of the paralogs: sub-functionalization, neo-functionalization, pseudogenization, or conservation. In this diagram it is showing a gene with four regulatory elements or protein domains, during sub-functionalization these are divided among the two duplicates, in neo-functionalization one the paralogs can evolve a new function, in pseudogenization one copy accumulates mutations that eventually make it non-functional, and during conservation both copies are kept the same.

REFERENCES

Albo MJ, Bilde T, Uhl G (2013) Sperm storage mediated by cryptic female choice for nuptial gifts. *Proc R Soc B* 280: 20131735

Anderson MJ, Dixson AF (2002) Motility and the midpiece in primates. *Nature* 416:496

Anderson MJ, Nyholt J, Dixson AF (2004) Sperm competition affects the structure of mammalian vas deferens. *J Zool Lond* 264:97-103

Anderson MJ, Chapman SJ, Videan EN, Evans E, Fritz J, Stoinski TS, Dixson AF, Gagneux P (2007) Functional evidence for differences in sperm competition in humans and chimpanzees. *American Journal of Physical Anthropology* 134:274-280

Anderson MJ, Dixson AF (2009) Sexual selection affects the sizes of the mammalian prostate gland and seminal vesicles. *Current Zoology* 55(1):1-8

Chapais B (2013) Monogamy, strongly bonded social groups, and the evolution of human social structure. *Evolutionary Anthropology* 22:52-65

Chapman T, Bangham J, Vinti G, Seifried B, Lung O, Wolfner MF, Smith HK, Partridge L (2003) The sex peptide of *Drosophila melanogaster*: female post-mating responses analyzed by using RNA interference. *PNAS USA* 100:9923-9928

Cheng Z, Ventura M, She X, Khaitovich P, Graves T, Osoegawa K, Church D, DeJong P, Wilson RK, Pääbo S, Rocchi M, Eichler EE (2005) A genome-wide comparison of recent chimpanzee and human segmental duplications. *Nature* 437:88-93

Darwin C (1871) *The Descent of Man and selection in relation to sex*. John Murray, Albemarle Street: London

Dewsbury, DA (1985) Interactions between males and their sperm during mulit-male copulatory episodes of deer mice (*Peromyscus maniculatus*). *Anim. Behav* 33:1266-1274

Dixson AF (1993) Sexual selection, sperm competition and the evolution of sperm length. *Folia Primatol* 61:221-227

Dixson AF (1998) Sexual selection and evolution of the seminal vesicles in primates. *Folia Primatol* 69:300-306

Dixson AF (2012) *Primate Sexuality: comparative studies of the prosimians, monkeys, apes, and humans.* 2nd edition. Oxford University Press: New York,NY

Dixson A, Anderson M (2001) Sexual selection and the comparative anatomy of reproduction in monkeys, apes, and human beings. *Annual Review of Sex Research* 12(1):121-144

Dixson AL, Anderson MJ (2002) Sexual selection, seminal coagulation and copulatory plug formation in primates. *Folia Primatol* 73(2-3):63-69

Eberhard WG, Cordero C (1995) Sexual selection by cryptic female choice on male seminal products – a new bridge between sexual selection and reproductive physiology. *Tree* 10(12):493-496

Eberhard WG (2009) Postcopulatory sexual selection: Darwin's omission and its consequences. *PNAS* 106(suppl.1):10025-10032

Fisher, R.A. 1915 The evolution of sexual preference, *Eugenics Review* **7**: 184–192

Fleagle JG (1999) *Primate Adaptation and Evolution*. 2nd edition. Academic Press: San Diego, CA.

Fontaine PM, Barrette C (1997) Megatestes: anatomical evidence for sperm competition in the harbor porpoise. *Mammalia* 61(1):65-71

Goodman M, Porter CA, Czelusniak J, Page SL, Schneider H, Shoshani J, Gunnell G, Groves CP (1998) Toward a phylogenetic classification of primates based on DNA evidence complemented by fossil evidence. *Molecular Phylogenetics and Evolution* 9(3):585-598

Gould JL, Gould CG (1989) *Sexual Selection*. Scientific American Library: New York,NY

Groves C (2001) *Primate Taxonomy.* Smithsonian Institution Press:Washington.

Gumucio DL, Heilstedt-Williamson H, Gray TA, Tarlé SA, Shelton DA, Tagle DA, Slightom JL, Goodman M, Collins FS (1992) Phylogenetic footprinting reveals a nuclear protein which binds to silencer sequences in the human γ and ε globin genes. *Molecular and Cellular Biology* 12(11):4919-4929

Helinski MEH, Deewatthanawong P, Sirot LK, Wolfner MF, Harrington LC (2012) Duration and dose-dependency of female sexual receptivity responses to seminal fluid proteins in *Aedes albopictus* and *Ae. aegypti* mosquitoes. *Journal of Insect Physiology* 58(10):1307-1313

Jensen-Seaman MI, Hooper-Boyd KA (2013) Molecular clocks: determining the age of the human-chimpanzee divergence. In: eLS. John Wiley & Sons, Ltd: Chinchester. DOI:10.1002/9780470015902.a0020813.pub2

Kappeler PM (1997) Intrasexual selection and testis size in strepsirhine primates. *Behav Ecol* 8:10-19

Lemon B, Tijan R (2000) Orchestrated response: a symphony of transcription factors for gene control. *Genes Dev.* 14:2551-2569

Lenhard B, Sandelin A, Carninci P (2012) Metazoan promoters: emerging characteristics and insights into transcriptional regulation. *Nature Reviews Genetics* 13:233-245

Li B, Carey M, Workman JL (2007) The role of chromatin during transcription. *Cell* 128:707-719

Maston et al. GA, Evans SK, Green MR (2006) Transcriptional regulatory elements in the human genome. *Annu. Rev. Genomics Hum. Genet.* 7:29-59

Mercer TR, Dinger ME, Mattick JS (2009) Long non-coding RNAs: insights into function. *Nature Reviews Genetics* 10:155-159

Moore HDM, Martin M, Birkhead TR (1999) No evidence for killer sperm or other selective interactions between human spermatozoa in ejaculates of different males *in vitro*. *Proc. R. Soc. Lond. B.* 266:2343-2350

Nascimento JM, Shi LZ, Meyers S, Gagneux P, Loskutoff NM, Botvinick EL, Berns MW (2008) The use of optical tweezers to study sperm competition and motility in primates. *J.R.Soc. Interface* 5:297-302

Ong C-T, Corcers VG (2011) Enhancer function: new insights into the regulation of tissue-specific gene expression. *Nat Rev Genet* 12(4):283-293

Parker GA (1970) Sperm competition and its evolutionary consequences in the insects. *Biol Rev.* 45:525-567

Perelman P, Johnson WE, Roos C, Seuánez HN, Horvath JE, Moreira MAM, Kessing B, Pontius J, Roelke M, Rumpler Y, Schneider MPC, Ailva A, O'Brien SJ, Pecon-Slattery J (2011) A molecular phylogeny of living primates. *PLoS Genetics* 7(3):e1001342

Perry GH, Dominy NJ, Claw KG, Lee AS, Fiegler H, Redon R, Werner J, Villnanea FA, Mountain JL, Misra R, Carter NP, Lee C, Stone AC (2007) Diet and the evolution of human amylase gene copy number variation. *Nat Genet* 39(10):1256-1260

Pomiankowski A, Iwasa Y (1998) Runaway ornament diversity caused by Fisherian sexual selection. *Proc. Nat. Acad. Sci. USA* 95:5106-5111

Prokupek A, Hoffmann F, Eyun SI, Moriyama E, Zhou M, Harshman L (2008) An evolutionary expressed sequence tag analysis of Drosophila spermatheca genes. *Evolution* 62(11):2936-2947

Ramm SA, Parker GA, Stockley P (2005) Sperm competition and the evolution of male reproductive anatomy in rodents. *Proc R. Soc B* 272:949-955

Rinn JL, Chang HY (2012) Genome regulation by long noncoding RNAs. *Annu. Rev. Biochem* 81:145-166

Rosenberg HF (1995) Recombinant human eosinophil cationic protein. *The Journal of Biological Chemistry* 270(14):7876-7881

Rouquier S, Blancher A, Giorgi D (2000) The olfactory receptor gene repertoire in primates and mouse: Evidence for reduction of the functional fraction in primates. *PNAS* 97(6):2870-2874

Schneider TD (1994) Reading sequence logos. *Nanotechnology* 5:445-455

Shi LZ, Nascimento J, Botvinick E, Durrant B, Berns MW (2011) An interdisciplinary systems approach to study sperm physiology and evolution. *WIREs Syst Biol Med* DOI:10.1002/wsbm.106

Snook RR (2005) Sperm in competition: not playing by the numbers. *TRENDS in Ecology and Evolution* 20(1):46-53

Steiper ME, Young NM (2006) Primate molecular divergence dates. *Molecular Phylogenetics and Evolution* 41:384-394

Tauber PF, Propping D, Schumacher GFB, Zaneveld LJD (1980) Biochemical aspects of the coagulation and liquefaction of human semen. *J Androl* 1:280-288

Tolhuis B, Palstra R-J, Splinter E, Grosveld F, de Laat w (2002) Looping and interaction between hypersensitive sites in the active β-globin locus. *Molecular Cell* 10:1453-1465

Wigby S, Chapman T (2004) Sperm competition. *Current Biology* 14(3):R100-R103

Zhang J, Rosenberg HF, Nei M (1998) Positive Darwinian selection after gene duplication in primate ribonuclease genes. *Proc. Natl. Acad. Sci. USA* 95:3708-3713

Zhang J (2003) Evolution by gene duplication: and update. *TRENDS in Ecology and Evolution* 18(6):292-298

Chapter 2: Rates of evolution of hominoid seminal proteins are correlated with function and expression, rather than mating system

Introduction

Sperm competition is a form of post-copulatory sexual selection, widespread in the animal kingdom and occurs when sperm of two or more males overlap temporally in the female reproductive tract (Parker 1970). Multiple mating has many direct and indirect benefits to females (reviewed in Møller 1998), but it creates a battlefield for males. There are several strategies and adaptations that males have adopted to increase their chance of successful fertilization. Increasing sperm count theoretically leads to a higher chance of paternity and is associated with an increase in testicular mass (Soulsbury 2010). As such, testes size is a common predictor of levels of sperm competition (Short 1979), demonstrated in a wide taxonomic range (birds, Lüpold et al. 2011; Rowe and Pruett-Jones 2011; mammals, Dixson and Anderson 2004; primates, Harcourt et al. 1981, 1995; insects, Gage 1994). Similarly, variation in sperm size, morphology, and velocity are also correlated with levels of sperm competition in a number of vertebrates and invertebrates (reviewed in Gomendio and Roldan 2008). Among primates in particular, the volume of the mitochondria-containing midpiece is significantly larger in those species whose females mate with multiple males (Anderson and Dixson 2002). Equally important are features of the seminal fluid that can provide an advantage in the presence of sperm competition, including the formation of a copulatory plug—a firm rubbery coagulum of semen within the female reproductive tract, commonly seen in rodents and primates (Sofikitis et al. 1990; Dixson and Anderson 2002), which is thought to act by reducing the chances of fertilization by subsequent males (Martan and Shepard 1976).

Additionally, seminal fluid has other functions, including the protection of sperm from the acidic environment of the vagina (Yanagimachi 1994; Fordney-Settlage 1981) and from female immune system attacks (Pandya and Cohen 1985; Barrat et al. 1990). Different species have different combinations of adaptations that best suit the battle at hand, but males that are best able to overcome sperm competition while maintaining the essential function of semen (fertilization) will prove most successful.

Among the hominoids, chimpanzees (*Pan troglodytes*) and bonobos (*P. paniscus*) are predicted to experience the most intense sperm competition, with multimale/multifemale mating systems (Hasegawa and Hiraiwa-Hasegawa 1990; Takahata et al. 1996). Their female promiscuity is reflected in males as large testes relative to body weight, large seminal vesicles, high sperm count, forcefully swimming sperm, and coagulation of semen into a copulatory plug (Tinklepaugh 1930; Nascimento et al. 2008; Dixson 1998, 2012). On the other end of the spectrum, gorillas (*Gorilla gorilla* and *G. beringei*) typically live in a single-male polygynous system with only minor levels of sperm competition. Consequently they have very small testes relative to body weight, low sperm count, and little semen coagulation (Robbins 1995; Dixson 2012). Human (*Homo sapiens*) and gibbon (*Hylobates sensu lato*) likely have low to moderate levels of sperm competition as they exhibit monogamy, or a mix of monogamy and polygyny in the case of human, with relative testes size, sperm count, sperm velocity, and coagulation all at moderate levels (Nascimento et al. 2008; Dixson 2009, 2012). Orangutans (*Pongo pygmaeus*) are a dispersed and solitary species with a proposed mating system of roving male promiscuity or dominant male centered 'communities' (van Schaik and van Hooff 1996). Genetic studies show, however, that both dominant

and subordinate males sire offspring (Utami et al. 2002; Goossens et al. 2006), which adds to the difficulty of classifying their mating system and predicting the resulting sperm competition levels.

Sexual selective pressures, which have molded anatomical and physiological changes have also resulted in adaptations at the molecular level (reviewed in Swanson and Vacquier 2002). These genetic signatures of sexual selection are seen throughout the metazoans—in broadcast spawners (Clark et al. 2009; Panhuis et al. 2006; Nydam and Harrison 2011), birds (Nadeau et al. 2007), butterflies (Walters and Harrison 2011), crickets (Fedorka and Zuk 2005), and the more extensively studied *Drosophila*, rodents, and primates. *Drosophila* single gene studies of testes proteins, accessory gland proteins, and seminal proteases have shown adaptive evolution in response to strong sexual selection (Haerty et al. 2007; Wagstaff et al. 2007; Almeida and DeSalle 2008; Kelleher et al. 2007; Wong et al. 2008). Additionally, variation at accessory gland protein (Acp) genes has been shown to affect male reproductive success (Clark et al. 1995; Fiumera et al. 2005); these proteins can induce changes in female physiology and mating receptivity (Wolfner 2002; Chapman and Davies 2004). Evidence for positive selection in rodents is also seen in seminal vesicle proteins (Karn et al. 2008), testes proteins (Turner et al. 2008), and ejaculatory proteins in general (Ramm et al. 2008). Likewise, numerous proteins in higher primates have been suggested to be evolving adaptively under the influence of strong sexual selection, including those involved in semen coagulation (Jensen-Seaman and Li 2003; Kingan et al. 2003; Dorus et al. 2004; Clark and Swanson 2005; Hurle *et al.* 2007; Carnahan and Jensen-Seaman 2008), liquefaction (Marques et al. 2012), sperm adhesion (Finn and Civetta 2010), egg-sperm interaction (Hamm et al.

2007; Herlyn and Zischler 2007), and immunity (Nunn et al. 2000; Wlasiuk et al. 2010). Furthermore, testes-specific genes also show elevated rates of evolution in relation to level of sperm competition (Wyckoff et al. 2000; Wu and Su 2004; Wong 2010).

Although it is commonly stated that reproductive proteins evolve faster than nonreproductive proteins, this conclusion is largely based on a handful of single gene studies, leaving the question of whether this statement is generally true across the genome unanswered (Findlay and Swanson 2010; Wong 2011). Moreover, rapid evolution of male reproductive genes in vertebrates is often attributed to sperm competition, but semen has many functions, and therefore the selective pressure could be in the form of pathogen resistance or species-recognition systems; untangling these forces remains a challenge (Wong 2011). Recent studies in murid rodents have shown "compartmentalized adaptation" with genes expressed in seminal vesicles evolving rapidly, while genes from other male reproductive tissues under strong constraint (Ramm et al. 2009; Dean et al. 2009). Similarly in primates, post-copulatory sexual selection does not appear to influence the overall evolution of secreted ejaculate proteins, but is effective on a handful of those proteins involved in specific functions such as immunity and peptidase activity (Good et al. 2013). In order to test the hypothesis that male reproductive proteins in primates are evolving rapidly in response to sexual selection (or other forces), and to avoid bias introduced by focusing on a subset of genes, we constructed and analyzed a dataset composed of all proteins found at appreciable abundance in human semen. We analyzed the patterns of nucleotide substitution across the hominoid primates; an advantage of this clade is the availability of complete genome sequences of five species,

all of which are closely related yet exhibit a wide range of mating systems and associated levels of sperm competition.

Methods

Sequence data

Two DNA sequence data sets were used in the analysis: the first is a seminal data set that contains 653 seminal plasma protein coding genes. This list was determined by a cross comparison of the human seminal plasma proteomic mass spectroscopy studies by Pilch and Mann (2006) and Batruch et al. (2011), and includes all proteins that were either identified in both studies or identified in one study with spectra $\geq 0.5\%$ of total. The second data set (control data set) contains 653 genes that were chosen randomly from an annotated list of protein coding genes with HCGN symbols from the Ensembl BioMart data-mining tool through Galaxy (Ensembl Genes 67, *Homo sapiens* genes (GRCh37); Goecks et al. 2010; Blakenberg et al. 2010; Giardine et al. 2005).

The seminal protein coding sequences were downloaded as a multispecies alignment from the UCSC genome browser's table browser (Human: GRCh37; Chimpanzee: CGSC 2.1.3; Gorilla: gorGor3.1; Orangutan: WUGSC 2.0.2; Rhesus: MGSC Merged 1.0) and Ensembl BioMart data mining tool through Galaxy (Gibbon: Nleu1.0) (Kent et al. 2002; Karolchik et al. 2004). The protein coding region sequences of the control gene set were downloaded from the Ensembl BioMart data-mining tool through Galaxy (Human: GRCh37; Chimpanzee: CHIMP2.1.4; Gorilla: gorGor3.1; Orangutan: PPYG2; Gibbon: Nleu1.0; Rhesus: MMUL_1.0). Gaps in the assemblies were manually filled in (to the best of the available data) using the Basic Local Alignment Search Tool to each species' nucleotide collection database (Altschul et al.

1990). Each alignment was manually curated to ensure gaps were in frame and stop codons were removed and replaced with gaps.

Each gene's multispecies alignment was then screened to ensure that each nonhuman primate species' sequence length was at least 70 percent of the human sequence, removing those species that did not meet the cut-off. Data manipulation and screening was accomplished using custom Perl scripts (available upon request). After the length filter was applied, any alignment containing less than three species (human and two others) was eliminated from further analyses. Final alignments are available as online supplementary information (Carnahan-Craig and Jensen-Seaman, *in press*).

Maximum likelihood estimates

Maximum likelihood estimations of the nonsynonymous substitution rate (*Ka*) and the synonymous substitution rate (*Ks*) were performed using the CodeML program of the PAML 4 package (Yang 2007). For this study we used three different PAML models of the data – model 0, model 1, and model 2. The unrooted tree used in the analysis is the canonical tree for the hominoid species with macaque as the outgroup (Goodman et al. 1998). Custom Perl scripts were used to automate PAML analyses.

The uniform model, model 0, constricts the program to calculate a uniform *Ka/Ks* ratio (or ω) across the entire tree. Model 1, or the free ratio model, relaxes the parameters to allow estimates of ω to be calculated for each branch of the tree independently. Model 2 was used to test deviation from neutral evolution on specific branches that were defined *a priori.* The background branches (everything except the selected branch) were set to have a uniform ratio while the foreground branch (selected branch) was tested both as a free ratio and as ω set to one (neutral). The likelihood of different models was compared

with a likelihood ratio test (LRT = twice the difference of the likelihood values compared to a chi square distribution where the degrees of freedom is equal to the difference in the number of parameters in each test). Human, chimpanzee, gorilla, orangutan, gibbon, macaque, and all internal branches were individually tested as 'foreground.' To correct for multiple testing, a false discovery rate (FDR) was implemented as described by Benjamini and Hochberg (1995). These data are included in Appendix 2 and available as online supplementary information (Carnahan-Craig and Jensen-Seaman, *in press*).

Any alignment with a human-chimp pairwise $Ks \geq 4$ times the average *Ks* was removed from further analysis to control for inclusion of non-orthologs. This filter removed 11 genes from the seminal data set and 13 genes from the control data set.

Expression

Tissue expression intensity values were calculated from the Human U133A/GNF1H Gene Atlas data (Su et al. 2004), which was downloaded from the BioGPS portal (Wu et al. 2009). The data set was modified so that the six cancerous tissues were removed, leaving 78 non-cancerous tissues. To determine tissue specificity, we calculated the tissue specificity index, τ, which is defined as:

$$\tau = \frac{\sum_{n-1}^{n}\left(1-\frac{V_t}{V_{max}}\right)}{n-1},$$

where n is the number of tissues, V_t is the expression intensity in tissue t, and V_{max} is the maximum expression intensity of that gene in any tissue (Yanai et al. 2005). τ ranges from 0 to 1, with a higher value indicating more tissue specific expression. So, a τ value of 1 indicates a gene expressed in only one tissue and a τ value of 0 corresponds to a gene expressed equally in all tissues. Tissue specificity was calculated for every gene in the Gene Atlas. For genes represented by more than one probe, an average of their tissue

specificity was used. These data are included in Appendix 2 and available as online supplementary information (Carnahan-Craig and Jensen-Seaman, *in press*).

Ejaculated semen is derived from multiple tissues. In order to partition the proteins by tissue of origin, we identified human-mouse orthologs with the vertebrate homology database curated by the Mouse Genome Database v5.13 (Bult et al. 2013), which is based on data from NCBI's HomoloGene (NCBI Resource Coordinators 2013), beginning with a published proteomic data set derived from individually dissected mouse tissues (Dean et al. 2009). Data from the anatomically distinct mouse anterior prostate, dorsolateral prostate, and ventral prostate were combined since hominoid primates do not have such divisions of the prostate. These data are included in Appendix 2 and available as online supplementary information (Carnahan-Craig and Jensen-Seaman, *in press*).

Gene Ontology

Gene ontology (GO) annotation was performed with the PANTHER classification system (Thomas et al. 2003). Annotations for biological process were queried and reduced to level 1 annotations. Differences among median ω and *Ka* estimates of genes in each GO category were assessed with a non-parametric one-way ANOVA. These data are included in Appendix 2 and available as online supplementary information (Carnahan-Craig and Jensen-Seaman, *in press*).

Statistical Analysis

All statistical analyses were performed with the GraphPad Prism version 6.0b for Mac OS X, GraphPad Software, La Jolla, California USA, (www.graphpad.com).

Results

Compilation of data sets

Of the 923 and 2022 human proteins identified via mass-spectroscopy by Pilch & Mann (2006) and Batruch et al. (2011), respectively, a nonredundant set of 653 genes was compiled after excluding very low abundant proteins (see Methods). Adding and aligning putative orthologs from other hominoid species and macaque reduced this to 642 genes with sequence from at least three species. Not all species are represented in all alignments (human, 642; chimpanzee 636; gorilla 590; orangutan 635; gibbon 615; and macaque 631). A similar dataset was constructed in parallel, beginning with genes chosen randomly from the annotated human genome but excluding any found in the seminal protein dataset. The randomly chosen genes, hereinafter referred to as the "control" dataset, also vary in species representation (human, 642; chimpanzee, 628; gorilla, 559; orangutan 614; gibbon, 598; and macaque, 602). The rank order of species by availability of suitable sequence is identical between the seminal genes and the control genes, and therefore we take any variation in number of genes found in each species to be a result of variation in completeness or quality of the genome assemblies, rather than variation in rates of pseudogenization of reproductive genes or genomic deletions thereof.

Seminal plasma genes evolve under evolutionary constraint

The median maximum likelihood estimate of ω, estimated from the 642 seminal genes and constrained to a single uniform rate across the tree, is significantly lower than that estimated from the 642 control genes (Mann-Whitney U test; $P = 0.009$; Fig 2.1). This trend of seminal genes evolving under more apparent constraint than the control genes is also consistently observed when comparing each individual species' ω (Mann-

Whitney U-test of median ω of terminal human, gorilla, and orangutan branches, $P < 0.05$; chimpanzee and gibbon not significant). However, this result is not driven by a lack of nonsynonymous changes in the seminal genes (seminal median *Ka* = 0.02385; control median *Ka* = 0.0233; Mann-Whitney U-test; $P = 0.7418$), but rather the seminal genes' significantly higher ratio of synonymous changes per synonymous site (Mann-Whitney U-test; seminal median *Ks* = 0.1351; control median *Ks* = 0.1186; $P = 0.0002$) (Fig 2.2).

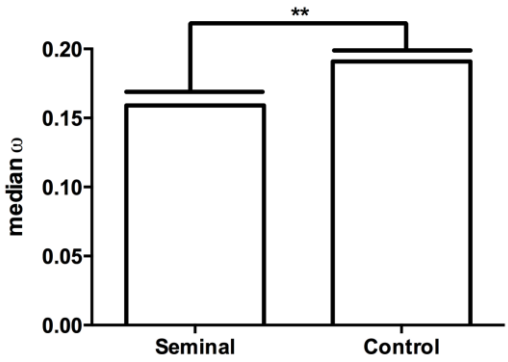

Figure 2.1: Seminal versus control median estimates of ω.
Median estimates of ω under a model constrained to a single uniform rate across the primate tree (PAML model 0) differ between 642 proteins found in human seminal plasma and a comparison set of 642 control proteins (median seminal ω = 0.1952; median control ω = 0.1909; two tailed Mann-Whitney U test, P = 0.009).

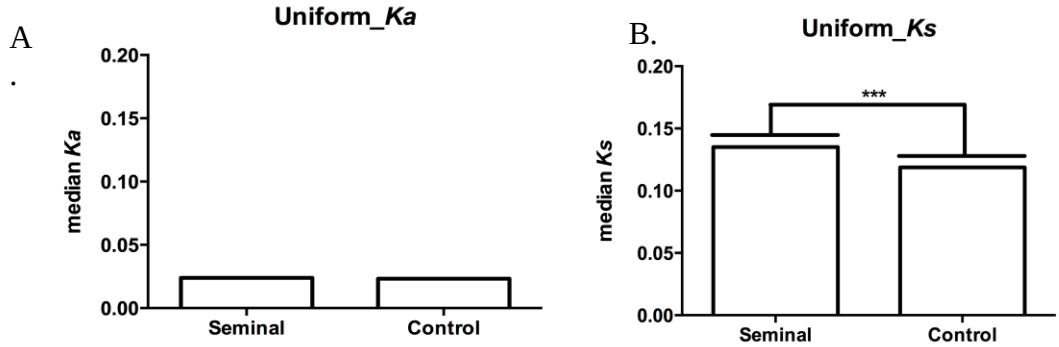

Figure 11: *Ka* and *Ks* estimates for seminal vs control
A: Uniform estimates of Ka of seminal genes and control genes. Seminal median = 0.02385; control median = 0.0233. Non-significant differences between medians (Mann-Whitney U test, p = 0.7481). B: Uniform estimates of Ks of seminal genes and control genes. Seminal median = 0.1351; control median = 0.1186. Significant differences between medians (Mann-Whitney U test, p = 0.0002; seminal > control).

We next allowed ω to vary freely among branches in the tree (PAML model 1), and asked whether species differed from one another considering their differences in mating systems (Fig 2.3). The median ω estimated along the terminal branches of ~640 genes in the data sets differ significantly among species (Kruskal-Wallis one-way ANOVA; $P < 0.0001$). The among-species difference in seminal proteins' ω is driven by the difference between human and gibbon, where human has the lowest median ω and gibbon the highest (Dunn's post-test; $P < 0.001$). A similar comparison of median values of ω of internal branches revealed significant variation in both the seminal protein-coding genes (Kruskal-Wallis one-way ANOVA; $P < 0.0001$) and the control dataset genes ($P < 0.0001$). Most notably, the stem-African ape has significantly greater median ω than the internal branch leading to the human-chimp ancestor following divergence from gorilla (Dunn's post-test; both seminal and control $P < 0.001$).

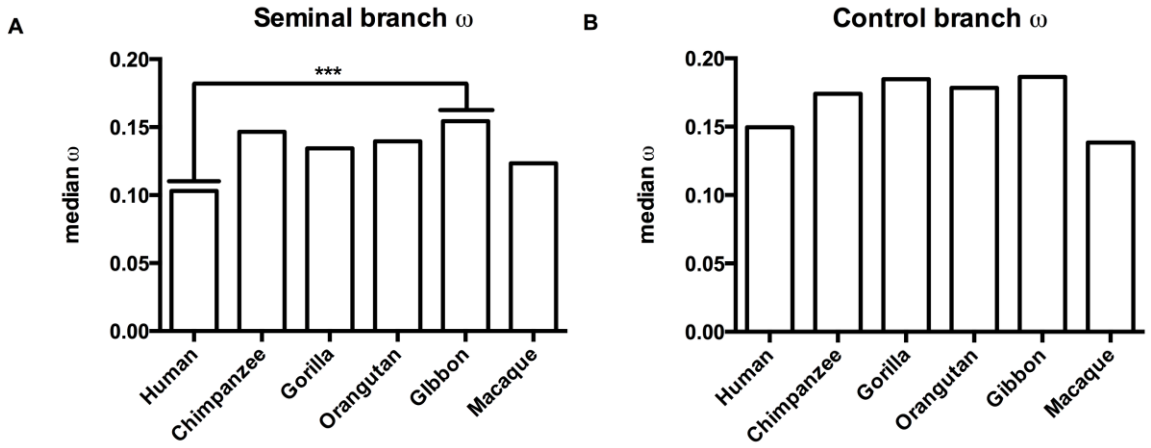

Figure 2.3: Seminal and Control branch estimates of ω
A: Seminal branch specific estimates (PAML model 2) of terminal branch ω value. Median human = 0.1030, chimp = 0.1465, gorilla = 0.1345, orang = 0.1395, gibbon = 0.1544, macaque = 0.1235. Medians significantly different under Kruskal-Wallis nonparametric ANOVA ($p<0.0001$), but only human-gibbon comparison was significant with Dunn's post-testing ($p \leq 0.001$). B: Control branch specific estimates (PAML model 2) of terminal branches. Median human = 0.1496, chimp = 0.1741, gorilla = 0.1847, orang = 0.1784, gibbon = 0.1864, macaque = 0.1384. Medians were significantly different under Kruskal-Wallis nonparametric ANOVA (≤ 0.0001), but no comparison was significant with Dunn's post-testing.

We searched for genes evolving under positive selection via recurrent selective sweeps in individual species by allowing the ω of a single terminal branch to vary while the rest of the tree is constrained to a uniform ω (PAML model 2, fix_omega=0), and comparing this estimate using a likelihood ratio test to that from a similar model where the same terminal branch estimate of ω is constrained to one, while the rest of the tree is constrained to a uniform ω (PAML model 2, fix_omega=1,omega=1). This was done for each of the five hominoid species for all genes. Among seminal proteins, only one gene in gorilla and five genes in gibbon showed significant evidence for ω>1, following correction for multiple testing. All species have many genes with evidence for purifying selection (ω significantly less than one). In the control dataset, a similar number of genes overall showed evidence of recurrent sweeps, with one gene each in chimpanzee, orangutan, and gibbon possessing a branch-specific ω significantly greater than one, following correction for multiple testing. As with the seminal protein dataset, all species have many genes with evidence for evolution under purifying selection.

Seminal genes' tissue specificity correlates with rate of protein evolution

The mean index of tissue specificity (τ), calculated from expression data in the gene atlas (Su et al. 2004), of seminal genes is greater than that of the control genes (P < 0.0001; two-tailed t-test; Fig 2.4), as well as that of all of the genes in the gene atlas (P < 0.0001).

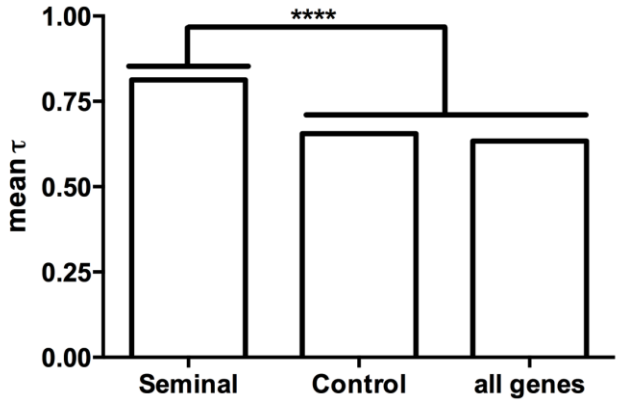

Figure 2.4: Mean tissue specificity index (τ) for seminal control and all genes
Mean tissue specificity index (τ) for seminal, compared to the control data set and all genes present in the Gene Atlas (Su et al. 2004) after removing those found in the seminal or control datasets (seminal $\tau = 0.8127$, n = 631; control $\tau = 0.6558$, n = 568; all $\tau = 0.6336$, n = 15,954; $p < 0.0001$, two-tailed t-test).

Tissue specificity is significantly and positively correlated with rates of seminal protein evolution, as estimated by ω in the human and chimpanzee lineages, whereas tissue specificity of the control dataset genes shows weakly negative, and marginally significant or non-significant correlations (Table 2.1). Considering the confounding effect of variation in *Ks* between seminal genes and control genes (see above), it important to note that a similar significant and positive correlation exists between *Ka* and τ in the seminal data set and significant negative correlation between *Ka* and τ in the control data set (Fig 2.5, Table 2.2). Genes that are found within both the top ten percent of tissue specificity values and human-chimpanzee pair-wise *Ka* values are: *A1BG, ACP5, CA6, COMP, CST1, DCXR, KLK3, LTF, MUC5B, ORM1, PAEP, PIP, SEMG1, SEMG2*, and *SPINT3*.

Table 2.2: Spearman's correlation coefficients (*r*) between branch-specific ω and τ

	Seminal *r* (*p*-value)	**Control *r* (*p*-value)**
Human ω	0.194 (<0.0001)	-0.0922 (0.030)
Chimp ω	0.110 (0.006)	-0.0818 (0.054)

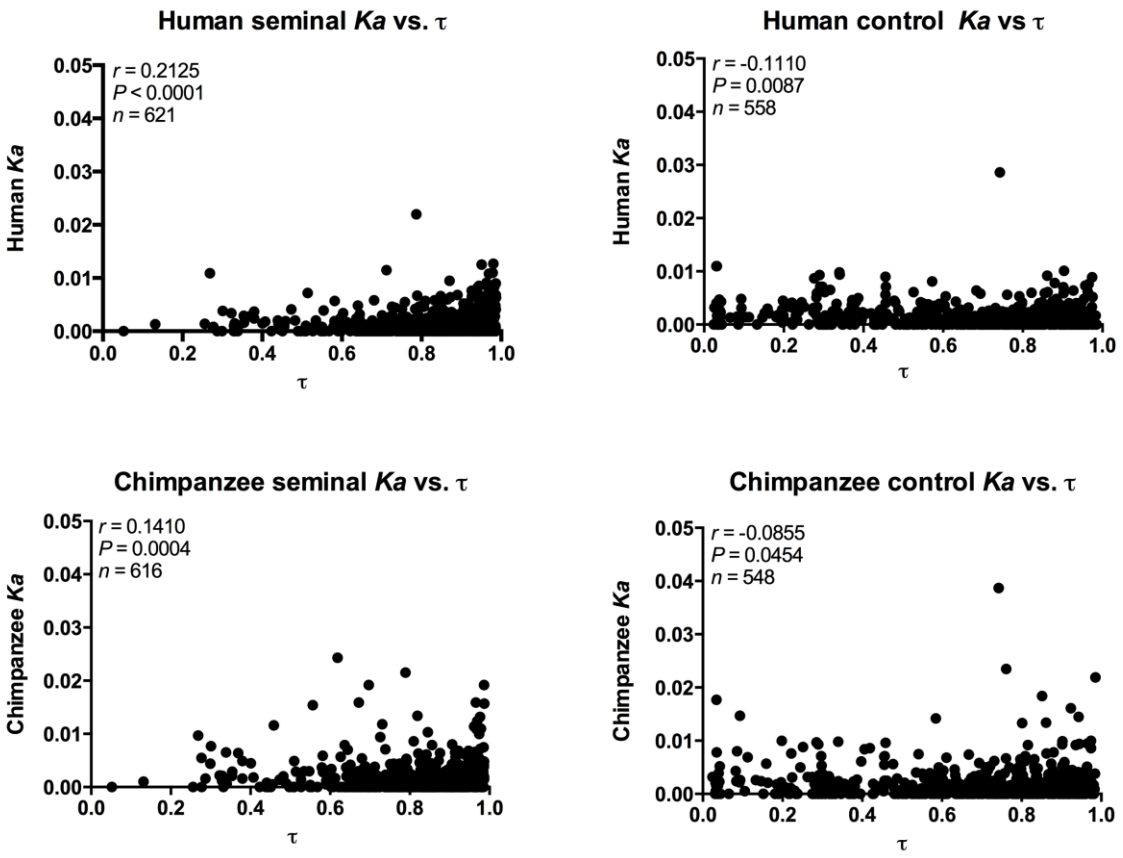

Figure 2.5: Branch specific *Ka* vs Tau
Scatterplots of the rate of human and chimpanzee branch-specific nonsynonymous substitutions (Ka) and the tissue specificity index (τ), for seminal and control genes. r = Spearman's correlation coefficient; p = p-value; n = number of genes.

Table 2.3: Spearman's correlation coefficients (*r*) between terminal branch-specific *Ka* and *τ*

	Seminal *r* (*p*-value)	**Control *r* (*p*-value)**
Human *Ka*	0.213 (<0.0001)	-0.111 (0.0087)
Chimpanzee *Ka*	0.140 (0.0004)	-0.0855 (0.0454)
Gorilla *Ka*	0.109 (0.0087)	-0.0821 (0.0678)
Orangutan *Ka*	0.238 (<0.0001)	-0.0129 (0.7659)
Gibbon *Ka*	0.135 (<0.0001)	-0.0629 (0.1495)

Tissue expression was further explored by parsing the seminal data set into the tissues from which the genes are expressed using the Dean et al. (2009) mouse proteomic data as a guide. Constrained to a uniform rate across the hominoid tree, the rate of evolution of these seminal genes differs significantly based on their tissue of maximal expression (Kruskal-Wallis one-way ANOVA; P =0.0096), with seminal vesicle derived

genes having a significantly higher median ω than the prostate and bulbourethral gland (Fig 2.6A; Dunn's post-test, $P \leq 0.05$). The median value of the human-chimp pairwise ω is also higher for genes expressed maximally from the seminal vesicles compared to other tissues, although not significantly so. The semenogelin genes (*SEMG1* and *SEMG2*) are not included in these analyses since there is not a clear one-to-one orthology with rodent genes; however, they are in a many-to-many homology relationship with the seminal vesicle expressed SVS genes of murid rodents, and are known to be expressed predominantly from the primate seminal vesicles (de Lamirande 2007). When *SEMG1* and *SEMG2* are added, the above trend of higher ω in seminal vesicle expressed genes is strengthened (Fig 2.6B; Kruskal-Wallis, P =0.0008; Dunn's post-test, $P \leq 0.05$).

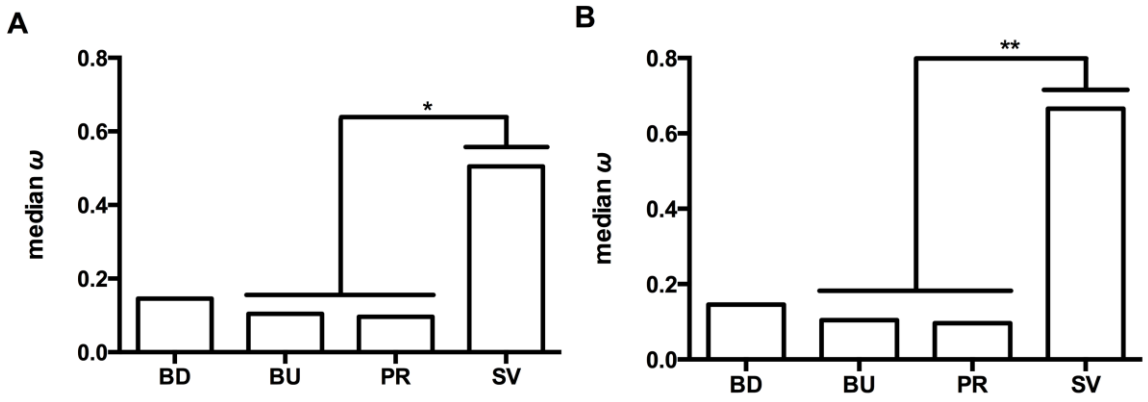

Figure 2.6: Median ω of genes expressed in different male tissues
A: Median estimates of ω constrained to a uniform ratio across hominoids (PAML model 0) of genes expressed maximally in different male reproductive tissues. BD = bulbourethral diverticulum (n = 28, median = 0.1455); BU = bulbourethral gland (n = 68, median = 0.1040); PR = prostate (combination of anterior prostate, ventral prostate, and dorsolateral prostate) (n = 47, median = 0.09607); SV = seminal vesicle (n = 4, median = 0.5047). B: Data from A with *SEMG1* and *SEMG2* added to SV (new SV n = 6, median = 0.6660).

Seminal plasma genes involved in reproduction, immune system processes, metabolic processes, and responses to stimuli evolve more rapidly

According to gene ontology (GO) characterization, the seminal genes fell into 15 level 1 biological processes categories and the control genes fell into 17 level 1. The median uniform, tree-wide ω of seminal protein coding genes varied significantly among categories (Kruskal-Wallis one-way ANOVA, $P < 0.0001$) but those of the control data set did not ($P = 0.0621$). Proteins involved in immune system processes, metabolic processes, response to stimuli, and reproduction had significantly higher ω estimates than did other (more ubiquitous) categories (Fig 2.7; Dunn's post-test). Although branch-specific estimates of ω do not differ significantly between human and chimpanzee when grouping all seminal genes together (see above), we hypothesized that proteins involved in some biological processes like reproduction or immune system may be evolving significantly differently between these species due to their differences in mating systems. However, estimates of ω for the human and chimpanzee branches did not differ for any of the 15 GO categories identified among the seminal proteins, nor for the 17 categories of the control proteins, following correction for multiple testing.

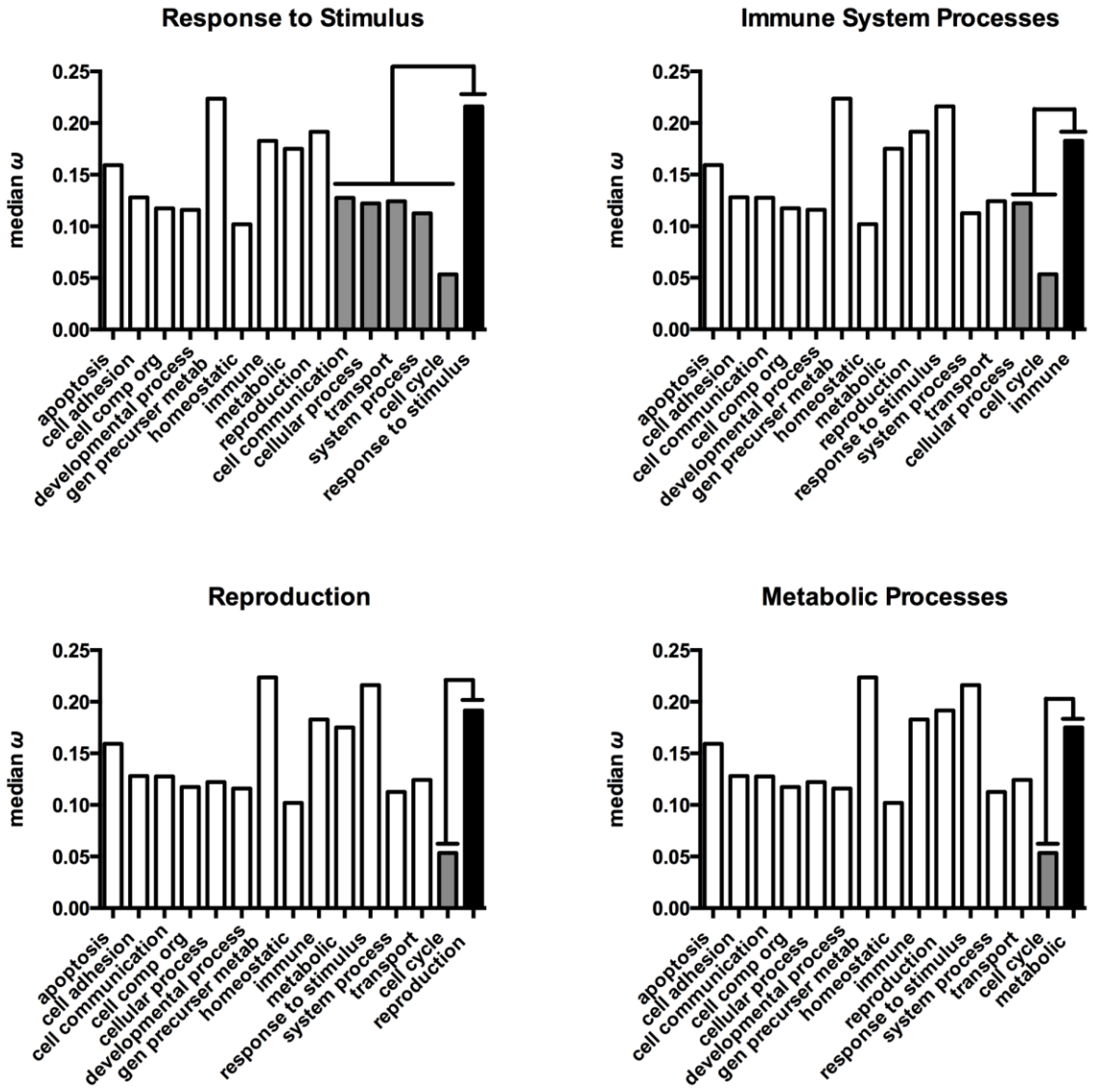

Figure 2.7: Gene ontology of seminal genes
Median estimates of ω under a model constrained to a single uniform rate across the primate tree (PAML model 0), for each biological process GO category. The same values are in each graph, but redrawn and colored to indicate significant differences among categories. Black bars represent categories with significantly higher median ω values than others, indicated by gray bars (Kruskal-Wallis nonparametric one-way ANOVA). White bars are neither significantly higher nor lower than any other category.

Discussion

Quality of the datasets

Beginning with an initial list of 653 seminal protein-coding genes, we were able to create alignments containing at least three species' orthologs for over 98% of these genes (642 of 653). Indeed, most (~88%) of these 642 alignments included all six

species, with an additional 11% missing only one species. This suggests that the quality of the current genome assemblies of these hominoid primates is in general sufficient for large-scale evolutionary analyses. It should be noted however, that we did observe variation in completeness by species, with the gorilla possessing the fewest identified orthologs followed by the gibbon. Although it has been shown that gorillas have lost function of several male reproductive genes (Jensen-Seaman & Li 2003), the reduced number in our dataset is not likely related to this observation, as there was a similar reduction among the control genes. The completeness of the dataset also did not follow any phylogenetic pattern, suggesting that the inability to identify some orthologs was not due to increasing evolutionary distance from humans. Therefore, we conclude that any variation among species in their representation is a function of quality and completeness of their genome assembly. We eliminated from our analyses eleven genes with a human-chimp pairwise *Ks* greater than four times the average pairwise *Ks* under the assumption that they represent non-orthologs. This cutoff is somewhat arbitrary; considering the very low *Ks* between the closely related human and chimpanzee (0.016), there will be many genes with two or three times the average *Ks* due to chance or variation in the local neutral mutation rate. Finally, we note that about 87% of the genes in our dataset are in the BioGPS expression database (Su et al. 2004) from which we calculated tissue specificity, confirming the value of this resource.

In our analyses we used both *Ka* and ω as the estimate of the rate of evolution. Although ω may be preferable because it conceivably controls for variation in the local mutation rate, *Ka* may be a more consistent measure for comparison between closely related species like the hominoid primates (Wang 2011). Interestingly, *Ks* drives the

decreased ω in the seminal data set compared to the controls. As this is based on over 600 genes it is difficult to imagine that this is caused solely by random fluctuations in small values of *Ks*, but rather may actually represent weaker purifying selection on synonymous sites in seminal genes compared to non-reproductive genes. Regardless, we found that the only qualitative difference in results using either *Ka* or ω was in the comparison with τ; the correlations between *Ka* and τ were much stronger than the correlation between ω and τ (see Tables 1 and 2).

Overall evolution of reproductive genes

The generalization that reproductive genes evolve more rapidly than non-reproductive genes was the overriding conclusion derived from studies examining individual genes. Such studies included genes that are testis specific (Wyckoff et al. 2000), male expressed (Clark & Swanson 2005), and those predicted to be under a particular selective pressure due to their known function including formation of a copulatory plug, modification of female behavior, species recognition, or polyspermy avoidance (Dorus et al. 2004; Carnahan & Jensen-Seaman 2008; Avila et al. 2011; Swanson & Vacquier 1998). In contrast, our data do not support this general conclusion as we saw that proteins found in human seminal plasma evolve at the same rate than a comparable control data set, as estimated by median *Ka*, or even more slowly when standardized by *Ks*. The most likely explanation of the discrepancy between our results and previous publications is that studies focusing on individual genes may have begun with an *a priori* expectation of positive selection based on function, combined with a publication bias toward rapidly evolving genes. However, our data are consistent with recent non-biased comprehensive seminal gene studies in mammals, in observing that

most genes coding for seminal protein are under strong selective constraint with only a few genes evolving rapidly (Dean et al. 2009; Findlay & Swanson 2010; Wong 2011; Good et al. 2013). This is perhaps not surprising given the many different functions of such proteins, with most of these functions unrelated to sexual selection.

We predicted that species that experience higher post-copulatory sexual selection (*e.g.* chimpanzee) would have higher average values of *Ka/Ks*, while species with low levels of sperm competition (*e.g.* gorilla) would have lower estimates of *Ka/Ks*. Our expectations were in part due to previous reports identifying faster protein evolution in chimpanzees at individual male reproductive genes, including *SEMG2* (Dorus et al. 2004) and *TGM4* (Carnahan & Jensen-Seaman 2008). However, our results are consistent with other large-scale studies of hominoid reproductive protein evolution in finding few differences among species (Wong 2011; Good et al. 2013). Considering that *Ka/Ks* values reflect a complex mix of positive selection at some sites, neutral substitutions at others, and fixation of slightly deleterious mutations under relaxed constraint—often at the same gene—it is perhaps not surprising that our simplistic expectation of higher *Ka/Ks* values in species with greater sperm competition was not met. The vast majority of amino acid substitutions differentiating humans and chimpanzees may be fixed due to relaxation of purifying selection (CSAC 2005). Further complicating any predictions are the fact that any observed behavioral phenotype in an extant species is an instantaneous view of the evolutionary history of the species, whereas the lineage-specific *Ka/Ks* values reflect the entire selective history of the lineage, including the possibility that its mating system may have changed repeatedly and as such specific selective pressures on any gene may have changed repeatedly. Therefore, species with transitions in mating behavior may

be expected to have higher *Ka/Ks* values because of an overall reduced intensity of purifying selection, a scenario proposed to explain patterns of evolution in seminal proteins seen in a comparison of two species of *Heliconius* butterflies (Walters & Harrison 2011).

Tempo of evolution related to function and expression

An interesting pattern that emerged upon data parsing was that seminal plasma genes are on average expressed in a more tissue-specific manner than the control set, and than all genes in the gene atlas (Su et al. 2004). Male reproductive genes, or at least those expressed from the testes, seem to have the ability to diverge in expression levels more rapidly than genes expressed from other tissues in hominoids (Khaitovich et al. 2005, 2006). Furthermore, we found that in the seminal data set the tissue specificity index (τ) is significantly positively correlated with ω, and even more strongly with *Ka*. Such a correlation has been previously reported in several genome-wide and tissue-wide studies in a variety of taxa (Liao et al. 2006; Kosiol et al. 2008; Haygood et al. 2010), with one explanation being that as a gene evolves to becomes more tissue specific it is released from the constraints of antagonistic pleiotropy imposed by differing functions in multiple tissue environments and becomes able to more freely respond to specific selective pressures. What is not as easily explained, however, is the much stronger correlation seen among the seminal proteins than in the control data set. Perhaps the general trend of a positive correlation between τ and ω or *Ka* is simply magnified by the intense selection of the reproductive environment. Our observation is consistent with the report of a much greater enrichment of positively selected genes among a set of testes-specific genes compared to liver- or breast-specific genes in mammals (Kosiol et al. 2008). Proteins

with highest expression from the seminal vesicles evolve significantly more rapidly than those from other male reproductive organs in our data set, as well as in murid rodents (Dean et al. 2009), suggesting that perhaps the uniqueness of this tissue is mammalian-wide.

While seminal plasma genes as a whole do not evolve more rapidly than a control set, certain functional GO categories of seminal plasma genes do indeed evolve more rapidly than others, namely: "reproduction", "immune response", "response to stimulus", and "metabolic processes". The first three categories may seem like obvious categories for elevated rates of protein change, whereas metabolism related proteins do not. However, putative adaptations to strong sperm competition—at least in chimpanzees—include the evolution of sperm that swim with more force, contain larger mitochondrial-containing midpieces, and have greater mitochondrial membrane potential (Anderson & Dixson 2002; Anderson et al. 2007; Nascimento et al. 2008), all of which may require adaptive evolution at proteins involved in energy metabolism. The categories with the lowest median ω values include those that may be considered to have many "housekeeping" genes, such as "cell cycle", "cell process", and "system process". Thus, the partitioning of the dataset into functional categories, combined with the tissue specificity index trends, and the tissue of origin, has revealed a subset of seminal proteins that show elevated rates of evolution. The genes coding for such proteins that are highly tissue specific, especially those from the seminal vesicles, and involved in reproductive, immune, stimulus response, and metabolism may be therefore be candidates for having been shaped by positive selection (or reduced purifying selection) driven by sexual selection.

References:

Almeida FC, DeSalle R (2008) Evidence of adaptive evolution of accessory gland proteins in closely related species of the *Drosophila repleta* group. Mol Biol Evol 25:2043-2053

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990) Basic local alignment search tool. J Mol Biol 215:403-410

Anderson MJ, Dixson AF (2002) Motility and the midpiece in primates. Nature 416:496

Anderson MJ, Chapman SJ, Videan EN, Evans E, Fritz J, Stoinski TS, Dixson AF, Gagneux P (2007) Functional evidence for differences in sperm competition in humans and chimpanzees. Am J Phys Anthropol 134:274-80

Avila Fw, Sirot LK, LaFlamme BA, Rubinstein CD, Wolfner MF (2011) Insect seminal fluid proteins: identification and function. Annu Rev Entomol 56:21-40

Barrat CLR, Bolton AE, Cooke ID (1990) Functional significance of white blood cells in the male and female reproductive tract. Hum reprod 5:639-648

Batruch I, Lecker I, Kagedan D, Smith CR, Mullen BJ, Grober E, Lo KC, Diamandis EP, Jarvi KA (2010) Proteomic analysis of seminal plasma from normal volunteers and post-vasectomy patients identifies over 2000 proteins and candidate biomarkers of the urogenital system. J Proteome Res 10:941-953

Benjamini Y and Hochberg Y (1995) Controlling the False Discovery Rate: a practical and powerful approach to multiple testing. J R Statist Soc B 57:289-300

Blakenberg D, Von Kuster G, Coraor N, Ananda G, Lazarus R, Mangan M, Nekrutenko A, Taylor J (2010) Galaxy: a web-based genome analysis tool for experimentalists. Curr Protoc Mol Bio. Chapter 19: Unit 19.10.1-21

Bult CJ, Eppig JT, Blake JA, Kadin JA, Richardson JE; Mouse Genome Database Group (2013) The mouse genome database: genotypes, phenotypes, and models of human disease. Nuc Acids Res 41:D885-D891

Carnahan SJ, Jensen-Seaman MI (2008) Hominoid seminal protein evolution and ancestral mating behavior. Am J Primatol 70:939-948

Carnahan-Craig SJ, Jensen-Seaman MI (*in press*) Rates of evolution of hominoid seminal proteins are correlated with function and expression, rather than mating system. Journal of Molecular Evolution

Chapman T, Davies SJ (2004) Functions and analysis of the seminal fluid proteins of male *Drosophila melanogaster* fruit flies. Peptides 25:1477-1490

Clark AG, Aguadé M, Prout T, Harshman LG, Langley CH (1995) Variation in sperm displacement and its association with accessory gland protein loci in *Drosophila melanogaster*. Genetics 139:189-201

Clark NL, Swanson WJ (2005) Pervasive adaptive evolution in primate seminal proteins. PLoS Genet 1:e35

Clark NL, Gasper J, Sekino M, Springer SA, Aguadro CF, Swanson WJ (2009) Coevolution of interacting fertilization proteins. PLoS Genet 5:e100570

CSAC (2005) Initial sequence of the chimpanzee genome and comparison with the human genome. Nature 437:69-87

Dean MD, Clark NL, Findlay GD, Karn RC, Yi X, Swanson WJ, MacCoss MJ, Nachman MW (2009) Proteomics and comparative genomic investigations reveal heterogeneity in evolutionary rate of male reproductive proteins in mice (*Mus domesticus*). Mol Biol Evol 26:1733-1743

de Lamirande E (2007) Semenogelin, the main protein of the human semen coagulum, regulates sperm function. Semin Thromb Hemost 33:60-68

Dixson AF (1998) Sexual selection and evolution of the seminal vesicles in primates. Folia Primatol 69:300-306

Dixson AF, Anderson MJ (2002) Sexual selection, seminal coagulation and copulatory plug formation in primates. Folia Primatol 73:63-69

Dixson AF, Anderson MJ (2004) Sexual behavior, reproductive physiology and sperm competition in male mammals. Physiol Behav 83:361-371

Dixson AF (2009) Sexual selection and the origins of human mating systems. Oxford University Press Inc, New York

Dixson AF (2012) Primate sexuality: comparative studies of the prosimians, monkeys, apes, and humans. 2nd edn. Oxford University Press Inc, New York

Dorus S, Evans PD, Wyckoff GJ, Choi SS, Lahn BT (2004) Rate of molecular evolution of the seminal protein gene *SEMG2* correlates with levels of female promiscuity. Nature Genet 36:1326-1329

Fedorka KM and Zuk M (2005) Sexual conflict and female immune suppression in the cricket, Allonemobious socius. J Evol Biol 18:1515-22

Findlay GD and Swanson WJ (2010) Proteomics enhances evolutionary and functional analysis of reproductive proteins. Bioessays 32:26-36

Finn S, Civetta A (2010) Sexual selection and the molecular evolution of ADAM proteins. J Mol Evol 71:231-240

Fiumera AC, Dumont BL, Clark AG (2005) Associations between sperm competition and natural variation in male reproductive genes on the third chromosome of *Drosophlia melanogaster*. Genetics 176:1245-1260

Fordney-Settlage D (1981) A review of cervical mucus and sperm interactions in humans. Int J Fertility 26:161-169

Gage MJG (1994) Association between body size, mating pattern, testis size and sperm lengths across butterflies. Proc R Soc Lond [Biol] 258:247-254

Giardine B, Riemer C, Hardison RC, Burhans R, Elnitski L, Shah P, Zhang Y, Blankenberg D, Albert I, Taylor J, Miller W, Kent WJ, Nekrutenko A (2005) Galaxy: a platform for interactive large-scale genome analysis. Genome Res 15:1451-1455

Goecks J, Nekrutenko A, Taylor J and The Galaxy Team (2010) Galaxy: a comprehensive approach for supporting accessible, reproducible, and transparent computational research in the life sciences. Genome Biol 11:R86

Gomendio M, Roldan ERS (2008) Implications of diversity in sperm size and function for sperm competition and fertility. Int J Dev Biol 52:439-447

Good JM, Wiebe V, Albert FW, Burbano HA, Kircher M, Green RE, Halbwax M, André C, Atencia R, Fischer A, Pääbo S (2013) Comparative population genomics of the ejaculate in humans and the great apes. Mol Biol Evol 30:964-976

Goodman M, Porter CA, Czelusniak J, Page SL, Schneider H, Shoshani J, Gunnell G, Groves CP (1998) Toward a phylogenetic classification of Primates based on DNA evidence complemented by fossil evidence. Mol Phylogenet Evol 9:585-98

Goossens B, Setchell JM, James SS, Funk SM, Chikhi L, Abulani A, Ancrenaz M, Lackman-Ancrenaz I, Bruford (2006) Philopatry and reproductive success in Bornean orant-utans (*Pongo pygmaeus*). Mol Ecol 15:2577-2588

Haerty W, Jagadeeshan S, Kulathinal RJ, Wong A, Ram KR, Sirot LK, Levesque L, Artieri CG, Wolfner MF, Civetta A, Singh RS (2007) Evolution in the fast lane: rapidly evolving sex-related genes in Drosophila. Genetics 177:1321-1335

Hamm D, Mautz BS, Wolfner MF, Aquadro CF, Swanson WJ (2007) Evidence of amino acid diversity-enhancing selection within humans and among primates at the candidate sperm-receptor gene *PKDREJ*. The Am J Hum Genet 81:44-52

Harcourt AH, Harvey PH, Larson SG, Short RV (1981) Testes weight, body weight and breeding system in primates. Nature 293:55-57

Harcourt AH, Purvis A, Liles L (1995) Sperm competition: mating system, not breeding season, affects testes size of primates. Funct Ecol 9:468-476

Hasegawa T, Hiraiwa-Hasegawa M (1990) Sperm competition and mating behavior. In: Nishida T (ed.) The chimpanzees of the Mahale mountains: Sexual and life history strategies, University of Tokyo Press, Japan, pp 115-132

Haygood R, Babbitt CC, Fedrigo O, Wray GA (2010) Contrasts between adaptive coding and noncoding changes during human evolution. Proc Natl Acad Sci U S A 107:7853-7

Herlyn H, Zischler H (2007) Sequence evolution of the sperm ligand zonadhesion correlates negatively with body weight dimorphism in primates. Evolution 61:289-298

Hurle B, Swanson W, NISC Comparative Sequencing Program, Green ED (2007) Comparative sequence analyses reveal rapid and divergent evolutionary changes of the *WFDC* locus in the primate lineage. Genome Res 17:276-286

Jensen-Seaman MI, Li WH (2003) Evolution of the hominoid semenogelin genes, the major proteins of ejaculated semen. J Mol Evol 57:261-270

Karn RC, Clark NL, Nguyen ED, Swanson WJ (2008) Adaptive evolution in rodent seminal vesicle secretion proteins. Mol Biol Evol 25:2301-2310

Karolchik D, Hinrichs AS, Furey TS, Roskin KM, Sugnet CW, Haussler D, Kent WJ (2004) The UCSC Table Brower data retrieval tool. Nucleic Acids Res 32:D493-496

Kelleher ES, Swanson WJ, Markow TA (2007) Gene duplication and adaptive evolution of digestive proteases in *Drosophila arizonae* female reproductive tracts. PLoS Genet 3:1541-1549

Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, Haussler D (2002) The human genome browser at UCSC. Genome Res 12:996-1006

Khaitovich P, Hellmann I, Enard W, Nowick K, Leinweber M, Franz H, Weiss G, Lachmann M, Pääbo S (2005) Parallel patterns of evolution in the genomes and transcripts of humans and chimpanzees. Science 309:1850-1854

Khaitovich P, Enard W, Lachmann, Pääbo S (2006) Evolution of primate gene expression. Nature Rev Genet 7:693-702

King MC, Wilson AC (1975) Evolution at two levels in humans and chimpanzees. Science 188:107-116

Kingan SB, Tatar M, Rand DM (2003) Reduced polymorphism in the chimpanzee semen coagulating protein, semenogelin I. J Mol Evol 57:159-169

Kosiol C, Vinar T, de Fonseca RR, Hubisz MJ, Bustamante CD, Nielsen R, Siepel A (2008) Patterns of positive selection in six mammalian genomes. PLoS Genet 4(8): e1000144

Liao BY, Scott NM, Zhang J (2006) Impacts of gene essentiality, expression pattern, and gene compactness on the evolutionary rate of mammalian proteins. Mol Biol Evol 23:2072-80

Lüpold S, Wistuba J, Damm OS, Rivers JW, Birkhead TR (2011) Sperm competition leads to functional adaptations in avian testes to maximize sperm quantity and quality. Reproduction 141: 595-605

Marques PI, Bernardino R, Fernandes T, NISC Comparative Sequencing Program, Green ED, Hurle B, Quesada V, Seixas S (2012) Birth-and-death of *KLK3* and *KLK2* in primates: evolution driven by reproductive biology. Genome Biol Evol 4:1331-1338

Martan J, Sheperd BA (1976) The role of copulatory plugs in reproduction in guinea pigs. J Reprod Fertil 85:79-83

Møller AP (1998) Sperm competition and sexual selection. In: Birkhead TR, Møller AP (ed.) Sperm competition and sexual selection, Academic Press, San Diego, pp 55-90

Nadeau NJ, Burke T, Mundy NI (2007) Evolution of an avian pigmentation gene correlates with a measure of sexual selection. Proc R Soc Lond [Biol] 274:1807-1813

NCBI Resource Coordinators (2013) Database resources of the National Center for Biotechnology Information. Nuc Acids Res 41:D8-D20

Nascimento JM, Shi LZ, Meyers S, Gagneux P, Loskutoff NM, Botvinick EL, Berns MW (2008) The use of optical tweezers to study sperm competition and motility in primates. J R Soc Interface 5:297-302

Nunn CL, Gittleman JL, Antonovics J (2000) Promiscuity and the primate immune system. Science 290:1168-1170

Nydam ML, Harrison RG (2011) Reproductive protein evolution in two cryptic species of marine chordate. BMC Evol Biol 11:18

Pandya IJ, Cohen J (1985) The leukocytic reaction of the human uterine cervix to spermatozoa. Fertil Steril 43:417-421

Panhuis TM, Clark NL, Swanson WJ (2006) Rapid evolution of reproductive proteins in abalone and *Drosophila*. Phil Trans R Soc London [Biol] 361:261-268

Parker GA (1970) Sperm competition and its evolutionary consequences in the insects. Biol Rev 45:525-567

Pilch B and Mann M (2006) Large-scale and high-confidence proteomic analysis of human seminal plasma. Genome Biol 7:R40

Ramm SA, Oliver PL, Ponting CP, Stockley P, Emes RD (2008) Sexual selection and the adaptive evolution of mammalian ejaculate proteins. Mol Biol Evol 25:207-219

Ramm SA, McDonald L, Hurst JL, Beynon RJ, Stockley P (2009) Comparative proteomics reveals evidence for evolutionary diversification of rodent seminal fluid and its functional significance in sperm competition. Mol Biol Evol 26:189-198

Robbins MM (1995) A demographic analysis of male life history and social structure of mountain gorillas. Behavior 132:21-48

Rowe M, Pruett-Jones S (2011) Sperm competition selects for sperm quantity and quality in the Austrailian maluridae. PLoS ONE 6:e15720

Short RV (1979) Sexual selection and its component parts, somatic and genital selection, as illustrated by man and the great apes. Advances in the Study of Behavior 9:131-158

Sofikitis N, Takahaski C, Nakamura I, Kadowaki H, Okazaki T, Shimamoto T, Miyagawa I (1990) The role of rat copulatory plug for fertilization. Acta Eur Fertil 21:155-158

Soulsbury CD (2010) Genetic patterns of paternity and testes size in mammals. PLoS ONE 5:e9581

Su AI, Wiltshire T, Batalov S, Lapp H, Ching KA, Block D, Zhang J, Soden R, Hayakawa M, Kreiman G, Cooke MP, Walker JR, Hogenesch JB (2004) A gene atlas of the mouse and human protein-encoding transcriptomes. PNAS 101:6062-6067

Swanson, WJ and Vacquier, VD (1998) Concerted evolution in an egg receptor for a rapidly evolving abalone sperm protein. Science 281:710-712

Swanson WJ, Vacquier VD (2002) The rapid evolution of reproductive proteins. Nature Rev Genet 3:137-144

Takahata Y, Ihobe H, Idani G (1996) Comparing copulations of chimpanzees and bonobos: do females exhibit proceptivity or receptivity? In: McGrew W, Marchant LF, Nishida T (ed.) Great ape societies. Cambridge University Press, Cambridge, pp 146-155

Thomas PD, Kejariwal A, Campbell MJ, Mi H, Diemer K, Guo N, Ladunga I, Ulitsky-Lazareva B, Muruganujan A, Rabkin S, Vandergriff JA, Doremieux O (2003)

PANTHER: a browsable database of gene products organized by biological function, using curated protein family and subfamily classification. Nucleic Acids Res 31:334-341

Tinkelpaugh OL (1930) Occurrence of vaginal plug in chimpanzee. Anat Rec 46:329-332

Turner LM, Hoekstra HE (2008) Causes and consequences of the evolution of reproductive proteins. Int J Dev Biol 52:769-780

Utami SS, Goossens B, Bruford MW, de Ruiter JR, van Hooff JARAM (2002) Male bimaturism and reproductive success in Sumantran orang-utans. Behav Ecol 13:643-652

van Schaik CP and van Hooff ARAM (1996) Toward an understanding of the orangutan's social system. In: McGrew WC, Mardchant NF, Nishida T, (eds.) Great Ape Societies. Cambridge: Cambridge University Press.

Wagstaff BJ, Begun DJ (2007) Adaptive evolution of recently duplicated accessory gland protein genes in desert *Drosophila*. Genetics 177:1023-1030

Walters JR, Harrison RG (2011) Decoupling of rapid and adaptive evolution among seminal fluid proteins in *Heliconius* butterflies with divergent mating systems. Evolution 65:2855-2871.

Wang D, Liu F, Wang L, Huang S, Yu J (2011) Nonsynonymous substitution rate (Ka) is a relatively consistent parameter for defining fast-evolving and slow-evolving protein-coding genes. Biol Direct 6:13

Wlasiuk G, Nachman MW (2010) Promiscuity and the rate of molecular evolution at primate immunity genes. Evolution 64:2204-2220

Wolfner MF (2002) The gifts that keep on giving: physiological functions and evolutionary dynamics of male seminal proteins in *Drosophila*. Heredity 88:85-93

Wong A, Turchin MC, Wolfner MF, Aquadro (2008) Evidence for positive selection on *Drosophila melanogaster* seminal fluid protease homologs. Mol Biol Evol 25:497-506

Wong A (2010) Testing the effects of mating system variation on rates of molecular evolution in primates. Evolution 64:2779-2785

Wong A (2011) The molecular evolution of animal reproductive tract proteins: what have we learned from mating-system comparisons? Int J Evolutionary Biol. doi:10.4061/2011/908735

Wu C, Orozco C, Boyer J, Leglise M, Goodale J, Batalov S, Hodge CL, Haase J, Janes J, Huss JW, Su AI (2009) BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. Genome Biol 10:R130

Wu HH, Su B (2004) Adaptive evolution of SCML1 in primates, a gene involved in male reproduction. BMC Evol Biol 8:192

Wyckoff GJ, Wang W, Wu CI (2000) Rapid evolution of male reproductive genes in the descent of man. Nature 403:304-309

Yanagimachi R (1994) Mammalian fertilization In: Eknobil & JD Neill (eds) The physiology of reproduction, 2nd edn., Raven Press, New York, pp189-317

Yanai I, Benjamin H, Shmoish M, Chalifa-Caspi V, Shklar M, Ophir R, Bar-Even A, Horn-Saban S, Safran M, Domany E, Lancet D, Shmueli O (2005) Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. Bioinformatics 21:650-659

Yang Z (2007) PAML 4: Phylogenetic Analysis by Maximum Likelihood. Mol Biol Evol 24:1586-1591

CHAPTER 3: Optimization of an *in vitro* system to study the evolution of transcriptional regulation -AND- *TGM4* trial and error: death by unrepeatability

INTRODUCTION

Understanding the link between genotype and phenotype is a central challenge in evolutionary biology especially in closely related species (i.e. low divergence in their genomes) with very different phenotypes. Trying to understand the relative importance between changes in the protein coding sequence and the regulatory sequence is not a new question; in 1975 Mary-Claire King and Allan C. Wilson hypothesized that the substantial anatomical difference between two closely related species (human and chimpanzee) is not due to the protein differences (caused my mutations in the protein-coding sequence) but due to the control of the expression of the proteins (i.e. changes in regulatory sequences).

Why study regulatory evolution?

The idea behind regulatory regions' importance in the evolution of gene expression is that a gene located in random DNA is inert because natural selection acts on a phenotype and not a genotype (Wray et al. 2003) and without the expression of a gene it cannot contribute to a phenotype. The phenotypic impact of a gene is therefore more than the biochemical activity of the protein but also in the specific conditions under which the gene is expressed. This relationship can result in significant phenotype changes if these instructions are modified (e.g. acceleration in growth resulting from earlier expression of a hormone or a duplicated structure from the ectopic expression of a transcription factor (TF) during development – reviewed in Wray et al. 2003). With such drastic

consequences to the misregulation of genes the obvious reaction would be to assume that all regulatory regions are under strong purifying selection, but there is no difference in the proportion of genes that have positive selection signatures in the coding region to those in the noncoding region (Planas and Serrat 2010). Furthermore, in the genome, one percent of genes' promoters have an experimentally verified single nucleotide polymorphism (SNP) of which 63 percent result in differential expression between alleles (Rockman and Wray 2002 – which may be a low estimate by today's technology). These observations suggest that gene expression is an important, dynamic process that may be 'fine tuned' by selection (Wray 2007) in order to achieve a more fit phenotype.

The primary determinant of overall gene expression is transcription initiation, which is controlled independently at each gene (Wray et al. 2003) and usually in a two-step process requiring DNA accessibility and PolII binding/elongation. The information about the status of the cell is integrated and transcription is modified accordingly at the promoter – a collection of transcription factor binding sites (TFBSs) that determine which TFs will bind. The distribution of TFBSs is skewed towards the transcription start site (TSS) (Rockman and Wray 2002; Tabach et al. 2007), so this basic unit of gene regulation (TF, TFBSs, and the target gene – Teichmann and Babu 2004) that is concentrated in the 5' proximal region is an important target for natural selection.

Another factor about *cis*-regulatory sequences that perhaps make them good targets for selection is that changes in this region can be pleiotropic and co-dominant. Promoters are often modular in their arrangement so a mutation may only effect a part of the transcriptional profile, but because most genes work as part of a network, altering the expression of one member may cause the other members to also change (Rockman and

Wray 2002). In fact, promoters for genes more central to the gene network have promoters that are under more positive selection than expected (Planas and Serrat 2010). Furthermore, selection may act on *cis*-regulatory regions faster because they can be seen in a heterozygous stage since the alleles may be codominant (a mutation in one allele is transcribed independently of the other allele) (Wray et al. 2003). Additionally, more highly expressed genes may have faster evolving promoters because it has been reported that selection and level of expression are correlated (Kudaravalli et al. 2008) and also that the level of expression is not a constraint in the evolution of a promoter (Planas and Serrat 2010). Changes in the promoter may happen through single nucleotide mutations, insertions by transposition, or retroposition. The consequence of these changes may be in the timing of expression, the spatial expression, responsiveness of expression to environmental cues, sex-specific gene expression, or more commonly gains or losses of functional regions (reviewed in Wray et al. 2003; Shibata et al. 2012).

Studying regulatory evolution

The study of regulatory regions provides a challenge because noncoding regions often work in a network and have pleiotropic effects so there is an indirect, nonlinear, context dependent relationship with the level of expression of the gene they are controlling (Wray et al. 2003). Because of this, sequence data can reveal what binding sites may be important and the organization of those sites, but alone it cannot predict what the *actual* resulting expression will be. Furthermore, by looking at expression levels it may be hard to determine regulatory elements that may have changed, because there is degeneracy in the binding requirements of many TFs. This may allow a buildup of conservative mutations in active binding sites, but also the emergence of new binding

sites, which are capable of satisfying the binding requirements (Dermitzakis and Clark 2002). However, using extensive computation in combination with comparative genomics, functional, and probabilistic models to look at noncoding regions, informative evolutionary changes can be elucidated.

A more definitive method of determining functional relevance of noncoding changes is to study them *in vitro*. Using methods like chromatin immunoprecipitation (ChIP) in combination with sequence identifying (ChIP-chip, ChIP-PCR, ChIP-seq) can determine which TFs are binding to which TFBSs within particular cells at particular physiological conditions (Dowell 2010). Binding can also suggested *in vitro* with footprinting and electromobility shift assays (EMSA). Additionally, chromatin modifications can provide insight to sequence differences between species by examining DNase hypersensitive sites (DHS) because different regulatory elements can recruit different chromatin modifiers to help turn on or turn off transcription by exposing or compacting the DNA (Li et al. 2007; Shibata et al. 2012). The downfall to these experiments is the requirement that the researcher has access to the tissue that the gene is expressed in under normal physiological conditions. For most gene studies in humans this is not a problem. However, this is a huge complication when trying to study reproductive genes, as most reproductive tissues are not available for culture, and even more so for cross-species comparisons. An alternative approach to directly assaying the native *in situ* DNA, is to use a reporter construct to investigate transcriptional strength of different isolated promoters based on their ability to drive expression of a unique protein reporter. One reporter gene that is commonly used is the firefly luciferase gene. Chabot et al. (2007) used the luciferase system to verify previously published microarray data that

showed differential levels of certain transcripts in human and chimp liver tissue. They found that for several of the genes identified there are significant differences between human- and chimpanzee-driven luciferase reporter constructs indicating that changes in the *cis*-regulatory region cloned into the reporter vector is responsible for differences in *in vivo* expression levels.

TGM4

A candidate gene for a promoter region under positive selection is the prostate specific transglutaminase, *TGM4*. This is a good candidate because the coding region shows a high level of selection in species with high levels of sperm competition like chimpanzees, as well as evidence for pseudogenization in the coding and non-coding regions in gorillas and gibbons, species with low levels of sperm competition (Clark and Swanson 2005; Carnahan and Jensen-Seaman 2008). It has also been further demonstrated that there is a difference in the protein level between human and chimpanzee (Chovanec and Jensen-Seaman, unpublished data); chimpanzee protein abundance is about four times higher than human in seminal plasma.

The function of TGM4 was thought to be in helping to mask surface antigens on the sperm to protect against a female immunological response (Mukherjee et al. 1983). But we know now that the main function of the transglutaminase is to cross link the structural proteins secreted from the seminal vesicle through the formation of ε(γ-glutamyl)lysine cross-linkages (Williams-Ashman 1984; Lin et al. 2002; Dean 2013). This is an essential function for appropriate seminal fluid activity, as *TGM4*-knockout mice do not form a copulatory plug and show reduced fertility (Dean 2013).

The gene coding for *TGM4* is located on human chromosome 3 and is expressed in a prostate specific manner (Dubbink et al. 1996; Dubbink et al. 1998; An 1999).

Additionally, several groups have characterized the promoter region of human *TGM4* (Fig 3.1). Basal promoter activity is located within 500 basepairs of the transcription start site and a critical region is located between -113 to -61 (Dubbink et al. 1998; Dubbink et al. 1999). Within this region a CATAA box is located at -49 and an essential Sp1 binding site is at -96 to -87 (Dubbink et al. 1999). The expression of *TGM4* can be upregulated by retinoic acid (Pasquali et al. 1999; Rivera-Gonzalez et al. 2012) and is down regulated by the steroid hormone androgen (Dubbink et al. 1998; Rivera-Gonzalez et al. 2012).

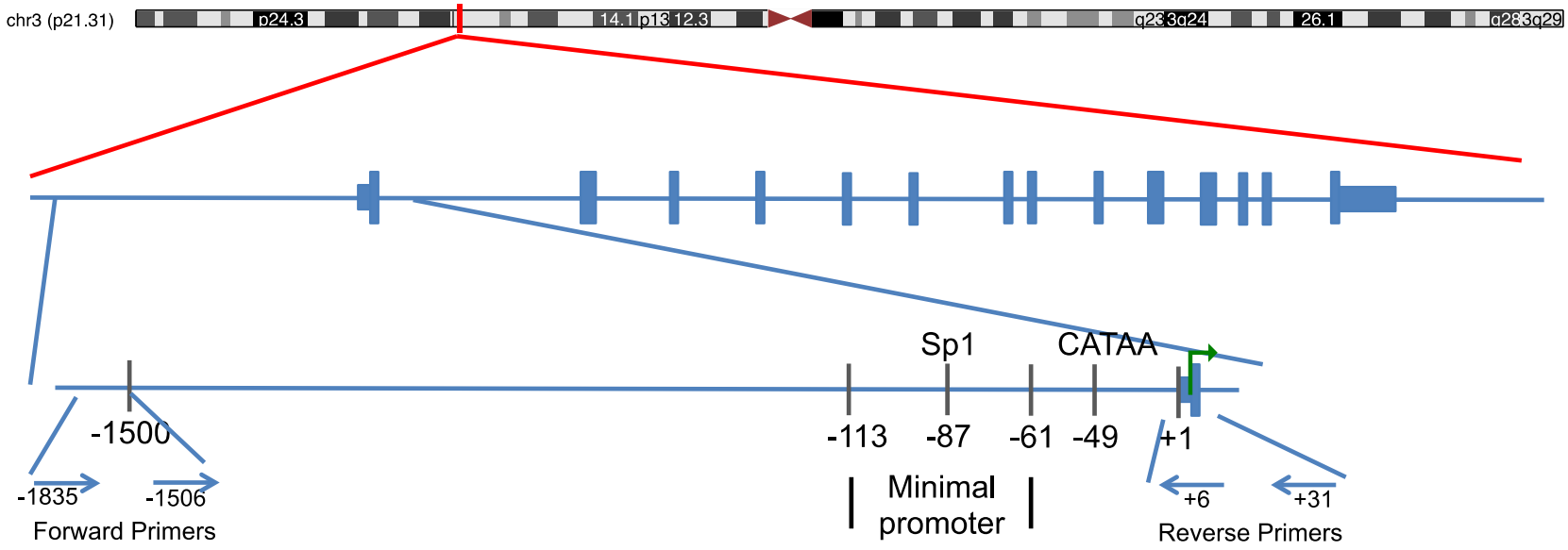

Figure 3.1: Genomic structure of *TGM4*

Genomic structure of *TGM4*. Chromosome ideogram is from the UCSC genome browser. The green arrow is the translation start site. Primers shown are -1835 = TGM4_up_F6; -1506 = RG_TGM4_1.5_For_SacI; +6 = RG_TGM4_Rev_EcoRV; +31 = TGM4_pro51R1

Interestingly, semen coagulation is a diverse trait in hominoids (Fig 1.6) that seemingly corresponds to the level of sperm competition. There is evidence of rapid coding sequence change and pseudogenization events in the coding and non-coding regions of *TGM4*, yet there has not been a cross-species investigation into the level of transcriptional control in hominoids.

METHODS

in vitro analysis

Expression construct creation

Luciferase reporter constructs were created both for this chapter and the next. The following text explains how these constructs were made. Specific instructions for *TGM4* are included later in this chapter and specifics for the semenogelins are included in the next chapter. First, the proximal promoter region was amplified from genomic DNA with polymerase chain reaction (PCR). This product was gel purified using a 1% crystal violet agarose gel and Wizard® SV Gel and PCR Clean-Up System (Promega). PCR conditions were optimized with standard primers and then repeated with primers that had a restriction enzyme site engineered into the sequence (5'-random sequence-restriction enzyme site-primer sequence-3'). A high-fidelity *Taq*-polymerase was used for PCR (iProof ™ High-Fidelity DNA Polymerase, BioRad). The final product were subject to complete sequencing to verify gene-specificity of the product and sequence integrity. The Sanger-sequencing method was used on the Applied Biosystem platform (BigDye® Terminator v3.1 Cycle sequencing kit, Applied Biosystems 3100 and 3130 Genetic Analyzer, Life Technologies). The promoter region for *TGM4, SEMG1,* and *SEMG2* were amplified from genomic DNA from the following species: human, chimpanzee (*Pan*

troglodytes -PR496, Coriell Institute), bonobo (*Pan paniscus* –PR251, Coriell Institute), gorilla (*Gorilla gorilla* –PR622, Coriell Institute), orangutan (*Pongo pygmaeus* –PR253, Coriell Institute), gibbon (*Hylobates syndactylus* –PR598, Coriell Institute), and macaque (*Macca mulatta* –NH4, generous gift from the lab of Dr. Ken Kidd, Yale University).

After the PCR product amplified with the high-fidelity polymerase was sequence verified it was then cloned into a TOPO® TA vector (Life Technologies). Briefly, the dNTP "A" needed to be added to the end of the purified product in order to be compatible with the "T" overhang on the TOPO® TA vector (standard *Taq* polymerases will add an additional "A" to the end of a PCR-product but high-fidelity polymerases such as iProof™ does not). This was accomplished by incubating the purified product with a standard *Taq* polymerase, *Taq* polymerase buffer, and dNTPs at 72°C for 15 minutes. This product was then incubated with the TOPO® TA vector at room temperature overnight (approximately 16-18 hours). Two DNA:vector molar ratios were used, 1:1 and 3:1. These ligation mixes were then transformed into One Shot® TOP 10 chemically competent cells, plated onto LB agar plates with kanamycin and X-Gal, and incubated at 37°C overnight. A blue-white/PCR screen was performed the following day: white colonies were picked as candidate constructs, added directly to a PCR reaction mix (M13 vector primers (see Table 3.1) and standard *Taq* polymerase), and streaked onto a replicate plate (LB-agar with kanamycin, incubated at 37°C). An additional five minutes of denaturing (95°C) was added prior to the beginning of the PCR cycling to facilitate bacterial cell lysis. After true positive candidate colonies were identified (a PCR product was visualized on an ethidium bromide stained 1% agarose gel at the appropriate size), two candidates were selected (usually those with the brightest bands on gel) and picked

from the replicate plate into a 4mL overnight culture (LB broth with kanamycin). From these cultures a freezer stock was made (750µL culture + 250µL 60% glycerol, stored at -80°C) and vector DNA was isolated (QIAprep spin miniprep kit (Qiagen) or PureYield™ plasmid miniprep system (Promega)). The isolated plasmid DNA was then subjected to DNA sequencing to verify the product. Once the TOPO® construct has been sequence verified, the vector was digested in order to isolate the inserted DNA (the promoter sequence of interest). The restriction enzymes used in this study are *Acc*65I, *Hin*dIII, or *Sac*I. These correspond to the restriction enzyme sites that are engineered into the forward (*Kpn*I/*Acc*65I) and reverse (*Hin*dIII or *Sac*I – depending on gene, see specific gene primer tables) primers. The digested product is gel purified using a 1% crystal violet gel with the Wizard® SV Gel and PCR Clean-Up System (Promega) and the plasmid DNA concentration was determined using a Qubit ® fluorometer (Life Technologies).

Table 3.1: Primers used in screening of TOPO or pGL constructs

Primer name	Purpose	Sequence 5' → 3'
M13_For(-21)mod	TOPO screen	GTTGTAAAACGACGGCCAGT
M13_Rev_mod	TOPO screen	CACAGGAAACAGCTATGACC
pGL4_92_R1	pGL4.10 screen	TTACCAACAGTACCGGATTG
pGL4_4223_F1	pGL4.10 screen	AGGTGCCAGAACATTTCTCT

The final step in the creation of the expression construct was the ligation of the promoter insert into the expression vector. We used the luciferase expression vector pGL4.10, which is a promoterless vector containing the coding sequence for the firefly luciferase enzyme. This vector was digested with *Acc*65I and *Hin*dIII or *Sac*I (to create complementary ends for the promoter insert) and subsequently gel purified with a 1% crystal violet agarose gel with the Wizard® SV Gel and PCR Clean-Up System (Promega). The purified, digested promoter insert was ligated into the purified, digested pGL4.10 using T4 DNA ligase (Promega). Ligation reactions were set up at the

DNA:vector molar ratios of 3:1 and 1:1 and incubated overnight (approximately 16-18 hours) in a refrigerated water bath set to 16°C. Ligation mixtures were transformed into chemically competent T1 *E.coli*, plated on LB-agar ampicillin or carbenicillin plates, and incubated at 37°C overnight. The transformation reaction was screened in a similar way to the TOPO® screen (minus the blue-white screen portion) – candidate colonies were picked from the plate, mixed into PCR mix with pGL primers (see table 3.1), and streaked onto a replicate plate (LB agar plus ampicillin). After the PCR screen, true positive candidates (appropriate band was seen on ethidium bromide stained agarose gel) were picked from the replicate plate into a 4mL overnight culture (LB broth with ampicillin at 37°C) from which freezer stocks were prepared (750µL culture + 250µL 60% glycerol, stored at -80°C) and vector DNA was isolated (QIAprep spin miniprep kit (Qiagen) or PureYield™ plasmid miniprep system (Promega)). The isolated plasmid DNA was then subjected to DNA sequencing to verify the product. Following sequence verification, positive constructs were streaked onto LB-ampicillin agar plates from the -80°C freezer stocks. Single colonies were picked into 1mL LB-ampicillin starter cultures, which were incubated at 37°C for 6-8 hours. The starter cultures where used to inoculate 50mL LB-ampicillin overnight cultures (37°C, 16-18 hours). These cultures were processed using Qiagen Plasmid Midi Kit (Qiagen) and resulting plasmid DNA concentration was determined using a Qubit ® fluorometer (Life Technologies). All sequence analysis for this study was performed with the SeqMan program from the Lasergene® software package (DNAStar).

Luciferase expression assays

Cell culture maintenance

A human prostate cell line (LNCaP clone FGC, ATCC® CRL-1740™) was kept in a humidified, 37°C, 5% carbon dioxide incubator in RPMI-1640 medium (ATCC) supplemented with 5% fetal bovine serum (FBS) and antibiotic (penicillin and streptomycin, which will be referred to as P/S) unless otherwise noted. All procedures were performed as per the protocols published in *Basic Techniques for Mammalian Cell Tissue Culture* (1998) with specifics as follows. Cultures were trypsinized and subcultured when cells reached >75% confluency (approximately every three days if cultures were split 1:3 or every 4 days if cultures were split 1:4).

Transfection and luciferase assay optimizations

When cultures reached >75% confluency, cells were trypsinized, counted using a hemocytometer, and plated in a 12-well cell culture plate at a density of 200,000 cells per well in 1mL of complete growth media. If multiple plates were being used for a particular experiment multiple flasks of cells were combined before counting to ensure enough cells for all the plates. 24 hours after plating, cells were transfected with the DNA constructs using Fugene® HD transfection reagent (Promega). This transfection reagent is a cationic lipid reagent, which will form a complex with DNA and because of the charge and lipid makeup, allow passage of the DNA into the mammalian cell across the cell membrane. All transfections were performed in triplicate unless otherwise noted. Firefly and *Renilla* luciferase activity was measured using Dual-Luciferase® Reporter Assay System (DLR™ Assay, Promega), the Luciferase Assay System (Promega), or the *Renilla* Luciferase Assay System (Promega) as indicated. The DLR™ assay system measures both firefly luciferase values and *Renilla* luciferase values: briefly, the firefly luciferase substrate is

added to the cell lysates and activity (light) is measured, then a second solution (Stop 'N Glo®) is added – which has two functions: quench the firefly reaction and act as substrate for *Renilla* luciferase – and activity is measured. Both the Luciferase Assay System and the *Renilla* Luciferase Assay System only contain the substrate for that particular enzyme but is done in the same way as the DLR® (substrate is added to cell lysate and light is recorded).

Luciferase vectors used in this study

pGL4.10 is a basic firefly luciferase vector with no promoter, but has a multiple cloning site for cloning a promoter of interest. It contains the coding region for a synthetic firefly (*Photinus pyralis*) luciferase gene, *luc2*, origin of replication, SV40 late poly(A) signal, and ampicillin resistance marker.

pGL4.70 is a basic *Renilla* luciferase vector with no promoter, but it has a multiple cloning site for insertion of promoter of choice. It contains the *hRLuc* coding gene (*Renilla* luciferase gene), SV40 late poly(A) signal, and an ampicillin resistance marker.

pGL4.74 is a *Renilla* luciferase promoter under the control of the TK promoter. It has the herpes simplex virus thymidine kinase (HSV-TK) promoter upstream of the *hRLuc* gene, a SV40 late poly(A) signal, and an ampicillin resistance marker.

Bradford assay

The Quick Start™ Bradford Protein Assay (BioRad) was used in accordance with manufacturer specifications for the 1mL assay. Readings for the assay were performed on a ThermoSpectronic Genesys 10 UV spectrophotometer.

TGM4 expression experiments

The proximal promoter region was amplified with polymerase chain reaction (PCR) with primers designed at approximately -1835 (TGM4_up_F6) and +31 (TGM4_pro51R1) to create a product that is approximately 1866 base pairs in length (Fig 3.1; primers: tables 3.2 and 3.3). The expression construct was made using the above outlined procedure. This was done in collaboration with an undergraduate mentee, Jason Hehr. He constructed the plasmids for human, and optimized PCR conditions for the other hominoids. The human construct was personally sequenced verified. The primers used for construction of these plasmids are in table 3.2 and location is marked on Fig 3.1.

Table 3.2: Primers used for cloning of *TGM4* proximal promoter region.
Kathryn Hooper-Boyd, 2007, designed primers designated with a star. Italics are restriction enzyme cut sites. Sarah Craig designed all other primers.

Primer name	Purpose	Sequence 5' → 3'
TGM4_up_F6*	PCR optimization	GCTGGCTCCTTTCAGTAGA
TGM4_F6_KpnI*	PCR for cloning	ACGTGCTACA*GGTACC*GCTGGCTCCTTTCAGTAGA
TGM4_F6_rev	Sequence verification	TCTACTGAAAGGAGCCAGC
TGM4_pro51R1*	PCR optimization	CCTTCAGATTCTCTCCTGCA
TGM4_pro51R1_SacI*	PCR for cloning	CTGTTTCCTG*GAGCTC*CTTCAGATTCTCTCCTGCA
TGM4_internal1_For	Sequence verification	CAATAGGAACAGCTCCATCTT
TGM4_internal1_Rev	Sequence verification	AAGATGGAGCTGTTCCTATTG
TGM4_internal2_For	Sequence verification	CATACGTCCATAATGGCACTG
TGM4_internal2_Rev	Sequence verification	CAGTGCATTATGGCGTATG
TGM4_internal3_For	Sequence verification	TGCCTAGCTGGATTGCAGA
TGM4_internal3_Rev	Sequence verification	TCTGCAATCCAGCTAGGCA
TGM4_internal4_For	Sequence verification	TCACCCACTGTTAGGCTCA
TGM4_internal4_Rev	Sequence verification	TGAGCCTAACAGTGGGTGA

During optimization experiments, it was noticed that the original human *TGM4* construct was not expressing higher than the promoterless vector (background expression). So, new primers were ordered according to a 2012 study by Rivera-Gonzalez et al., in which they showed *TGM4* expression in a pGL3 vector was significantly greater than the promoterless vector (Table 3). The forward primer was moved 300 base pairs closer to the transcription start site (TSS) and the reverse primer was moved 25 base pairs closer to the TSS (so the product is ~325 base pairs shorter than the original, -1535 → +6; Fig 3.1).

Table 3.3: Primers used in the creation of additional *TGM4* constructs
Constructs based off the study by Rivera-Gonzalez et al., 2012 (only modification was the restriction enzyme site on the reverse primer from *Xho*I to *Eco*RV)

Primer name	Purpose	Sequence 5' → 3'
RG_TGM4_1.5_For_SacI	PCR for cloning	TATCGATAGGTACCGAGCTCAATAGGAACAGCTCCATCTTGCCA
RG_TGM4_Rev_EcoRV	PCR for cloning	GATCGCAGATCTATAGAATGCCAGGGAAGACTCTATCTCTGAT

RESULTS

Luciferase optimization

The first optimization used the transfection conditions for the LNCaP cells using the Fugene® HD transfection reagent product literature (Promega). There were two optimization experiments that were performed: Fugene:DNA (µl:µg) ratio, and time post-transfection to assay. The Fugene:DNA (µl:µg) ratios of 3:2, 4:2, 5:2, 6:2, and 7:2 were all tested as suggested by the manufacturer. The *SEMG1* human construct (chapter 4) was transfected and the luciferase assay was performed 24 hours post-transfection using the DLR™ Assay System. To optimize the time to assay after transfection to assay, the time points of 24, 48, and 72 hours post transfection were assayed. The *SEMG1* and *SEMG2*

human constructs (chapter 4) were transfected using a 3:2 Fugene:DNA ratio; the Luciferase Assay System were used. These experiments were not repeated, but transfections were done in triplicate.

The constructs tested at the different Fugene:DNA ratios had significantly different mean values (One-way ANOVA, $P = 0.0013$). In post-testing (Turkey's multiple comparison tests) it was determined that the 3:2 ratio was significantly lower than the 5:2 ($P > 0.05$), 6:2 ($P \leq 0.05$), and 7:2 ($P > 0.05$) ratios and the 4:2 ratio was significantly lower than 6:2 ($P \leq 0.05$) (Fig 3.2). The time points for *SEMG1* did not show significant variation in the mean relative luciferase activity (One-way ANOVA, $P = 0.1960$, Fig 3.3). However, *SEMG2* showed significant variation in the mean relative luciferase activity across the different experimental groups (One-way ANOVA, $P = 0.0017$), with significant variation between 24 and 48 hours (Turkey's multiple comparison tests, $p \leq 0.05$, Fig3.3). The ratio and time that provided the best luciferase activity were the 6:2 (Fig 3.2) ratio and 48 hours (Fig 3.3). These were the conditions used for expression assays in this chapter (for *TGM4* expression) and chapter 4 (for semenogelin expression).

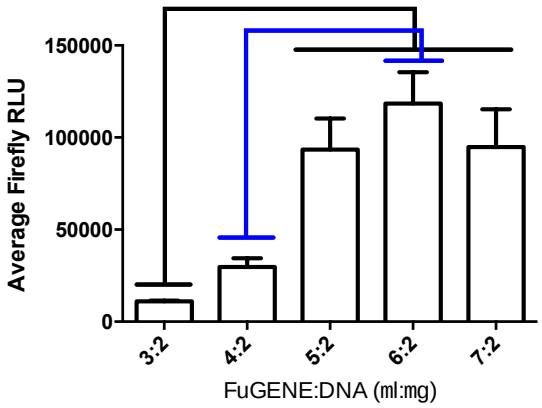

Figure 3.2: Fugene:DNA ratio optimization experiment.
***SEMG1* human construct was transfected.**

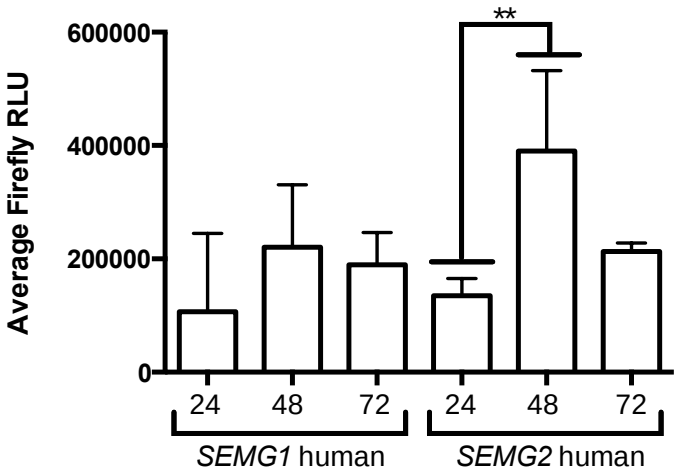

Figure 3.3: Time-post transfection to assay experiment.
X-axis is hours post-transfection to assay. *SEMG1* human one-way ANOVA $P = 0.1960$; *SEMG2* human one-way ANOVA $P = 0.0017$, Turkey's post testing 24 hours versus 48 hours $P \leq 0.05$.

Another optimization point was finding an internal control that would be useful in normalizing the luciferase data. Two controls were explored: an internal co-transfected control vector, and protein concentration. First, use of the internal control vector containing the *Renilla* (*Renilla reniformis*) luciferase was explored. Both the promoterless vector and the vector with TK promoter (pGL4.70 and pGL4.74 respectively, Promega) were tested for low, consistent expression and found to not show any difference between the expression of the two vectors (data not shown). pGL4.74 was used in all further optimization experiments since, in theory, it should provide a more consistent expression level due to its constitutive promoter; so when referring to the *Renilla* control vector, I am referring to pGL4.74.

Ideally, *Renilla* control vector would control for transfection efficiency and be expressed at a constant, low level regardless of the presence of other reporter vectors (Schagat et al. 2007). To test that *Renilla* control vector would be expressed as such in my system I transfected LNCaP cells with 0.1μg of pGL4.74 and increasing

concentrations of pGL4.10 containing the *SEMG1* human promoter (assayed after 24 hours with the Renilla Luciferase Assay System; experiment done twice). The *Renilla* control vector proved, however, not to be a good control vector in our system because as the expression of the firefly luciferase vector (*SEMG1* human pGL4.10) increases, the expression level of *Renilla* control vector also increased (Fig 3.4). This was also tested with lower concentrations of the control vector and the same trend was found (pGL4.74 at either 0.01 μg or 0.001 μg was transfected along with increasing concentration of *SEMG1* human pGL4.10, assayed at 24 hours with *Renilla* Luciferase Assay System). So, there is a degree of cross talk between the two co-transfected vectors with the firefly vector expression affecting the *Renilla* vector expression.

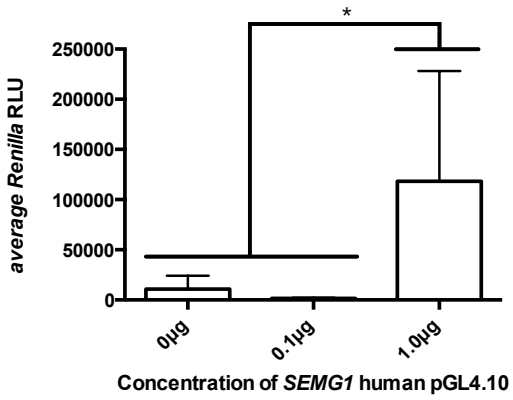

Figure 3.4: Firefly luciferase effect on *Renilla* luciferase
Average Renilla control vector relative light units. One-way ANOVA P = 0.0111; Turkey's multiple comparisons significant between 0 and 1.0μg and 0.1 and 1.0μg (P > 0.05).

To validate that the previous result is due to cross-talk between the experimental (firefly pGL4.10) vector and the control (*Renilla* pGL4.74) vector, and not due to inherent flaws in the assay, the dual luciferase protocol (see methods) was also tested for appropriate activity (i.e. testing that all luciferase activity that is attributed to the *Renilla* control vector is just the *Renilla* control vector activity and not bleed-over from the firefly experimental vector, i.e. failure of the Stop 'N Glo® to quench the firefly

luciferase activity). To do this LNCaP cells were transfected with 1µg of *SEMG1* human pGL4.10 and 0µg of pGL4.74. These were incubated for 24 hours and then a dual-luciferase assay was performed (DLR™). For this experimental purpose only the *Renilla* luciferase results are shown.

Renilla luciferase values with 1µg pGL4.10 were consistent with *Renilla* luciferase values from a mock experiment (no pGL4.10 or pGL4.74 present) (two-tailed t-test $P = 0.0554$; Fig 3.5). Therefore the quenching by Stop-N-Glo is complete and there is no bleed-over.

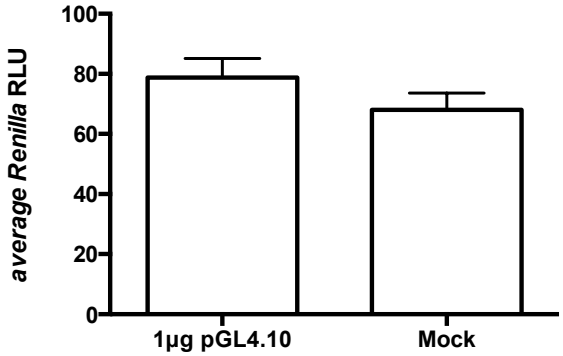

Figure 3.5: Effectiveness of Stop-N-Glo
Average Renilla luciferase relative light units. 1µg pGL4.10 = LNCaP cells were transfected with 1 µg of *SEMG1* human pGL4.10 experimental vector and 0µg Renilla control vector. Mock = 0µg of both vectors were transfected.

The final control vector optimization experiment was to determine if the cross talk between the *Renilla* control vector and the firefly experimental vector was a one-way or two-way street. For this experiment 1µg of *SEMG1* human pGL4.10 and increasing concentration of pGL4.74 were co-transfected. There was evidence of cross talk from *Renilla* control vector to firefly luciferase vectors at concentrations of 0.01µg and 0.001µg as evidence from the increased relative light units (Fig 3.6), but there was no effect of the *Renilla* control vector on the firefly experimental vector at 0.0001µg (Fig 3.6).

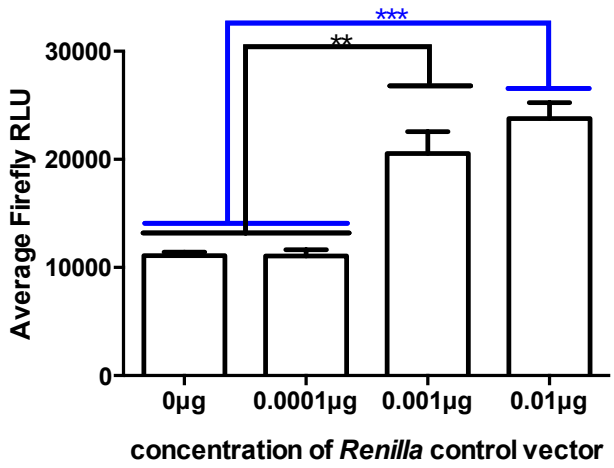

Figure 3.6: *Renilla* luciferase effect on firefly luciferase expression
Reverse cross-talk experiment. Graph shows firefly luciferase relative light units with increasing concentrations of pGL4.70. This experiment was done with a Fugene:DNA ratio of 1.5:1 (experiment done twice, data shown) and 3:1 (experiment done one time, data not shown), both had similar trends. One-way ANOVA P = 0.0002; Turkey's multiple comparison – firefly RLU with 0µg and 0.0001µg Renilla control vector vs. firefly RLU with 0.001µg Renilla control vector, P ≤ 0.05; firefly RLU with 0µg and 0.0001µg Renilla control vector vs. firefly RLU with 0.01µg Renilla control vector, P ≤ 0.001.

As an additional measure of control, consistent cell number was also tested. This was accomplished by performing a Bradford assay on the cell lysates; if there is a consistent cell number in the wells on the plate between experimental conditions at the time of assay (i.e. the experimental conditions did not cause cells to die or speed up growth in one well and not the others) there should not be a difference in protein concentration. Using the standard set provided with the Quick Start™ Protein Assay, a standard curve was created (Fig. 3.7). The formula for the line (y=0.226x-0.0586) was determined in Excel (Microsoft Office 2010) by adding a linear trendline and subsequently was used to determine the protein concentration of the experimental samples (Table 3.3). While there was significant overall differences, there are no significant differences between the cell lysate protein concentrations of cells transfected of any of the specific experimental conditions (Fig. 3.8).

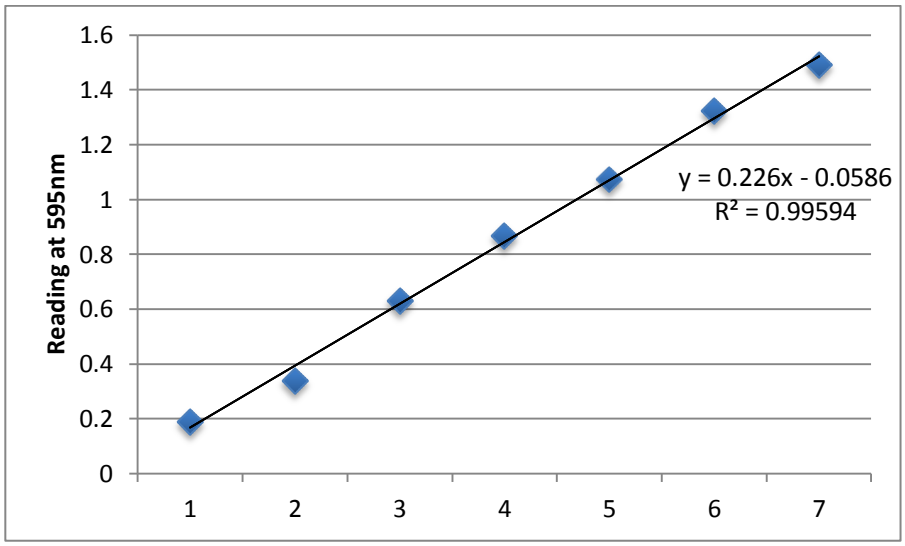

Figure 3.7: Standard Curve for Bradford Assay.
1=0.125mg/ml (0.189)*, 2 = 0.25mg/ml (0.338), 3 = 0.5mg/ml (0.631), 4 = 0.75mg/ml (0.868), 5 = 1mg/ml (1.075), 6 = 1.5mg/ml (1.324), 7 = 2mg/ml (1.493). *number in parentheses is the reading of sample in spectrophotometer at 595nm.

Table 3.4: Spectrophotometer readings and calculated average concentrations from Bradford assay

Gene_Species	First reading at 595nm	Second reading at 595nm	Third reading at 595nm	Average concentration mg/ml
*SEMG1*_human	0.854	0.775	0.802	0.1245
*SEMG1*_chimp	0.809	0.831	0.806	0.1257
*SEMG1*_bonobo	0.786	0.744	0.700	0.1094
*SEMG1*_gorilla	0.823	0.753	0.815	0.1215
*SEMG1*_orang	0.771	0.754	0.866	0.1215
*SEMG1*_gibbon	0.791	0.741	0.670	0.1073
*SEMG1*_macaque	0.826	0.824	0.829	0.1282
*SEMG2*_human	0.771	0.716	0.681	0.1047
*SEMG2*_chimp	0.784	0.676	0.705	0.1045
*SEMG2*_bonobo	0.751	0.731	0.766	0.1107
*SEMG2*_gorilla	0.760	0.742	0.799	0.1147
*SEMG2*_orang	0.823	0.739	0.867	0.1244
*SEMG2*_gibbon	0.778	0.785	0.840	0.1244
*SEMG2*_macaque	0.791	0.783	0.806	0.1207
Promoterless_pGL4.10	0.894	0.822		0.1354
*TGM4*_human	0.757	0.768	0.785	0.1154
Mock	0.774			0.1163

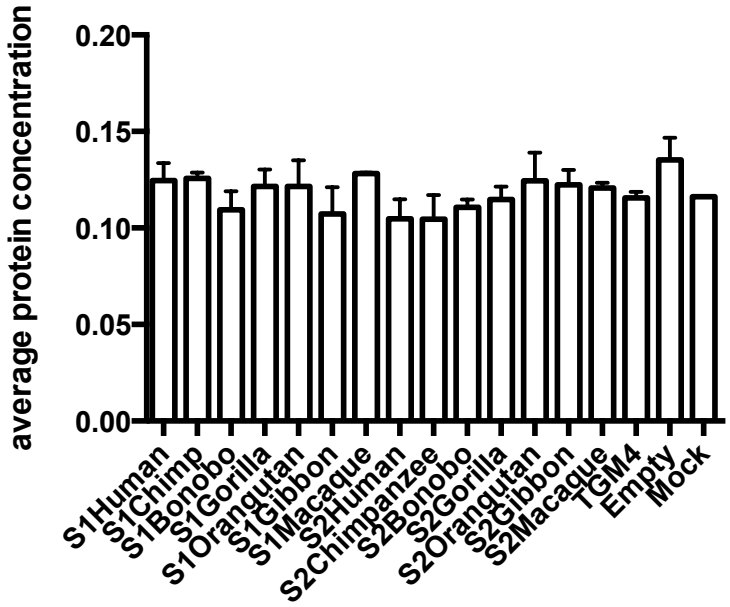

Figure 3.8: Protein concentrations of cell lysates
Average protein concentration of cell lysates transfected with *SEMG1* (S1) constructs, *SEMG2* (S2) constructs, *TGM4* construct, empty = pGL4.10 with no insert, or mock (transfected with only Fugene reagent). One-way ANOVA *P* = 0.0120, no significant comparisons in post-testing (Turkey's multiple comparison tests).

TGM4 expression

The 5' proximal promoter region of *TGM4* was amplified from human DNA and cloned into the pGL4.10 expression vector. This expression vector was tested in the human LNCaP cell line. Contradictory to prior studies that show this region is transcriptionally active, expression of this vector in our system failed to show expression higher than an empty pGL4.10 expression (background expression) (Fig. 3.9). To ensure that we did not inadvertently and unknowingly including a repressor sequence, we moved the primer location to exactly match the location of the primer in prior published results (Rivera-Gonzalez et al. 2012; see Fig 3.1). However, similar to our previous results, this new construct still failed to show expression higher than background (Fig. 3.9). Further testing of the other hominoid constructs was not performed due to these results.

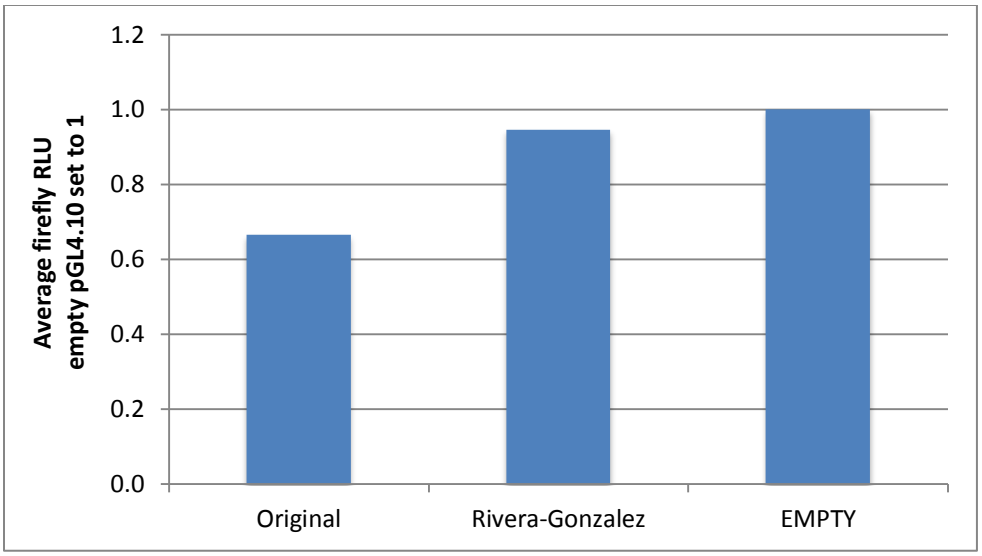

Figure 3.9: Average relative light unit (RLU) of the *TGM4* proximal promoter driven pGL4.10. Original = insert amplified using original primers from the study, Rivera-Gonzalez = insert amplified using primers from Rivera-Gonzalez et al. 2012, empty = promoter-less pGL4.10. Each bar represents three separate experiments, each done in triplicate.

DISCUSSION

Optimal transfection conditions and the use of an internal control

From the optimization experiments it was determined that a 3:1, Fugene:DNA (µl:µg) ratio and a 48-hour post-transfection time to assay were optimal. Additionally, *Renilla* was found to be unreliable and not useful as an internal control. This is because its expression level varies with the strength of an experimental vector (Fig. 3), which is not due to bleed-over from incomplete stoppage of the luciferase enzyme activity (Fig 4). This observation was seen by others in our lab (Ranajit Das, Scott Hergenrother, personal communication). The *Renilla* vector also may be affecting the expression of the experimental vector (Fig 5), although this effect can be overcome by decreasing the *Renilla* vector concentration. Furthermore, it was concluded that variation in the amount of luciferase activity is due directly to the amount of luciferase produced by the expression construct driven by the cloned promoter region and not due to an unequal cell

number (due to cells being plated at inconsistent number or cells dying due to transfection procedure or expression of a foreign construct). Although *Renilla* is commonly used as an internal control in transfection assays, including several studies important for the regulatory evolution in humans and other hominoids (e.g. Babbitt et al. 2009), for several genes examined in the LNCaP cell line, its expression is inconsistent. This result is not entirely unsupported in the literature, as others have also commented on the effectiveness and cautioning the use of co-transfecting the *Renilla* control vector as a means to normalize firefly luciferase data (e.g. Shifera and Hardin 2010; Zhang et al. 2003). Therefore, I recommend not using an internal vector control, but instead increasing the number of true replicates of each experiment to account for variation that may be present on an experiment-to-experiment basis. Or, if an internal vector is to be used as a control, that sufficient validation experiments are performed to ensure consistent expression.

Expression of *TGM4*

Previous studies performing promoter bashing on the proximal regulatory region of *TGM4* show that expression driven by a 1.5kb piece of this region will drive expression of that vector higher than a promoterless expression vector (Dubbink et al. 1998, 1999; Pasquali et al. 1999; Rivera-Gonzalez et al. 2012). However, in our system, the expression of a *TGM4* driven expression vector was never greater than the promoterless vector. This trend was upheld whether using unique primers or primers ordered according to prior studies. The main difference between the constructs that I created in this study and the constructs created in Rivera-Gonzalez et al. (2012, for example) is the vector backbone – I used pGL4.10 and they used pGL3 basic vector. I

don’t believe that using pGL3 over pGL4.10 would be beneficial because of the nature of the backbone itself. pGL4.10 was engineered to have fewer regulatory sequences and is codon optimized for expression in mammalian cell lines; otherwise they are the same (Promega). Furthermore, pGL3 has been shown to be more responsive to steroid hormones than pGL4.10, which could influence the observed luciferase expression controlled by promoters of genes that are potentially steroid hormone regulated (Dougherty and Sanders 2005), which indicates that pGL4.10 is a superior vector to use in these cases (*TGM4* is thought to be partially regulated by androgen). Therefore, I am left with no satisfactory explanation for my inability to replicate the results of Dubbink et al. (1998, 1999), Pasquali et al. (1999), and Rivera-Gonzalez et al. (2012).

REFERENCES

An G, Meka CSR, Bright SP, Veltri RW (1999) Human prostate-specific transglutaminase gene: promoter cloning, tissue-specific expression, and down-regulation in metastatic prostate cancer. *Urology* 54:1105-1111

Babbitt CC, Silverman JS, Haygood R, Reininga JM, Rockman MV, Wray GA (2009) Multiple functional variants in *cis* modulate *PDYN* expression. *Mol.Biol.Evol.* 27(2):465-479

Cabot A, Shrit RA, Blekhman R, Gilad Y (2007) Using reporter assays to identify *cis* regulatory differences between humans and chimpanzee. *Genetics* 176:2069-2076

Carnahan SJ, Jensen-Seaman MI (2008) Hominoid seminal protein evolution and ancestral mating behavior. *Am J Primatol* 70:939-948

Clark NL, Swanson WJ (2005) Pervasive adaptive evolution in primate seminal proteins. *PLoS Genetics* 1(3):e35

Dean MD (2013) Genetic disruption of the copulatory plug in mice leads to severely reduced fertility. *PLoS Genetics* 9(1):e1003185

Dermitzakis ET, Clark AG (2002) Evolution of transcription factor binding sites in mammalian gene regulatory regions: conservation and turnover. *Mol. Biol. Evol.* 19(7):1114-1121

Dougherty DC, Sanders MM (2005) Comparison of the responsiveness of the pGL3 and pGL4 luciferase reporter vectors to steroid hormones. *BioTechniques* 39:203-207

Dowell RD (2010) Transcription factor binding variation in the evolution of gene regulation. *Trends in Genetics* 26(11):468-475

Dubbink HJ, Verkaik NS, Faber PW, Trapman J, Schröder FH, Romijn JC (1996) Tissue-specific and androgen-regulated expression of human prostate-specific transglutaminase. *Biochem J* 315:901-908

Dubbink HJ, de Waal L, van Happeren R, Verkaik NS, Trapman J, Romijn JC (1998) The human prostate-specific transglutaminase (*TGM4*): genomic organization, tissue-specific expression, and promoter characterization. *Genomics* 51:434-444

Dubbink HJ, Cleutjens KBJM, van der Korput HAGM, Trapman J, Romijn JC (1999) An Sp1 binding site is essential for basal activity of the human prostate-specific transglutaminase gene (*TGM4*) promoter. *Gene* 240:261-267

King MC and Wilson AC (1975) Evolution at two levels in humans and chimpanzees. *Science* 188(4184):107-116

Kudaravalli S, Veyrieras J-B, Stranger BE, Dermitzakis ET, Pritchard JK (2008) Gene expression levels are a target of recent natural selection in the human genome. *Mol. Biol. Evol.* 26(3):649-658

Kwasnieski JC, Mogno I, Myers CA, Corbo JC, Cohen BA (2012) Complex effects of nucleotide variants in a mammalian *cis*-regulatory element. *PNAS* 109(47):19498-19503

Lin H-J, Luo C-W, Chen Y-H (2002) Localization of the transglutaminase cross-linking site in SVS III, a novel glycoprotein secreted from mouse seminal vesicle. *Journal of Biological Chemistry* 277(5):3632-3639

Mukherjee DC, Agrawal AK, Manjunath R, Mukherjee AB (1983) Suppression of epididymal sperm antigenicity in the rabbit by uteroglobin and transglutaminase in vitro. *Science* 219(4587):989-991

Pasquali D, Rossi V, Prezioso D, Gentile V, Colantuoni V, Lotti T, Bellastella A, Sinisi AA (1999) Changes in tissue transglutaminase activity and expression during retinoic acid-induced growth arrest and apoptosis in primary cultures of human epithelial prostate cells. *Endocrinol Metab* 84:1463-1469

Planas J, Serrat JP (2010) Gene promoter evolution targets the center of the human protein interaction network. *PLoS One* 5(7):e11476

Rivera-Gonzalez G, Droop AP, Rippon HJ, Tiemann K, Pellacani D, Georgopoulos LJ, Maitland NJ (2012) Retinoic acid and androgen receptors combine to achieve tissue specific control of human prostatic transglutaminase expression: a novel regulatory network with broader significance. *Nucleic Acids Research* 40(11):4825-4840

Rockman MV, Wray GA (2002) Abundant raw material for *cis*-regulatory evolution in humans. *Mol. Biol. Evol.* 19(11):1991-2004

Schagat T, Paguio A, Kopish K, Promega Corporation (2007) Normalizing genetic reporter assays: approaches and considerations for increasing consistency and statistical significance. *Cell Notes* 17:9-12

Shibata Y, Sheffield NC, Fedrigo O, Babbitt CC, Wortham M, Tewari AK, London D, Song L, Lee B-K, Iyer VR, Parker SCJ, Margulies EH, Wray GA, Furey TS, Crawford GE (2012) Extensive evolutionary changes in regulatory element activity during human origins are associated with altered gene expression and positive selection. *PLoS Genetics* 8(6):e1002789

Shifera AM, Hardin JA (2010) Factors modulating expression of *Renilla* luciferase from control plasmids used in the luciferase reporter gene assays. *Anal Biochem* 396(2):167-172

Tabach Y, Brosh R, Buganim Y, Reiner A, Zuk O et al. (2007) Wide-scale analysis of human functional transcription factor binding reveals a strong bias towards the transcription start site. *PLoS One* 2(8):e807

Teichmann SA, Babu MM (2004) Gene regulatory network growth by duplication. *Nature Genetics* 36(5):492-496

Williams-Ashman HG (1984) Transglutaminases and the clotting of mammalian seminal fluids. *Molecular and Cellular Biochemistry* 58:51-61

Wray GA, Hahn MW, Abouheif E, Balhoff JP, Pizer M, Rockman MV, Romano LA (2003) The evolution of transcriptional regulation in eukaryotes. *Mol. Biol. Evol.* 20(9):1377-1419

Wray GA (2007) The evolutionary significance of *cis*-regulatory mutations. *Nature Reviews: Genetics* 8:206-216

Zhang X, Chen H, Rovin BH (2003) Unexpected sensitivity of synthetic *Renilla* luciferase control vectors to treatment with a cyclopentenone prostaglandin. *BioTechniques* 35:1144-1148

Chapter 4: Evolution in the expression of the duplicated primate semenogelin genes

Introduction

A special case of the evolution of gene regulatory elements is the evolution after gene duplication. The duplication of a gene provides evolution raw material for genetic innovations and can arise in one of three ways: unequal crossing over, retroposition, or chromosomal (genome) duplication (Ohno 1970; Zhang 2003). After a gene has been duplicated the paralogs (duplicated copies of a gene that originate from the same ancestral gene) will either be maintained in the genome or lost via pseudogenization. Pseudogenization is the gradual accumulation of mutations, which will render a gene functionless. After an extended period of time the pseudogene will be unrecognizable to the paralog or deleted from the genome. Maintenance of duplicated genes in the genome can happen in three different ways – conservation, subfunctionalization, or neofunctionalization. Conservation of gene function occurs simply by purifying selection keeping both of the paralogs in their ancestral state, which is beneficial if extra copies of the gene product are advantageous to the organism; however, this is uncommon. More frequently, subfunctionalization, splitting of parent gene function between two daughter genes, or neofunctionalization, acquirement of a new function by a daughter gene, occur (Zhang 2003). Subfunctionalization occurs through a complementary degeneration process to differentiate the function of certain aspects from the parent gene to the duplicated daughter genes in order for both to be stably maintained (Papp et al. 2003; Zhang 2003). It has been suggested that subfunctionalization is the most common outcome of gene duplication (Lynch and Force 2000; Papp et al. 2003) and one form of

this is the division of the regulatory elements to adjust the transcription of the genes according to what is needed (Papp et al. 2003; Zhang 2003).

Evolution of duplicated *cis*-regulatory sequences

After gene duplication, changes occur in the coding and non-coding sequences that lead to the eventual fate of the gene (see above), which may be driven by positive or relaxed selection. Interestingly, there are a large number of gene families that have a history of positive selection, which have also rapidly expanded in copy number in primates indicating that selection is an important factor on the retention of duplicated genes and the expansion of gene families (Han et al. 2009). In fact, it has been shown by several studies that a larger fraction of young gene duplicates have a significantly greater rate of non-synonymous coding substitutions than a comparable set of single-copy orthologs (Castillo-Davies 2004; Han et al. 2009). In addition to coding sequence changes, the regulation of genes also plays an important role in the divergence of duplicated genes to change level of expression, timing of expression, tissue specificity, or alternative splicing (Gagnon-Arsenault et al. 2013). These changes are most likely a combination of epigenetic (chromatin, DNA methylation, or nucleosome occupancy) and genetic (*cis*-regulatory sequence) alterations (Zou et al. 2012; Gagnon-Arsenault et al. 2013). Rapid, *cis*-regulatory changes and subsequent expression changes seem to be universally routine after gene duplication (reviewed in Zhang 2003). As an example, in yeast, there is a 10-fold increase in the initial rate of expression and regulatory evolution shortly after a gene duplication event, which may serve as a mechanism to maintain both duplicate copies of the gene (Gu et al. 2005).

It sometimes is hard to investigate a gene duplication event through its initial or early stages of sub- [or neo- and pseudo-] functionalization due to the rapid changes that are occurring to the sequence at that point. So there is no go-to method for regulatory divergence as there is for coding sequence divergence. Two different ways in which researchers usually approach *cis*-regulatory evolution: determining the tempo and mode of natural selection on the non-coding sequences through nucleotide substitutions (for example see Haygood et al. 2007), or using conservation between orthologs to identify potentially important sequences that could be important transcription factor binding sites (TFBSs) or *cis*-regulatory modules (CRMs) (for example see Lenhard et al. 2003). The problem with either of these approaches, however, is the lack of consensus in the field of how these should be modeled and yet it is difficult to say one is better than the other. Yet, over the past decade there has been a growing trend to use phylogenetic footprinting to identify genomic regions that are potentially important in the regulation of gene expression with decreasing chance of missing functionally important sequences (Wasserman and Sandelin 2004). The idea behind this method stems from the observations that functionally important sequences will have fewer substitutions than a non-functional region (Bagheri-Fam et al. 2001; Ureta-Vidal et al. 2003).

Phylogenetic footprinting uses four steps: define orthologous regions, align promoter sequences, visualize or identify regions of significant conservation, and then determine which transcription factors (TFs) may bind to that area. Using this method decreases the input sequence that will be searched (focusing just on conserved sequences) and greatly reduces the number of sites that are predicted, yet retaining experimentally validated sites (Gumucio et al. 1992; Aparicio et al. 1995; Wasserman et al. 2000;

Wasserman et al. 2004), which helps distinguish TFBSs that have an *in vivo* role with those that do not. Using the same logic that orthologs will be under similar selective pressures, paralogs may be under different (or diverging) selective pressures (Ureta-Vidal et al. 2003) and therefore the phylogenetic footprinting approach can be tweaked to identify possible key TFBSs changes that drive expression divergence. This approach plays off the idea of the duplication-degeneration-complementation (DDC) model of *cis*-regulatory evolution following gene duplication. DDC states that subfunctionalization can be the result of division of regulatory modules (either symmetrically, Duarte et al. 2005 or asymmetrically, Gu et al. 2005) and that neofunctionalization will be the result of the gain of regulatory modules (Force et al. 1999; Duarte et al. 2005). These changes (division or gain) can be visualized through sequence comparisons of paralogous regulatory sequences.

Characterization and function of the semenogelins

Semenogelin 1 (SEMG1) and semenogelin 2 (SEMG2) are the predominant proteins in seminal fluid (Lilja et al. 1985, 1987, 1989). The genes encoding these proteins are duplicated genes that are tandemly located on human chromosome 20q12-13.1 (Ulvsbäck et al. 1992). The locus in which they are located is called the Wap four-disulfide core (*WFDC*) domain locus, which contains the semenogelin genes, *PI3, EPPIN, SLPI,* 3 *SPINT* genes, and 11 *WFDC* genes (Peter et al. 1998; Clauss et al. 2002). The human semenogelin genes have a conserved gene structure consisting of three exons – the first exon having a leader sequence and a signal peptide coding sequence, the second exon encoding the complete secreted protein, and a third non-coding exon. Because of their compact structure they span only 2.7 kb (*SEMG1*) and 3.1 kb (*SEMG2*)

with 11.5 kb between the two sequences (Lilja et al. 1989; Lilja and Lundwall 1992; Ulvsbäck et al. 1992, Fig 4.1). In humans, the two genes share 78 per cent identity in their amino acid sequence (Lilja et al. 1989; Lilja 1990; Lilja et al. 1992) yet differ in molecular weight by approximately 20 kilodaltans (SEMG1 ~52 kDa; SEMG2 ~ 71 and 76 kDa – depending on glycosylation state; Lilja et al. 1985; Lilja and Lundwall 1992; Malm et al. 1996). The size difference between the two genes is due to a difference in the number of 180 base pair repeat units that are present in the second exon. These repeat units account for greater than 80 per cent of the coding sequence, and can be split into three groups based on sequence similarity (although structurally similar so believed to have common origin and created through multiple duplications; Lundwall and Lazure 1995). As shown in figure 4.1, *SEMG1* exon 2 has two of each type of repeat (I, II, and III) and *SEMG2* exon 2 has four repeat type I, and two repeat types II, and III (Lilja and Lundwall 1992). It is interesting that the two genes differ mainly only in the number of type I repeats because this is the putative site for transglutaminase cross-linking (Zalensky et al. 1993; Robert et al. 1997; Ulvsbäck and Lundwall 1997; Robert and Gagnon 1999) which is believed to be important in the functionality of the protein.

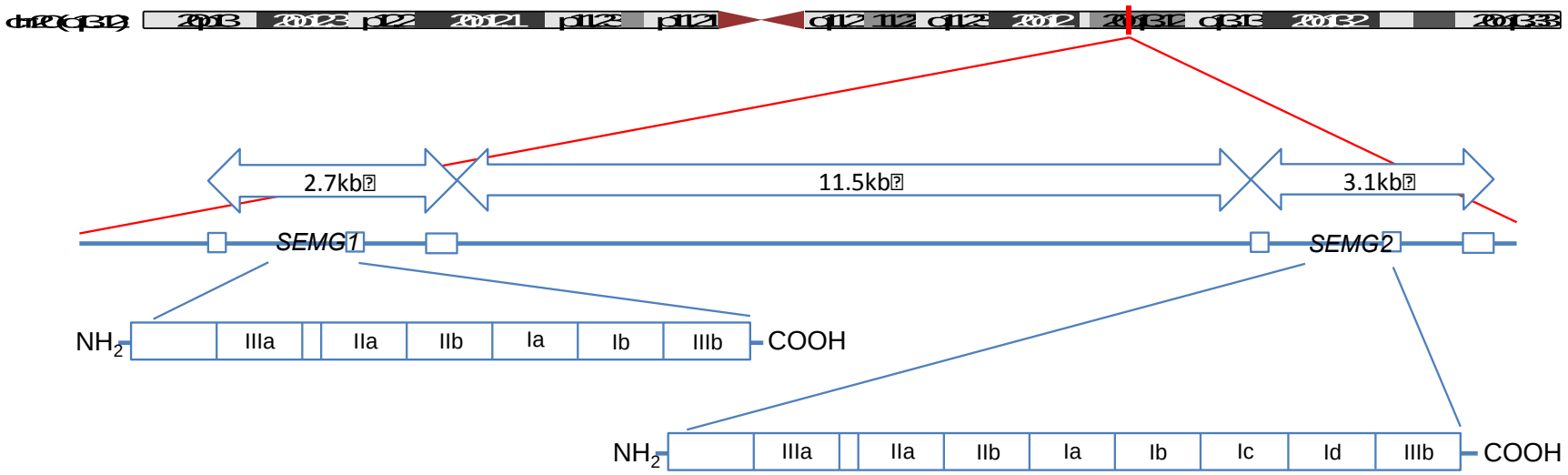

Figure 4.1: Genomic arrangement of the semenogelin genes.
The image shows a chromosomal ideogram of chromosome 20 from the UCSC genome browser with the red line marking the location on the q-arm where the semenogelin genes are located. Expanding this area shows the genomic arrangement of the semenogelin genes in the chromosomal DNA. The blue line represents the DNA of the chromosome, white boxes are untranslated regions, and blue boxes represent translated exons (redrawn from the UCSC genome browser). The number in the arrows above this schematic shows the length of the region of both semenogelin genes and the interspacing DNA. The mature peptide SEMG1 and SEMG2 comes entirely from the translated portion of exon 2 and the translated portion of exon 1 codes for a signal peptide and is cleaved. The mature peptide is diagramed with the repeated segments indicated within each protein.

After ejaculation, human semen is turned into a viscous gel and then subsequently liquefied through proteolysis. These consistency changes are due to changes in the semenogelin proteins (Lilja 1987; Peter et al. 1998). As stated above, the SEMG1 and SEMG2 are the major component of ejaculate and contain transglutaminase cross-linking sites. The covalent cross-linking of semenogelins along with noncovalent interactions creates a coagulum, which is stabilized by zinc, traps spermatozoa, and is hypothesized to help prevent backflow of the semen from the vagina (Jonsson et al 2006; Malm et al. 2007). In other mammals such as murid rodents, homologs to the semenogelins are cross-linked into a firm rigid copulatory plug hypothesized to block subsequent male partners' ejaculates access to fertilization potential (Martan and Shepherd 1976; Voss 1979). In addition to providing the scaffolding for the ejaculate coagulum, semenogelin has important functions in inhibiting sperm motility, sperm capacitation, and antimicrobial properties (Robert and Gagnon 1995; de Lamirande et al. 2001; Bourgeon et al. 2003; Edström et al. 2008; Mitra et al. 2010). The surface of the spermatozoa presents a CD52 antigen that binds to the C-terminus domain of semenogelin, of which epitopes have been detected on the head, midpiece, and tail of spermatozoa (Bjartell 1996; Zalensky et al. 1993; Flori et al. 2008). The binding of semenogelin to the antigen is then thought to affect the sperm's membrane potential and permeability, which may contribute to the sperm's motility (Yoshida et al. 2009). Similarly, semenogelin inhibits sperm capacitation in a dose-dependent manner by inhibiting hyperactivation (the whiplash like movement sperm display during capacitation) (de Lamirande et al 2001). In mouse the inhibition of capacitation has been shown to decrease fertility (Kawano and Yoshida 2006) but perhaps this is a way to keep the sperm decapacitated until they reach further

into the female reproductive tract (a preservation mechanism so to speak). These three actions of semenogelin (structural component of coagulated ejaculate, inhibitor of sperm motility, and inhibition of capacitation) are all reversible events triggered by the cleavage of the semenogelin proteins by PSA (prostate specific antigen, aka KLK3; Lilja 1985) and to a lesser extent by ACPP (prostate acid phosphatase, aka PAP; Brillard-Bourdet et al. 2002). Semenogelins are a specific substrate for PSA and are quickly fragmented when incubated together (Peter et al. 1998; Robert and Gagnon 1999; Jonsson et al. 2006). The cleavage of semenogelin releases the trapped sperm bound by semenogelin (Robert et al. 1997; Flori et al. 2008). Even after the semenogelin proteins are cleaved, they still function in assisting the sperm survival in the female reproductive tract. It has been shown that the 18 kDa N-terminal region that is cleaved by PSA has antimicrobial activity (Bourgeon et al. 2004). The antimicrobial activity is potentiated by low pH (of which the vagina is), the addition of zinc (which happens when mixed with fluid from the prostate) (Edström et al. 2008) and facilitated through binding with the protein EPPIN, which is also bound to the surface of newly ejaculated spermatozoa (Wang et al. 2005).

Expression and regulation of the semenogelins

SEMG1 and *SEMG2* are largely and mainly expressed in the seminal vesicles (Bjartell et al. 1996; Lundwall et al. 2002; Koistinen et al. 2002; Yoshida et al. 2003), but are also shown to be expressed to a much lower extent in the vas deferens, prostate, epididymis, and trachea. In addition to the above, *SEMG1* has some expression in the gastro-intestinal tract and skeletal muscle, while *SEMG2* has some expression in the kidney and testes (Lundwall et al. 2002). The promoter region for the human *SEMG1* has

begun to be characterized (Fig 4.2, Zhang et al. 2009) and shown to have a CAATT protein binding domain at -302, GATA-1 binding sites at -214 and -101, CpG at -11, and a TATA box at -28. The sequence between the two GATA binding domains has been shown through promoter bashing to be the minimal core promoter, while the areas at -349 to -302 and -28 to -1 have suppressive activity on the expression, and the sequence around the CAATT site has enhancing expression influence. Additionally, it is thought that androgen may play a role in the regulation of these genes. In mouse, the SVSIII gene is not detected in castrated mice but expression is recovered after androgen hormone stimulation (Lin 2002). In humans, SEMG1 is greatly decreased in seminal fluid from males who have had a radical prostatectomy and had preoperative anti-androgen treatment (Robert and Gagnon 1999). These results suggest that androgen may play a role in the regulation of this gene.

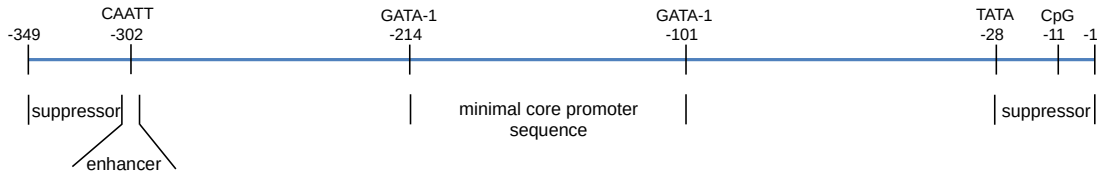

Figure 4.2: Important functional elements in the promoter of *SEMG1*
Elements were identified through promoter bashing by Zhang et al. 2009. Redrawn from Zhang et al. 2009.

The evolution of *SEMG1* and *SEMG2* in primates

SEMG1 and *SEMG2* belong to a group of genes called the rapidly evolving substrates for transglutaminases (REST) which includes the semenogelins in primates, seminal vesicle secretory protein genes in rodents, and seminal vesicle protein genes in guinea pig (Lundwall and Lazure 1995; Hagstrom et al 1996; Ulvsbäck and Lundwall 1997; Lundwall and Olsson 2001; Lundwall et al. 2003; Hurle et al. 2007). There are long stretches of sequence similarity between human semenogelin and rat SVSII except

for in the second exon, which encodes the entire secreted protein, which means that while the genes are homologous the protein produced will be much different (Lundwall and Lazure 1995). The timing of the gene duplication, which resulted in the primate *SEMG1* and *SEMG2*, is estimated to be 61 million years ago (after the split of the haplorhines and strepsirrhines, Fig 4.9) and is perhaps thought to be the result of homologous recombination between LINE - L1 elements (Lundwall 1996). Since the duplication, the genes have undergone numerous rearrangements, pseudogenizations, open reading frame expansions, deletions, and homogenizations. Two species of New World Monkey only have one semenogelin gene: the owl monkey (*Atous nancymaae*) locus contains a single chimeric semenogelin due to an *Alu* insertion which resulted in a *SEMG1*-like exon 1 and intron 1 and a *SEMG2*-like exon 2, intron 2, and exon 3 (Hurle et al. 2007). Similarly, the cotton-top tamarin (*Saguinus oedipus*) only has one semenogelin (*SEMG1*) due to the deletion of the *SEMG2* gene by insertion of a LINE1 element (Ulvsbäck and Lundwall 1997; Lundwall and Olsson 2001). It is also hypothesized that gene conversion has been occurring to homogenize the coding region of *SEMG1* and *SEMG2* in the squirrel monkey (*Saimiri boliviensis*) (Hurle et al. 2007). Additionally there is some evidence to suggest that gene conversion is a factor in the evolution of these genes in marmoset – between paralogs there is 100 per cent identity in exon 1, and almost 100 per cent identity in intron 1 extending into the first 0.9 kb of exon 2 (Valtonen-André et al. 2006).

Another feature of these genes that has undergone a multitude of changes is the expansion of the repeat regions located in the second exon (see above). The number of repeats in *SEMG1* exon 2 is more variable than the number of repeats in *SEMG2* (Table 4.1). It is hypothesized that the variability of the gene sequence in this area may account

for some of the rapid evolution and divergence of these two genes (Ulvsbäck and Lundwall 1997; Jensen-Seaman and Li 2003).

Table 4.1: Number of repeats of the Ia repeat in primate semenogelins.
Data is from Jensen-Seaman and Li 2003 unless otherwise noted. A dash indicates no data has been reported. Table modified from Jensen-Seaman and Li 2003

Species		*SEMG1*	*SEMG2*
Human		5-6	8
Chimpanzee		10-12	8
Bonobo		8-9	8
Gorilla	Western	8-9, 11[1]	-
	Eastern	8-9	8
Orangutan		13	8
Gibbon		6	7
Macaque		-	10[2]
Baboon		-	12
Proboscis		-	10

1: Carnahan and Jensen-Seaman 2008
2: Ulvsbäck and Lundwall 1997

Another factor in the evolution of these genes is the wide distribution of premature stop codons within the protein coding sequence (summarized for the hominoids in Fig 4.3). Of the primates who have had this region characterized for both genes, only human, orangutan, vervet, colobus, and marmoset seem to have full-length, functional copies of *SEMG1* and *SEMG2*. Chimpanzees, bonobos, and baboons have a premature stop codon in the coding region of *SEMG2* and gibbons have a premature stop codon in *SEMG1* (Jensen-Seaman and Li 2003; Dorus et al. 2004; Hurle et al. 2007). Gorillas have premature stop codons in exon 2 of both *SEMG1* and *SEMG2*. In *SEMG1*, gorillas are polymorphic for three premature stop codons. Both eastern and western lowland gorillas have the 5' most stop codon, while only western lowland gorilla have the two 3' stop codons (Carnahan and Jensen-Seaman 2008), and 2 premature stop codons in *SEMG2* (Jensen-Seaman and Li 2003). These changes beg to question whether there is an ongoing trend toward pseudogenization in this region (Hurle et al. 2007).

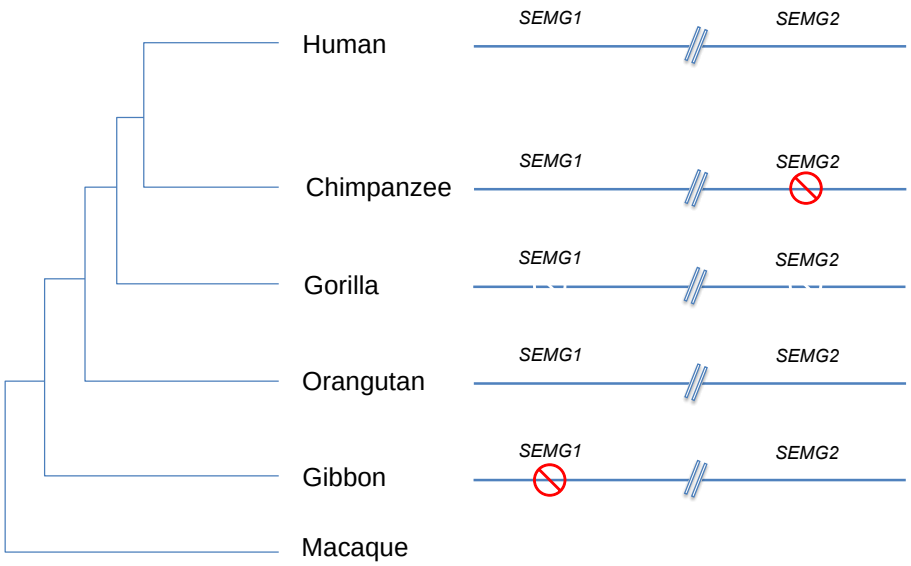

Figure 4.3: Stop codons in the hominoid semenogelin genes
Schematic of stop codon presence in the *SEMG* genes for hominoids. Red signs are for stop codons that are fixed in a species and white signs indicate polymorphic stop codons.

The coding region of the semenogelins also show evidence of rapid change. The *Ka/Ks* ratio (see first chapter) for the hominoids over all is approximately 0.6 (Jensen-Seaman and Li 2003). This is higher than the average *Ka/Ks* of 0.126 from all human-chimp orthologous pairs in the genome (CACS 2004) and higher than the average of all genes that code for proteins found in human seminal plasma (see chapter 2). Interestingly, the pattern of selection on both genes seem to correlate with level of female promiscuity and degree of semen coagulation (Dorus et al. 2004) with the more rapidly evolving lineages being those that have the highest level of sperm competition. *SEMG1* specifically shows a reduced level of polymorphism in chimpanzee and marginally reduced polymorphism in humans, which may indicate a selective sweep, whereas gorillas have higher levels of polymorphism (Kingan et al. 2003). Furthermore, at *SEMG1* there is elevated human-chimp sequence divergence and higher human-chimpanzee *Ka/Ks* ratio in comparison to human-chimp estimates of other genes (Kingan

et al. 2003). Similarly, *SEMG2* also shows higher *Ka/Ks* values on the lineages leading to chimpanzee and bonobo (Dorus et al. 2004).

In addition to looking at the evolutionary rate in the coding region, a few studies have estimated the evolutionary rate in the non-coding regions (5' non-coding, introns, 3' non-coding) of these genes. The results for these regions are contrary to the results from the coding region. The non-coding regions appear to be changing *slower* than control regions: the *SEMG2* 5' flanking region (minus the 200 bases proximal promoter), second intron (minus the sites flanking the splice sites), and two downstream sequences had a mutational rate for human of 0.84 substitutions/10^9 years and macaque had a mutation rate of 1.22 substitutions/10^9 years which is slower than the control (beta-globin) (Ulvsbäck and Lundwall 1997). Additionally Hurle et al. (2007) showed that the noncoding pairwise divergence (estimated from the introns) is less than the pairwise divergence for the coding regions. These results suggest that positive selection may be driving the evolution of the coding sequence (Metz et al 1998; Johnson et al. 2001).

Using semenogelin as a model for transcriptional divergence post gene duplication

The regulatory regions of semenogelins have not been well studied. The promoter bashing done in the initial characterization (Zhang et al. 2009) was done under the pretext of a possible marker for prostate cancer and only one of the semenogelins was studied. Furthermore sequence analysis of the divergence of the promoter regions for the two genes indicates that they are evolving slower than expected so there would not be much divergence expected. However, it has been shown that SEMG1 is five to ten times higher than SEMG2 in human semen (Malm et al. 1996; Malm et al. 2007) and early proteomic

data indicates that these proteins are at different abundances in both human and chimp semen (Chovanec and Jensen-Seaman, unpublished data).

In order to begin to investigate if there is divergence in the regulatory sequences of *SEMG1* and *SEMG2*, I am developing a modified phylogenetic footprinting approach (see Fig 4.4). By using ancestral sequence reconstruction and a combination of conservation (what sequences are conserved between extant and ancestral sequences) and uniqueness (what are unique sequences for each gene) it is possible to find differences that occur during the initial divergence that could account for differential regulation between the two genes.

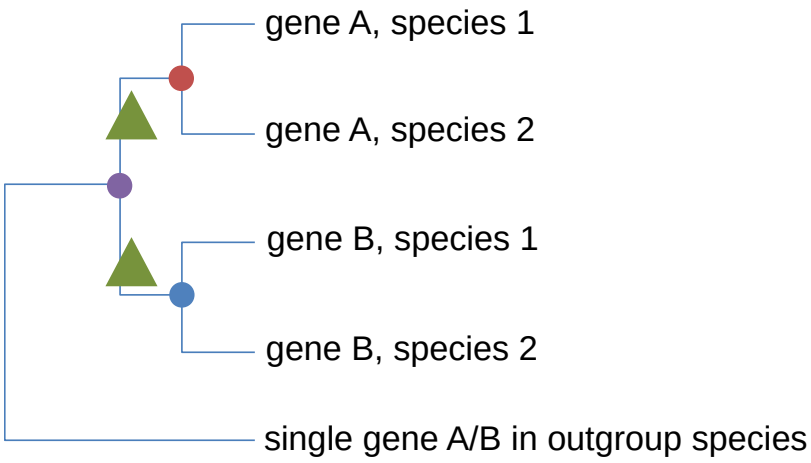

Figure 4.4: Modified phylogenetic footprinting incorporating DDC
Schematic of my hypothesis for the divergence of transcriptional regulation after gene duplication. The purple circle represents the ancestral gene A/B. After gene duplication there will be rapid divergence in the sequence (represented by the green triangles) of the newly duplicated gene resulting in two paralogous genes, A and B that will have novel regulatory regions (with respect to the ancestral gene). After the genes have diverged there will be stasis in the evolutionary pressures to diverge A from B but there may also be selective pressures for variation between species.

Methods

in vitro analysis

Expression construct creation

The proximal promoter region was amplified with polymerase chain reaction (PCR) with primers designed at approximately -453 (500_forward primer) and +28 (500_reverse primer) to create a product that is approximately 480 base pairs in length (see tables 4.2 and 4.3 for primers used). After initial amplification failed due to low efficiency of the reverse primer, a semi-nested approach was employed. Briefly, a primer that was designed at +400 (900_reverse) and used in conjunction with the 500_forward primer. (Besides the above mentioned detail, complete instructions on construction of constructs are found in methods for chapter 3; table 4.4 are primers used in cloning screening steps). Sequences are available in Appendix 3.

Table 4.2: Primers used for *SEMG1*.
Restriction enzyme cut sites are in italics.

Primer name	Purpose	Sequence 5' → 3'
SEMG1_500forward	PCR optimization / sequencing	AAAATAGAACGTGTCTCAAGATCAT
SEMG1_500_forward_Kpn	PCR for Cloning	ACGTGCTACA*GGTACC*AAAATAGAACGTGTCTCAAGATCAT
SEMG1_900_reverse	Semi-nested PCR	CTTTGGATTCAGTTTGTTGCTTGCC
SEMG1_500reverse	PCR optimization / sequencing	GGGAAAGTACAAAGATGATGTTGGG
SEMG1_500reverse_Hind	PCR for cloning	GACACTATGCCT*AAGCTT*GGGAAAGTACAAAGATGATGTTGGG
S1_rev_HIND	PCR for Cloning	GACACTATGCCT*AAGCTT*GTTGGGCTTCATCTTGCTTG
S1mut_rev_HIND	PCR for cloning	GACACTATGCCT*AAGCTT*GTTGGGCTTCTTCTTGCTTG

Table 4.3: Primers used for *SEMG2*.
Restriction enzyme cut sites are in italics.

Primer name	Purpose	Sequence 5' → 3'
SEMG2_500_forward	PCR optimization	AAAACAGAATGTGTCTCAGGATTAC
SEMG2_500_forward_Kpn	PCR for cloning	ACGTGATACA*GGTACC*AAAACAGAATGTGTCTCAGGATTAC
SEMG2_900_reverse	Semi-nested PCR	CTTTGGATTTAGTATGTTGTTGGTC
SEMG2_500_reverse	PCR optimization	GGGAAAGGACAAAGAGGATGATGGA
SEMG2_500_reverse_Hind	PCR for cloning	GACACTATGCCT*AAGCTT*GGGAAAGGACAAAAGAGGATGATGAGA
S2_rev_HIND	PCR for cloning	GACACTATGCCT*AAGCTT*ATGGACTTCATCTTGCTTG
S2mut_rev_HIND	PCR for cloning	GACACTATGCCT*AAGCTT*ATGGACTTCTTCTTGCCTTG
SEMG2_internal_For	Sequencing	CACTGAGCAGGGGTGAGGAA
SEMG2_internal_Rev	Sequencing	AGGAAGGAGACTAGCTTCAG

Table 4.4: Vector primers used in screening steps

Primer name	Purpose	Sequence 5' → 3'
M13_For(-21)mod	TOPO screen	GTTGTAAAACGACGGCCAGT
M13_Rev_mod	TOPO screen	CACAGGAAACAGCTATGACC
pGL4_92_R1	pGL4.10 screen	TTACCAACAGTACCGGATTG
pGL4_4223_F1	pGL4.10 screen	AGGTGCCAGAACATTTCTCT

Luciferase expression assays

Cell culture maintenance

A human prostate cell line (LNCaP clone FGC, ATCC® CRL-1740™) was kept in a humidified, 37°C, 5% carbon dioxide incubator in RPMI-1640 medium (ATCC) supplemented with 5% fetal bovine serum (FBS) and antibiotic (penicillin and streptomycin, which will be referred to as P/S) unless otherwise noted. All procedures were performed as per the protocols published in *Basic Techniques for Mammalian Cell Tissue Culture* (1998) with specifics as follows. Cultures were trypsinized and subcultured when cells reached >75% confluency (approximately every three days if cultures were split 1:3 or every 4 days if cultures were split 1:4).

Transfection and luciferase assay

When cultures reached >75% confluency, cells were trypsinized, counted using a hemocytometer, and plated in a 12-well cell culture plate at a density of 200,000 cells per well in 1mL of complete growth media. If multiple plates were being used for a particular experiment multiple flasks of cells were combined before counting to ensure enough cells for all the plates. After 24 hours LNCaP cells were transfected with 1μg of vector DNA (either promoter expression construct or promoterless pGL4.10 vector) and FuGENE® HD transfection reagent (Promega) at a ratio of 3μL:1μg of vector DNA. Transfection reactions were mixed and delivered to the cells in unsupplemented RPMI-1640 medium. Mock transfections were also performed alongside the experimental transfections to control for background luminescence. This reaction mixture contained only 3 μL of FuGENE® HD transfection reagent in unsupplemented RPMI-1640. Transfection reactions were incubated at room temperature for five minutes and then 50μL was added to each well in a clockwise-dropwise fashion. Transfected cells were kept in a humidified, 37°C, 5% carbon dioxide incubator for 48 hours. Each experimental condition was assigned to three wells of the 12-well plate (and the mock reaction to one well). A luciferase assay was performed using the Luciferase Assay System (Promega) according to the instructions provided by the supplier with the exception of the lysis buffer. A passive lysis buffer (Promega) was used in place of the reporter lysis buffer that accompanied the luciferase assay system. 20 μL of the cell lysates were added to a 96-well luminometer plate and read on a Turner Biosystems Veritas microplate luminometer.

The remaining cell lysate was kept at -20°C in a 96-well, non-skirted PCR plate. This experimental set-up was repeated four times unless otherwise noted.

Androgen treatment

Cells were plated as described above at a density of 200,000 cells per well in 800μL of complete media consisting of RPMI-1640 medium, charcoal-stripped FBS, and P/S. 24 hours after plating cells were transfected as described above. 24 hours post-transfection cells were treated with 10nM methytrieolone (R1881, Perkin Elmer Life Sciences, Inc.) or a vehicle control (100% ethanol). To add the hormone (or control) to the cells, R1881 (or an equivalent volume of EtOH) was diluted from a 100μM stock (or 100% EtOH) in RPMI-1640 medium and then 200μL of this mixture was added to the cells. Following a 24-hour incubation time, a luciferase assay was performed as described above. This experiment was done in triplicate and not repeated.

Data analysis

Background luminescence was removed from raw luciferase values for experimental and control vectors by subtracting the mock transfection relative light unit (RLU) from the RLU of all experimental wells. An average RLU of the triplicate wells was taken for each experimental condition and this value was then normalized to the average RLU of the empty pGL4.10 vector. This normalization allowed comparison of results across experimental set-ups. This part of the data analysis was performed in Excel. Statistical tests were then performed using the Prism 6 software (www.graphpad.com).

in silico **analysis**

Phylogenetic analysis and ancestral sequence reconstruction

Human, chimpanzee, bonobo, gorilla, orangutan, gibbon, and macaque sequences for the 5' *cis*-regulatory region were generated from the creation of the luciferase expression constructs. Additional primate sequences were obtained from GenBank nucleotide database: baboon (*Papio Anubis* – DP000036), colobus monkey (*Colobus guereza* – DP000038), galago (*Otolemur garnettii* – DP000040), lemur (*Lemur catta* – DP000042), marmoset (*Callithrix jacchus* – DP000044), owl monkey (*Aotus nancymaae* – DP000046), squirrel monkey (*Saimiri boliviensis* – DP000047), and vervet (*Chlorocebus aethiops* – DP000048) (originated from Hurle et al. 2007). From the GenBank sequences, human *SEMG1* or *SEMG2* were aligned with the downloaded sequence using ClustalW in order to determine orthologous sequences. Alignments available in Appendix 3.

The resulting sequence files were concatenated and submitted to ClustalW for alignment. The alignment file was submitted to jModelTest 2 (Darriba et al. 2012) to detect the best model of nucleotide substitution to recreate the phylogenetic relationships between the species for phylogenetic analysis. This alignment was converted into MEGA format using MEGA5.2 (Tamura et al. 2011). Using the tools in MEGA, phylogenetic trees were created and ancestral sequences were inferred. Both the neighbor-joining and maximum likelihood methods were used to create a phylogenetic tree. The neighbor-joining tree was created using the number of differences method including both transitions and transversions and gaps/missing data were completely deleted. The resulting phylogeny was tested using 1000 replicates of the bootstrap method. For the maximum likelihood tree the Hasegawa-Kishino-Yano model was used with uniform rates among sites, the nearest-neighbor-interchange (NNI) heuristic method, and a

bootstrap method of testing with 1000 replicates. The maximum likelihood method was also used for ancestral sequence reconstruction with the Hasegawa-Kishino-Yano model; uniform rates among sites, and all sites were used in the inference.

Phylogenetic footprinting

The online tool, ConSite (Sandelin et al. 2004a), was used to identify conserved TFBSs between two sequences. This program uses a built-in alignment tool named ORCA, and queries to the JASPAR database to predict TFBSs (Sandelin et al. 2004b). The search was limited by the following filters: transcription factors (TFs) were selected from the vertebrate taxonomic supergroup, no specificity on a minimum specificity bit, a conservation cut off of 96%, and TF score threshold of 80%.

To determine if there are predicted TFBSs that are conserved between extant hominoid *SEMG1* or *SEMG2* and the first ancestral sequences after the gene duplication (the haplorhine ancestral gene) that are also unique to either gene (Fig 4.10), I first compared the sequence for the haplorhine ancestral gene to the ancestral *SEMG1/2* sequence. After doing this for both *SEMG1* haplorhine ancestral gene and *SEMG2* haplorhine ancestral gene I compared the results to see where they overlapped and which of the predicted TFBSs were unique to each gene. Then I compared *SEMG1* or *SEMG2* hominoid LCA gene sequence to the haplorhine LCA sequence to find predicted TFBSs that are both common between these sequences and were also identified in the previous step as unique to that gene and conserved from the ancestor. The TFBSs identified were further analyzed for conservation in all the extant hominoid sequences (comparing all hominoid sequences to the hominoid LCA and identifying sites conserved, Fig 4.10). The TFBSs sites identified here are called unique, conserved sites (unique to *SEMG1* or

SEMG2 and conserved from the duplication through the hominoids). These sites were verified for transcription factors that are relevant for expression in the prostate by filtering the results based on expression using the BioGPS interface (Wu et al. 2009; Wu et al. 2013) and excluding all factors that did not show prostate expression.

In order to determine if there are differences in the TFBSs predictions for *SEMG2* hominoids and *SEMG2* macaque I compared the *SEMG2* macaque to the *SEMG2* catarrhine LCA and also the *SEMG2* catarrhine LCA to the *SEMG2* hominoid LCA to identify TFBSs that are different between macaque and the hominoid LCA that have their origin on the branch from the Catarrhine LCA to the Haplorhine LCA (Fig 4.13). I then compared the *SEMG2* hominoid LCA to the each extant hominoid sequences and identified all sites that are conserved among all hominoids but are unique to the group as identified by the first comparison (see Fig 4.13).

Results

Mating system does not have an effect on transcriptional regulation of the semenogelins

Average relative light units (RLU) were calculated from the raw data of each experiment (which is basically the measure of the amount of light produced) and normalized to the promoterless luciferase vector average RLU. Unless otherwise state, all results shown are from four independent replicates of the experiment, where each experiment included triplicate transfections. There is significant variation among the level of transcriptional activity from the different species promoters within *SEMG1* (one-way ANOVA, $p < 0.0001$, Fig 4.5a) and but not within *SEMG2* (one way ANOVA, $p > 0.05$, Fig 4.5b). While there were differences between individual species comparisons,

in neither the case of *SEMG1* or *SEMG2* did the sexual selective pressures from sperm competition seem to influence the activity of the promoter (Fig 4.6a, i.e. species from multimale mating systems did not have more active promoters than species with unimale mating systems; *SEMG1* two-tailed unpaired t test, $P = 0.1605$; *SEMG2* two-tailed, unpaired t test, $P = 0.8573$). Differences between genes remained significant when grouped by mating system (Fig 4.6b, multimale unpaired t test, $P = 0.0002$; unimale unpaired t test, $P = 0.0004$).

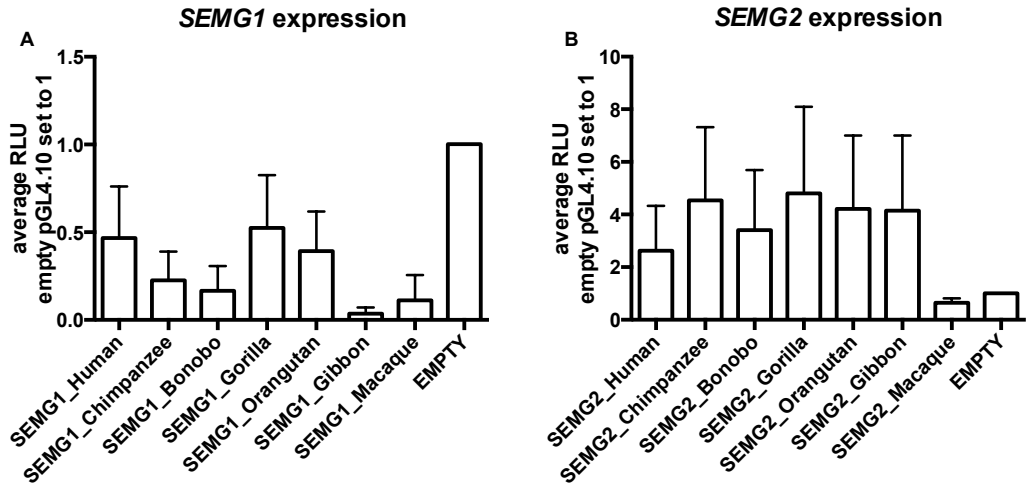

Figure 4.5: Expression of the hominoid semenogelin promoter regions
Histograms representing the expression of the luciferase gene under the control of the hominoid (and macaque) *SEMG1* and *SEMG2* proximal promoters. A: Results on the expression activity of the *SEMG1* promoter. The empty pGL4.10 expression level was set to one and the other species were normalized to this. B: Results of the expression activity of the *SEMG2* promoter. Similarly, the empty pGL4.10 expression level was set to one and the other species were normalized to this value. Error bars indicate standard deviation.

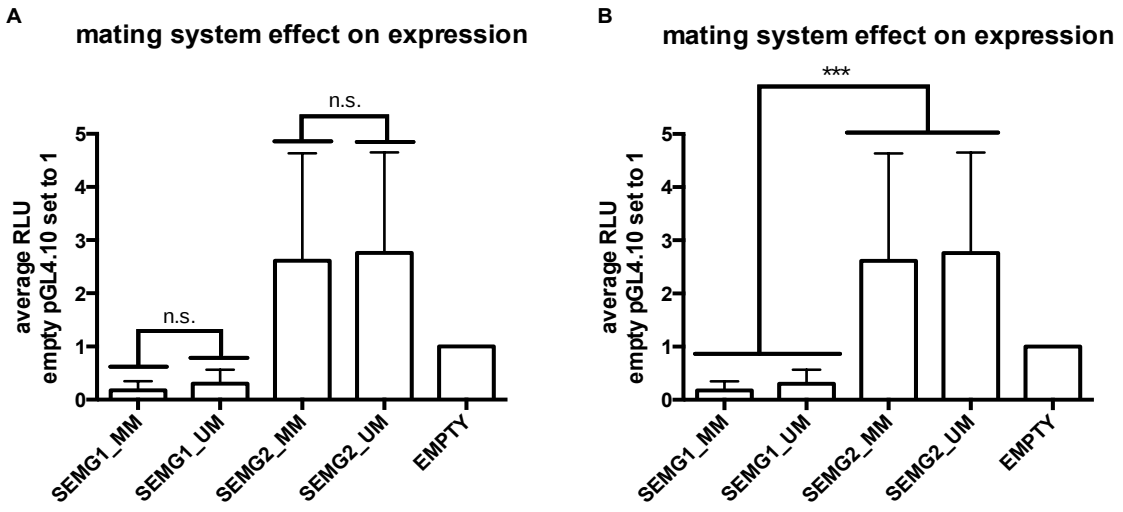

Figure 4.6: Mating system effect on expression
Average luciferase expression for *SEMG1* and *SEMG2* under the conditions of mating system: MM= multimale system (chimpanzee, bonobo, orangutan, and macaque), UM= unimale system (human, gorilla, and gibbon), empty = promoterless pGL4.10. A) No significant difference within a gene based on mating system. B) Significant difference between *SEMG1* and *SEMG2* even after grouping species based on mating system.

SEMG2 proximal promoter drives expression higher than *SEMG1*

Significant variation was found when comparing between *SEMG1* and *SEMG2* (one way ANOVA $p<0.0001$, Fig 4.7; even with grouping of species based on mating system, Fig 4.6b). When looking at the data there are two splits in the data. First, for every hominoid, the *SEMG2* promoter drove expression greater than the *SEMG1* promoter. And second, all hominoid *SEMG2* promoters drove expression of the luciferase enzyme greater than the promoter of the macaque.

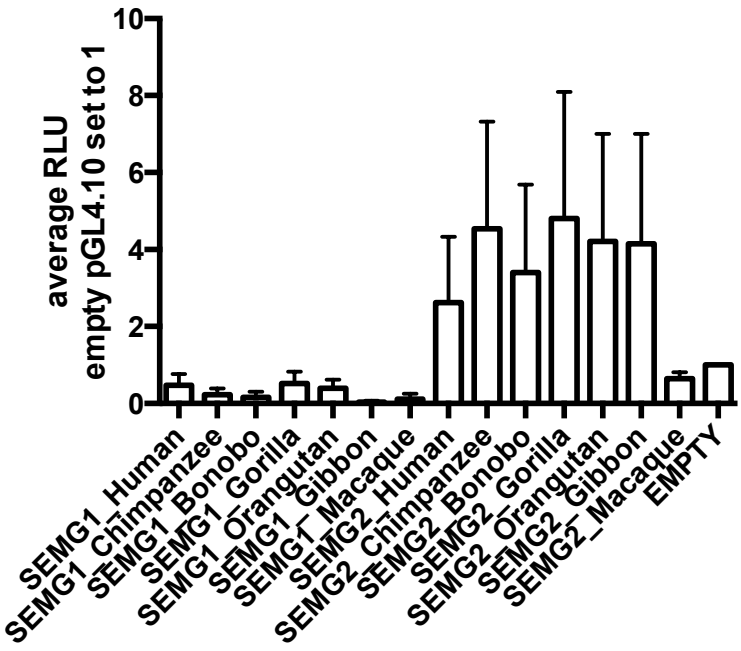

Figure 4.7: *SEMG1* and *SEMG2* expression
Histogram displaying the expression of all reporter constructs created in this study. *SEMG2* has greater expression than *SEMG1*.

Androgen does not affect the transcriptional control of the proximal promoter of the semenogelins

The putative proximal promoters of human and chimpanzee *SEMG1* and *SEMG2* were also tested in an environment supplemented with a synthetic androgen, R1881, and no difference in expression was detected from that of the control (Fig 4.8). This experiment was only repeated once, with triplicate transfections in the experiment.

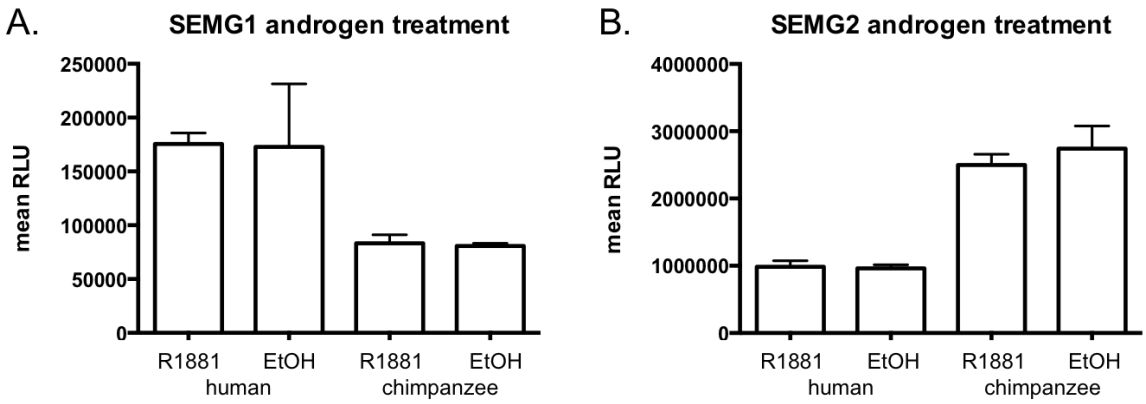

Figure 4.8: Androgen effect on semenogelin expression
Expression of the *SEMG1*(A) and *SEMG2*(B) proximal promoter in response to a synthetic androgen, R1881, or a vehicle control, EtOH. Treatment had no difference than the control. Data shown is raw data and not normalized.

Reconstruction of ancestral semenogelin sequences

Phylogenetic trees were constructed using sequences of the semenogelin genes for the hominoids and macaque that were sequenced in the creation of the reporter constructs, as well as the orthologous sequences from Hurle *et al.* (2007), with the maximum likelihood method based on the Hasegawa-Kishino-Yano model (Figure 4.9). The best model for the tree using jModelTest 2 was the HKY model with gamma distribution. However, previous research in this field uses the normal HKY model and since the resulting tree is identical, the HKY tree was used. The sequences for the hominoid *SEMG1* and *SEMG2* last common ancestor (LCA), catarrhine *SEMG1* and *SEMG2* LCA, haplorhine *SEMG1* and *SEMG2* LCA, and the *SEMG1/SEMG2* LCA were determined by maximum likelihood in MEGA5.2. These reconstructed sequences used were reconstructed with the HKY model, as the HKY-gamma model derived sequences are almost identical. These sequences used in further analysis are available in Appendix 3.

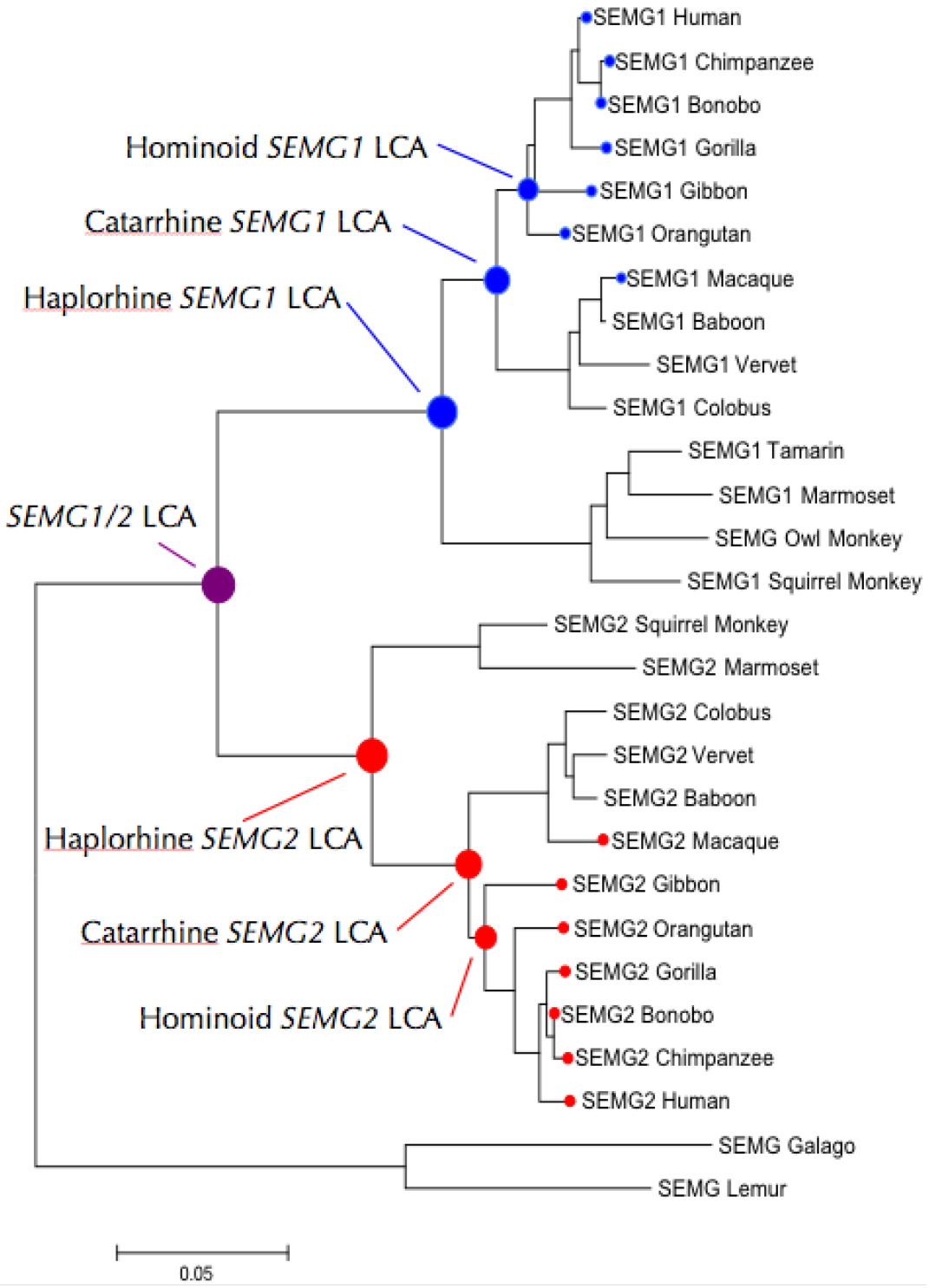

Figure 4.9: Phylogenetic tree of the semenogelins
Maximum likelihood phylogenetic tree made in the program MEGA5.2 inferred using the Hasegawa-Kishino-Yano model. The tree is drawn to scale and branch lengths are measured in number of nucleotide substitutions per site. Small colored dots signify species used in reporter constructs assays; larger colored dots indicate hypothetically reconstructed sequences used in TFBSs prediction analyses.

Modified phylogenetic footprinting identified candidate transcription factor binding sites that may account for expression differences between *SEMG1* and *SEMG2*

When comparing the *SEMG1* and *SEMG2* haplorhine LCA to the *SEMG1/SEMG2* LCA, it was found that there are 95 and 135 (respectively) conserved TFBSs between the two sequences (Fig 4.10). Of those identified there are 52 predicted TFBSs that are further conserved between the *SEMG1* haplorhine LCA and the *SEMG2* haplorhine LCA. The purple asterisks in figures 4.11 and 4.12 represent these 52 'shared' TFBSs. The gene specific TFBSs (i.e. the 'unique TFBSs') were submitted to further comparisons to identify gene specific predicted TFBSs that are conserved throughout the lineages created in the hominoid radiation (i.e. 'unique, conserved TFBSs'). Figure 4.10 shows the line of comparisons used to identify these sites. The blue line represents the sequences that were considered to find unique, conserved *SEMG1* TFBSs and the red for *SEMG2* unique, conserved TFBSs. To further refine the TFBSs predictions any TF that is not expressed in the prostate is removed. This result in 21 unique conserved predictions for *SEMG1* (Fig 4.11) and 37 for *SEMG2* (Fig 4.12).

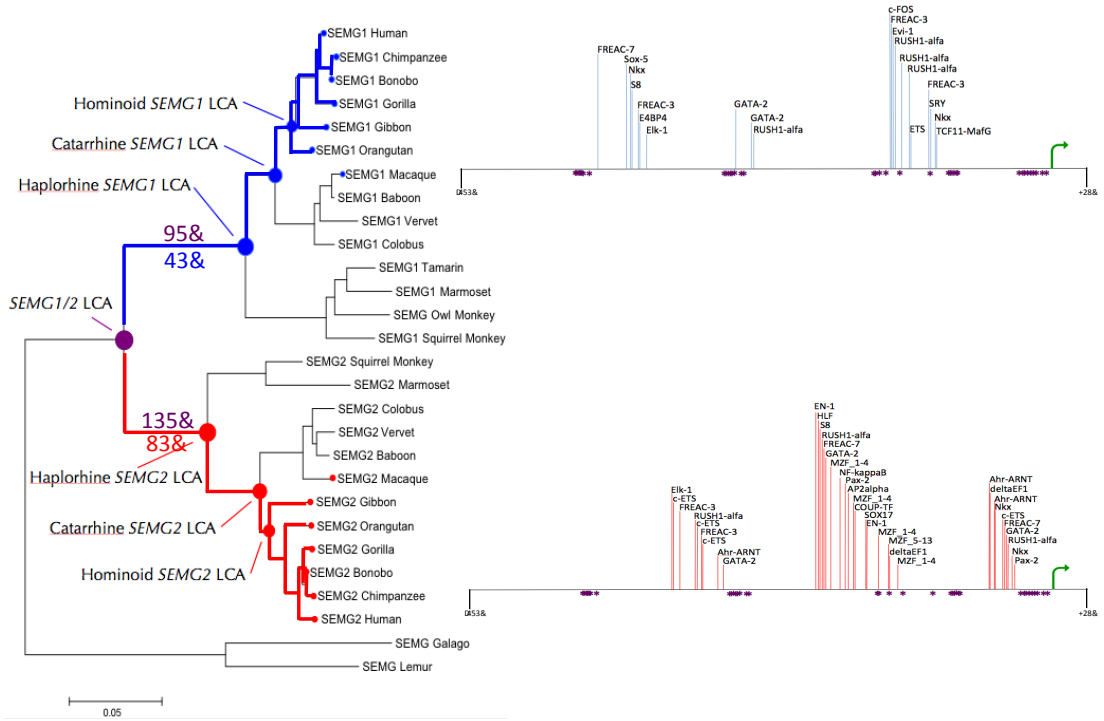

Figure 4.10: Schematic of the method to find unique, conserved TFBSs.
The number on the top of the branches (95 and 135) is the total number of predicted TFBSs conserved between the *SEMG1*/2 LCA to the haplorhine *SEMG1* LCA and *SEMG1*/2 LCA to the haplorhine *SEMG2* LCA (respectively). Comparing the results of these data to each other found that there are 52 TFBSs predictions in common. Subtracting these 52 from the initial comparisons leaves a total of 43 and 83 unique TFBSs for *SEMG1* and *SEMG2* (number below the branches).

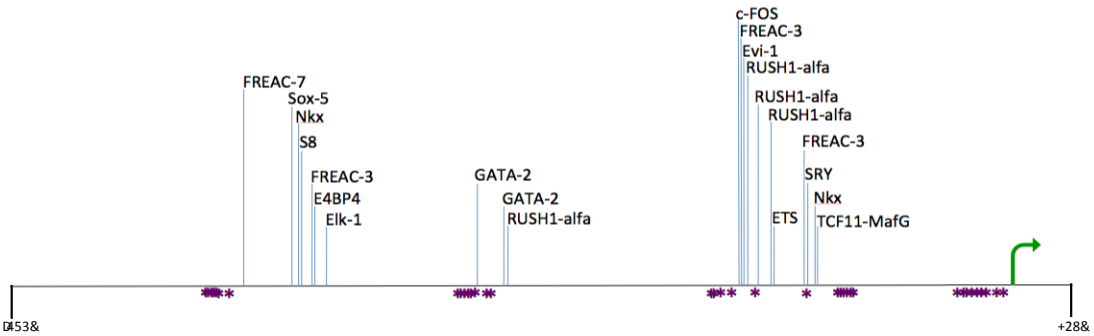

Figure 4.11: Unique, conserved *SEMG1* TFBSs
Unique (to *SEMG1*), conserved (throughout the tree to terminal hominoid) transcription factor binding sites in the hominoid *SEMG1* proximal promoter.

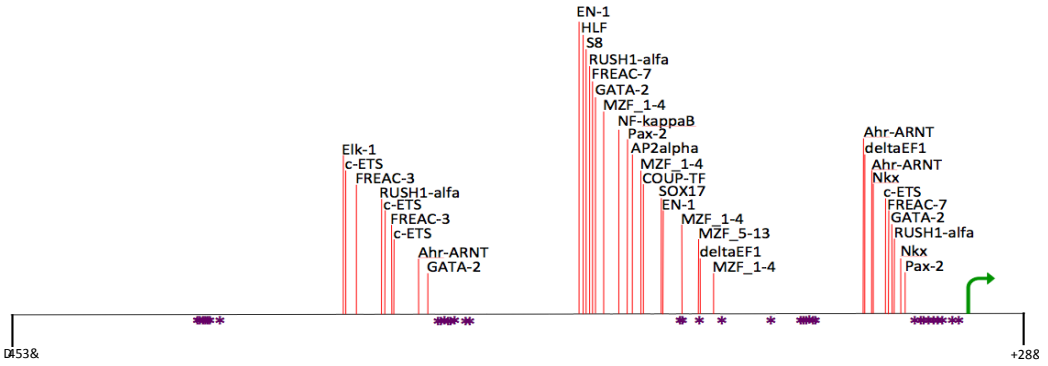

Figure 4.12: Unique, conserved *SEMG2* TFBSs
Unique (to *SEMG2*), conserved (throughout the tree to terminal hominoid) transcription factor binding sites in the hominoid *SEMG2* proximal promoter.

Identifying candidate TFBSs to explain expression differences between hominoid *SEMG2* expression and macaque *SEMG2* expression

There are 136 conserved TFBSs predicted when comparing macaque *SEMG2* to the catarrhine *SEMG2* LCA and 246 conserved TFBSs predicted when comparing the catarrhine *SEMG2* LCA to the hominoid *SEMG2* LCA (Fig 4.13). Between these two comparisons there are 109 binding sites that are unique to the hominoid lineage – 48 of which are conserved among all hominoids. Further filtering this data set using tissue expression of the TFs, there are 24 predicted TFBSs that could potentially impact a differential regulation between *SEMG2* macaque and *SEMG2* hominoids (Fig 4.14).

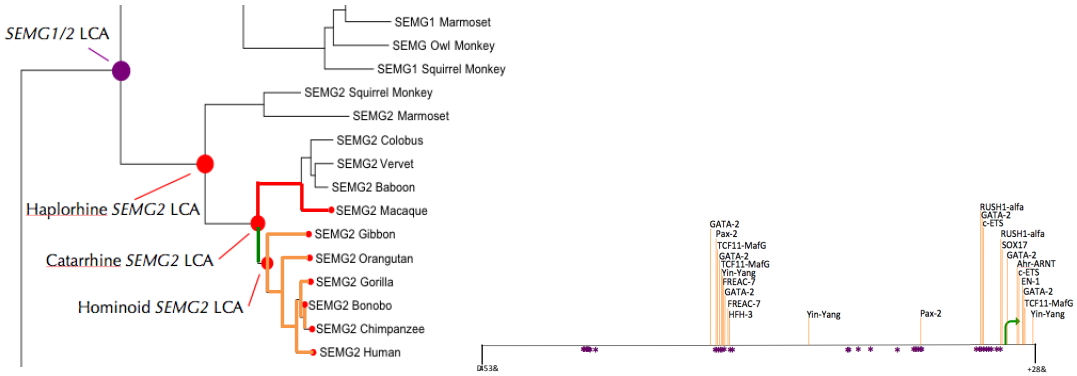

Figure 4.13: Schematic to find differences in TFBSs between macaque and hominoid *SEMG2*

Schematic of the method to identify possible important TFBSs between the extant hominoids (orange branches) and the macaque (red branch) – i.e. what changes have occurred on the green branch.

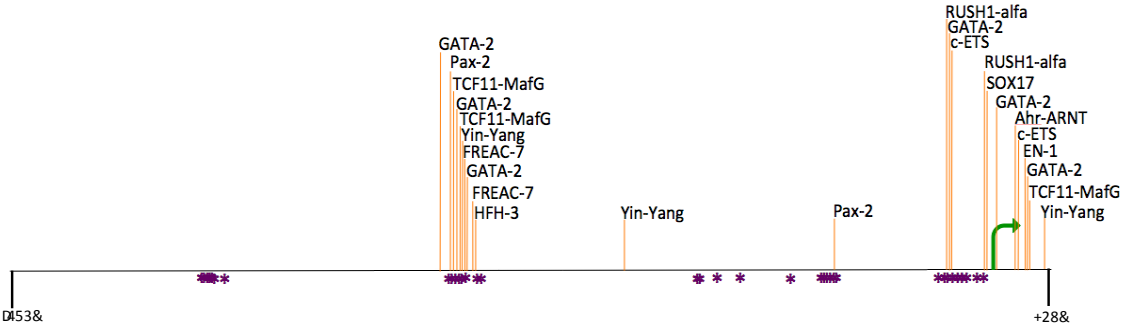

Figure 4.14: Hominoid unique, conserved TFBSs in *SEMG2*
Conserved transcription factors in the hominoid *SEMG2* proximal promoter that are unique to just the hominoids.

DISCUSSION

An uncoupling of non-coding and coding region evolution in the semenogelins

Semenogelins are the predominant protein in semen and are cross-linked by the prostate specific transglutaminase, TGM4, to form a coagulum of semen after ejaculation (Jonsson et al. 2006; Malm et al. 2007). In the hominoids there is a spectrum of semen coagulation levels that correlates with mating system (Dixson and Anderson 2002) and investigations into the level of selection on the protein-coding region of these genes reveals patterns that also correlate with mating system (more promiscuous species have higher rates of protein evolution than species with less promiscuous mating systems, Jensen-Seaman and Li 2003; Kingan et al. 2003; Dorus et al. 2004). However, the coding sequence also indicates that there have been pseudogenization events in both *SEMG1* (gorilla and gibbon) and *SEMG2* (chimpanzee and gorilla) (Fig 4.3); and SEMG1 is more abundant in seminal plasma than SEMG2 (Malm et al. 2007). In contrast, my expression data from the proximal promoter region does not show a correlation with mating system (Fig 4.6), evidence of psuedogenization that corroborates with predictions based on coding sequence predictions, or greater expression of *SEMG1* relative to *SEMG2* (Fig

4.5). This evidence suggests that there may be a decoupling of the evolution of the regulatory and the coding regions of the gene. Or, that the *in vitro* expression assay does not accurately recapitulate the *in vivo* expression of those genes, perhaps because there is a distal regulatory element required for the *in vivo* expression.

Semenogelins: evolution by gene duplication

After gene duplication it is important for the new paralogs to diverge and it has been shown that divergence via regulatory region changes is important for changing the level, timing, or tissue specificity of the promoter regions (Gagnon-Arsenault et al. 2013). One model for the evolution of these regions is duplication-degeneration-complementation (DDC), which hypothesizes that the state of subfunctionalization can be the result of splitting of parental regulatory modules, and neofunctionalization will be the result of a gain of regulatory module. A common method to compare sequences and predict functional regions is phylogenetic footprinting, which uses conservation as a means of detection. However, if the question is not what do these sequences have in common, but rather, how do these sequences differ, there is not a model for how to investigate this. I, therefore, am proposing to use a modified phylogenetic footprinting/ DDC method that utilizes not only extant sequences but ancestral sequences as well, in order to predict regulatory sequence changes differences between the semenogelin genes.

Using this method I have identified 21 and 37 unique, conserved TFBSs predictions in the regulatory region of *SEMG1* and *SEMG2* that could have a role in the divergent expression observed in the *in vitro* expression assay. Furthermore, I also identified 24 sites that are potential TFBSs gains in the hominoid lineage of *SEMG2* that causes an increase expression level compared to other species' *SEMG2*. I am predicting

that the difference between macaque and the hominoids in this case is a *gain* of factors by the hominoids and not a *loss* of factors by the macaque. One main reason for this hypothesis is that the expression of the macaque *SEMG2* is higher than the expression of *SEMG1* – similar to the result of the hominoid *SEMG1* vs. *SEMG2.* So, the most parsimonious explanation is that the change in expression between macaque and hominoid *SEMG2* is due to changes along the branch leading from the catarrhine LCA to the hominoid LCA. Adding additional Old World monkeys and New World monkeys to the *in vitro* expression system can test this hypothesis and allow us to more fully understand when divergence in expression occurred between these two genes. Furthermore, after making predictions, it would be useful to make mutant promoter constructs (adding or deleting TFBSs) to determine which of the predicted changes are contributory to expression differences.

References

Aumüller G, Seitz J, Lilja H, Abrahamsson P-A, von der Kammer H, Scheit K-H (1990) Species- and organ- specificity of secretory proteins derived from human prostate and seminal vesicles. *The Prostate* 17:31-40

Bagheri-Fam S, Ferraz C, Demaille J, Scherer G, Pfeifer D (2001) Comparative genomics of the *SOX9* region in human and *Fugu rubripes:* conservation of short regulatory sequence elements within large intergenic regions. *Genomics* 78:73-82

Bjartell A, Malm J, Möller C, Gunnarsson M, Lundwall Å, Lilja H (1996) Distribution and tissue expression of semenogelin I and II in man as demonstrated by *in situ* hybridization and immunocytochemistry. *Journal of Andrology* 17(1):17-26

Bourgeon F, Evrard B, Brillard-Bourdet M, Colleu D, Jégou B, Pineau C (2004) Involvement of semenogelin-derived peptides in the antibacterial activity of human seminal plasma. *Biology of Reproduction* 70:768-774

Brillard-Bourdet M, Réhault S, Juliano L, Ferrer M, Moreau T, Gauthier F (2002) Amidolytic activity of prostate acid phosphatase on human semenogelin-derive synthetic substrates. *Eur. J. Biochem.* 269:390-395

Carnahan SJ, Jensen-Seaman MI (2008) Hominoid seminal protein evolution and ancestral mating behavior. *Am J Primatol* 70:939-948

Canacci AM, Izumi K, Zheng Y, Gordetsky J, Yao JL, Miyamoto H (2011) Expression of semenogelins I and II and its prognostic significance in human prostate cancer. *The Prostate* 71:1108-1114

Castillo-Davis CI, Hartl DL, Guillaume A (2004) *cis*-Regulatory and protein evolution in orthologous and duplicate genes. *Genome Res* 14:1530-1536

Christensen TH, Prentice H, Gahlman R, Kedes L (1993) Regulation of the human cardiac/slow-twitch Troponin C gene by multiple, cooperative, cell-type-specific, and MyoD-Responsive elements. *Molecular and Cellular Biology* 13(11):6752-6765

Clauss A, Lilja H, Lundwall Å (2002) A locus on human chromosome 20 contains several genes expressing protease inhibitor domains with homology to whey acidic protein. *Biochem J.* 368:233-242

Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: more models, new heuristics and parallel computing. *Nature Methods* 9:772

De Lamirande E, Yoshida K, Yoshiike M, Iwamoto T, Gagnon C (2001) Semenogelin, the main protein of semen coagulum, inhibits human sperm capacitation by interfering

with the superoxide anion generated during this process. *Journal of Andrology* 22(4):672-679

de Lamirande E (2007) Semenogelin, the main protein of the human semen coagulum, regulates sperm function. *Semin Thromb Hemost* 33:60-68

Dorus S, Evans PD, Wyckoff GJ, Choi SS, Lahn BT (2004) Rate of molecular evolution of the seminal protein gene *SEMG2* correlates with levels of female promiscuity. *Nature Genetics* 36(12):1326-1329

Dixson AL and Anderson MJ (2002) Sexual selection, seminal coagulation and copulatory plug formation in primates. *Folia Primatol (Basel)* 73(2):63-69

Duarte JM, Cui L, Wall PK, Zhang Q, Zhang X, Leebens-Mack J, Ma H, Altman N, dePamphilis CW (2005) Expression pattern shifts following duplication indicative of subfunctionalization and neofunctionalization in regulatory genes of *Arabidopsis*. *Mol. Biol. Evol.* 23(2): 469-478

Edström AML, Malm J, Frohm B, Martellini JA, Giwercman A, Mörgelin M, Cole Am, Sørensen OE (2008) The major bactericidal activity of human seminal plasma is zinc-dependent and derived from fragmentation of the semenogelins. *The Journal of Immunology* 181:3413-3421

Ferreira Z, Seixas S, Andrés AM, Kretzschmar WW, Mullikin JC, Cherukuri PF, Cruz P, Swanson WJ, NISC Comparative Sequencing Program, Clark AG, Green ED, Hurle B. Reproduction and immunity-driven natural selection in the human *WFDC* locus. *Mol Biol Evol* 30(4):938-950

Flori F, Ermini L, La Sala GB, Nicoli A, Capone A, Focarelli R, Rosati F, Giovampaola CD (2008) The GPI-anchored CD52 antigen of the sperm surface interacts with semenogelin and participates in clot formation and liquefaction of human semen. *Molecular Reproduction and Development* 75:326-335

Gagnon-Arsenault I, Blanchet FCM, Rochette S, Diss G, Dubé AK, Landry CR (2013) Transcriptional divergence plays a role in the rewiring of protein interaction networks after gene duplication *Journal of Proteomics* 81:112-125

Gu X, Zhang Z, Huang W (2005) Rapid evolution of expression and regulatory divergences after yeast gene duplication. *PNAS* 102(3)707-712

Gumucio DL, Heilstedt-Williamson H, Gray TA, Tarlé SA, Shelton DA, Tagle DA, Slightom JL, Goodman M, Collins FS (1992) Phylogenetic footprinting reveals a nuclear protein which binds to silencer sequences in the human ϒ and ε globin genes. *Molecular and Cellular Biology* 12(11): 4919-4929

Hagstrom JE, Fautsch MP, Perdok M, Vrabel A, Wieben (1996) Exons lost and found: unusual evolution of a seminal vesicle transglutaminase substrate. *The Journal of Biological Chemistry* 271(35):21114-21119

Han MV, Demuth JP, McGrath CL, Casola C, Hahn MW (2009) Adaptive evolution of young gene duplicates in mammals. *Genome Res* 19:859-867

Haygood R, Fedrigo O, Hanson B, Yokoyama K-D, Wray GA (2007) Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution. *Nature Genetics* 39(9):1140-144

Hurle B, Swanson W, NISC Comparative Sequencing Program, Green ED (2007) Comparative sequence analyses reveal rapid and divergent evolutionary changes of the *WFDC* locus in the primate lineage. *Genome Research* 17:276-286

Jensen-Seaman MI, Li W-H (2003) Evolution of the hominoid semenogelin genes, the major proteins of ejaculated semen. *J Mol Evol* 57:261-270

Jonsson M, Linse S, From B, Lundwall Å, Malm J (2005) Semenogelins I and II bind zinc and regulate the activity of prostate-specific antigen. *Biochem J.* 387:447-453

Jonsson M, Lundwall Å, Linse S, From B, Malm J (2006) Truncated semenogelin I binds zinc and is cleaved by prostate-specific antigen. *Journal of Andrology* 27(4):542-547

Jonsson M, From B, Malm J (2009) Binding of semenogelin I to intact human spermatozoa studied by flow cytometry and surface plasmon resonance. *Journal of Andrology* 31(6):560-565

Kawano N, Yoshida M (2007) Semen-coagulating protein, SVS2, in mouse seminal plasma controls sperm fertility. *Biology of Reproduction* 76:353-361

Kingan SB, Tatar M, Rand D (2003) Reduced polymorphism in the chimpanzee semen coagulating protein, semenogelin I. *J Mol Evol* 57:159-169

Koistinen H, Soini T, Leinonen J, Hyden-Granskog C, Salo J, Halttunen M, Stenman UH, Seppala M, Koistinen R (2002) Monoclonal antibodies, immunoflourometric assay, and detection of human semenogelin in male reproductive tract: no association with in vitro fertilizing capacity of sperm. *Biol. Reprod* 66(3):624-628

Lenhard B, Sandelin A, Mendoza L, Engström P, Jareborg N, Wasserman WW (2003) Identification of conserved regulatory elements by comparative genome analysis. *Journal of Biology* 2:13

Lilja H (1985) A kallikrein-like serine protease in prostatic fluid cleaves the predominant seminal vesicle protein. *J. Clin. Invest.* 76:1899-1903

Lilja H, Oldbring J. Rannevik G, Laurell C-B (1987) Seminal vesicle-secreted proteins and their reactions during gelation and liquefaction of human semen. *J. Clin. Invest.* 80:281-285

Lilja H Oldbring J, Rannevik G, Laurell CB (1987) Seminal vesicle-secreted proteins and their reactions during gelation and liquefaction of human semen. *J. Clin. Invest.* 80:281-285

Lilja H (1990) Cell biology of semenogelin. *Andrologia* 22:132-141

Lilja H, Abrahamsson P-A, Lundwall Å (1989) Semenogelin, the predominant protein in human semen. *The Journal of Biological Chemistry.* 264(3): 1894-1900

Lilja H, Lundwall Å (1992) Molecular cloning of epididymal and seminal vesicular transcripts encoding a semenogelin-related protein. *Proc. Natl. Acad. Sci.* 89:4559-4563

Lin H-J, Luo C-W, Chen Y-H (2002) Localization of the transglutaminase cross-linking site in SVS III, a novel glycoprotein secreted from mouse seminal vesicle. *The Journal of Biological Chemistry* 277(5):3632-3639

Lundwall Å, Lazure C (1995) A novel gene family encoding proteins with highly differing structure because of a rapidly evolving exon. *FEBS Letters* 374:53-56

Lundwall Å (1996) The cloning of a rapidly evolving seminal-vesicle-transcribed gene encoding the major clot-forming protein of mouse semen. *Eur. J. Biochem.* 235:424-430

Lundwall Å (1996) The structure of the semenogelin gene locus: nucleotide sequence of the intergenic and the flanking DNA. *Eur. J. Biochem.* 235:466-470

Lundwall Å and Ulvsbäck M (1996) The gene of the protease inhibitor SKALP/Elafin is a member of the rest gene family. *Biochemical and Biophysical Research Communications* 221:323-337

Lundwall Å (1998) The cotton-top tamarin carries an extended semenogelin I gene but no semenogelin II gene. *Eur. J. Biochem.* 255:45-51

Lundwall Å, Olsson AYM (2001) Semenogelin II gene is replaced by a truncated LINE1 repeat in the cotton-top tamarin. *Biology of Reproduction* 65:420-425

Lundwall Å, Bjartell A, Olsson AY, Malm J (2002) Semenogelin I and II, the predominant seminal plasma proteins, are also expressed in non-genital tissues. *Molecular Human Reproduction* 8(9):805-810

Lundwall Å (2007) A locus on chromosome 20 encompassing genes that are highly expressed in the epididymis. *Asian J. Androl* 9:540-544

Lundwall Å, Clauss A (2011) Genes encoding WFDC- and kunitz-type protesase inhibitor domains: are they related? *Biochem. Soc. Trans*. 39:1398-1402

Malm J, Hellman J, Magnusson H, Laurell C-B, Lilja H (1996) Isolation and characterization of the major gel proteins in human semen, semenogelin I and semenogelin II. *Eur. J. Biochem* 238:48-53

Malm J, Jonsson M, Frohm B, Linse S (2007) Structural properties of semenogelin I. *FBS Journal* 274:4503-4510

Martan J, Shepherd BA (1976) The role of the copulatory plug in reproduction of the guinea pig. *J Exp Zool* 196(1):79-98

Mitra A, Richardson RT, O'Rand MG (2010) Analysis of recombinant human semenogelin as an inhibitor of human sperm motility. *Biology of Reproduction* 82:489-496

Miyano S, Yoshida K, Yoshiike M, Miyamoto C, Furuichi Y, Iwamoto T (2003) A large deletion of the repeat site in semenogelin I is not involved in male infertility. *Int J Mol Med* 11(4):435-440

Papp B, Pál C, Hurst LD (2003) Evolution of *cis*-regulatory elements in duplicated genes of yeast. *TRENDS in Genetics* 19(8):417-422

Peter A, Lilja H, Lundwall Å, Malm J (1998) Semenogelin I and semenogelin II, the major gel-forming proteins in human semen, are substrates for transglutaminase. *Eur. J. Biochem.* 252:216-221

Rajesh A Madhubabu G, Yenugu S (2011) Identification and characterization of *Wfdc* gene expression in the male reproductive tract of the rat. *Molecular Reproduction and Development.* DOI 10.1002/mrd.21361

Robert M, Gagnon C (1995) Sperm motility inhibitor from human seminal plasma: association with semen coagulum. *Human Reproduction* 10:2192-2197

Robert M, Gagnon C (1999) Semenogelin I: a coagulum forming, multifunctional seminal vesicle protein. *Cell. Mol. Life Sci* 55:944-960

Sandelin A, Wasserman WW, Lenhard B (2004a) ConSite: web-based prediction of regulatory elements using cross-species comparison. *Nucleic Acids Research* 32:W249-W252

Sandelin A, Alkema W, Engström P, Wasserman WW, Lenhard B (2004b) JASPAR: an open-access database for eukaryotic transcription factor binding profiles. *Nucleic Acids Research* 32:D91-D94

Sato I, Yoshiike M, Yamasaki T, Yoshida K, Takano S Mukai T, Iwamoto T (2001) A dot-blot-immunoassay for semen identification using a polyclonal antibody against semenogelin, a powerful seminal marker. *Forensic Science International* 122:27-34

Ureta-Vidal A, Ettwiller L, Birney E (2003) Comparative genomics: genome-wide analysis in metazoan eukaryotes. *Nature Review Genetics* 4:251-261

Ulvsbäck M, Lazure C, Lilja H, Spurr NK, Rao VVNG, Löffler C, Hansmann I, Lundwall Å (1992) Gene structure of semenogelin I and II. *The Journal of Biological Chemistry.* 267(25):18080-18084

Ulvsbäck M, Lundwall Å (1997) Cloning of the semenogelin II gene of the rhesus monkey: Duplications of 360 bp extend the coding region in man, rhesus monkey and baboon. *Eur J. Biochem.* 245:25-31

Valtonen-André C, Olsson AY, Nayudu PL, Lundwall Å (2005) Ejaculates from the common marmoset (*Callithrix jacchus*) contain semenogelin and beta-microseminoprotein but not prostate-specific antigen. *Molecular Reproduction and Development* 71:247-255

Valtonen-André C, Olsson AY, Kullberg M, Nayudu PL, Lundwall Å (2007) The common marmoset (*Callithrix jacchus*) has two very similar semenogelin genes as the result of gene conversion. *Biology of Reproduction* 76:604-610

Voss R (1979) Male accessory glands and the evolution of copulatory plugs in rodents. *Occasional Papers in Zoology*, University of Michigan 689:1-27

Wang Z, Widgren EE, Sivashanmugam P, O'Rand MG, Richardson RT (2005) Association of eppin with semenogelin on human spermatozoa. *Biology of Reproduction* 72:1064-1070

Wasserman WW, Palumbo M, Thompson W, Fickett JW, Lawrence CE (2000) Human-mouse genome comparisons to locate regulatory sites. *Nature Genetics* 26:225-228

Wasserman WW, Sandelin A (2004) Applied bioinformatics for the identification of regulatory elements. *Nature Reviews Genetics* 5:276-287

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-entric information. *Nucl. Acids Res.* 41(D1): D561-D565.

Wu C, Orozco C, Boyer J, Leglise M, Goodale J, Batalov S, Hodge CL, Haase J, Janes J, Huss JW 3rd, Su AI (2009) BioGPS: an extensible and customizable portal for querying and organizing gene annotation resources. *Genome Biol.* 10(11):R130.

Yoshida K, Yamaskai T, Yoshiike M, Takano S, Sato I, Iwamoto T (2003) Quantification of seminal plasma motility inhibitor/semenogelin in human seminal plasma. *Journal of Andrology* 24(6):878-884

Yoshida K, Krasznai ZT, Yoshiike M, Kawano N, Yoshida M, Morisawa M, Tóth Z, Bazsáné T, Iwamoto T (2009) Functional implications of membrane modification with semenogelins for inhibition of sperm motility in humans. *Cell motility and the cytoskeleton* 66:99-108

Zalensky AO, Yau P, Breneman JW, Bradbury EM (1993) The abundant 19-kilodalton protein associated with human sperm nuclei that is related to seminal plasma α-inhibins. *Molecular Reproduction and Development* 36:164-173

Zani M-L, Brillard-Bourdet M, Lazure C, Juliano L, Courty Y, Gauthier F, Moreau T (2001) Purification and characterization of active recombinant rat kallikren rK9. *Biochimica et Biophysica Acta* 1547:387-396

Zhang J (2003) Evolution by gene duplication: an update. *TRENDS in Ecology and Evolution* 18(6):292-298

Zhang Y, Want Z, Zhang J, Farmer B, Lim SH (2008) Semenogelin I expression in myeloma cells can be upregulated pharmacologically. *Leuk Res* 32(12):1889-1894

Zhang Y, Wang Z, Zhang J, Lim SH (2009) Core promoter sequence of SEMG I spans between the two putative GATA-1 binding domains and is responsive to IL-4 and IL-6 in myeloma cells. *Leuk Res.* 33(1):166-169

Zou Y, Su Z, Huang W, Gu X (2012) Histone modification pattern evolution after yeast gene duplication. *BMC Evolutionary Biology* 12:111

Chapter 5: Final Thoughts

Recently Antony Dean stated that the in study of evolution there are only two questions asked: what makes things different and what makes them the same (2010). In primate biology a lot is known anatomically and behaviorally of what groups species and what separates them. Also, through comparative genomics, the similarities between different species' genomes are now known. For instance, a recent comparison of human, chimpanzee, and bonobo showed that the genomes range from 98.7 percent to 99.6 percent identical (Prüfer et al. 2012). Yet, there are very large phenotypic differences between these three species. What accounts for this? What makes them different? King and Wilson (1975) hypothesized that the differences lie in the regulatory sequences. While there has been evidence that supports this hypothesis, there is also evidence to support the importance of phenotypic changing coding sequence differences (reviewed in Carroll 2005). Which leads to the reasonable assumption that it has to be both; therefore this study is a combination of coding and noncoding sequence analysis and functional noncoding sequence testing.

The first study is a computational study that looked at 653 seminal plasma protein-coding genes, estimated the rate of selection, and investigated if that rate is related to mating system. The hypothesis was driven, perhaps naively, by single gene studies showing elevated rates of evolution for reproductive proteins and thereby leading to conclusions that reproductive genes evolve rapidly. However, do seminal plasma genes (a reproductive fluid, and therefore made of reproductive proteins) *as a whole* respond to selection in the same way because known *subsets* are under positive selection? While the data overall did not support this hypothesis (and in fact was the opposite; Fig 2.1),

through parsing the data and examining it from a functional perspective, interesting trends were discovered. First, that seminal plasma genes are highly tissue specific and the rate of protein change is positively correlated with the level of tissue specificity (Fig 2.5). This was not a trend observed for the control data set, but is consistent with other tissue specific gene sets. Furthermore, when grouped into functional categories according to their role in specific biological processes, the seminal plasma genes in the categories of reproduction, immune system function, response to stimulus, and metabolic processes evolve more rapidly than genes in more ubiquitous functions (e.g. cell cycle, homeostasis; Fig 2.7). The fact that these categories were singled out as being more rapidly evolving is perhaps not surprising; reproductive genes, immune system genes, and metabolic genes have all been implicated in positive selection in other (single gene) studies. Additionally, these functions are important functions for the general purpose of semen – making sure the sperm survive the harsh environment of the female reproductive tract, making sure the sperm have enough energy to swim to the egg, and fertilization of the egg. Interestingly, the function of the genes that fall in the overlap between the top ten percent of tissue specific genes and the top ten percent of *Ka/Ks* are in these four categories. So selection must be acting on these genes due to these functional attributes.

To further investigate this, it would be interesting to do another large-scale analysis of the corresponding 653 noncoding regions associated with these genes. While there is not a common, method in the field of studying noncoding regions, there are several approaches that have have been published. The first is a similar test to *Ka/Ks* where *Ka* is the nucleotide substitution rate in the *promoter* region and *Ks* is the synonymous substitution rate of the coding sequence and then analyzed in a similar way

to how one would analyze coding sequences (Wong and Nielson 2004). A second method is to compare the substitution rate of the promoter to the substitution rate in the intronic regions (taking into account and removing the first intron, which may contain regulatory elements, as well as splice sites) to see if there is a different rate of substitution in the regulatory noncoding sequence versus other gene-proximal noncoding regions (Haygood et al. 2007). However, even with sophisticated models of testing sequences, there still has to be a way to functionally test if predictions reflect the *in vivo* system. The ideal experiment would be to test the specific reproductive tissues in which these genes are expressed using chromatin immunoprecipitation (ChIP) and its derivatives to find specific binding proteins that could be regulating the transcription of the genes and then comparing the results across species. However, as stated earlier there is limited availability to these tissues, so this study would be difficult. Studying proteomics or transcritptomics of seminal plasma in different species are great methods to determine what the end point of transcription and translation, but they don't approach the question of which regulatory sequences are important for species specific differences, rather just that there are (or are not) differences.

One way to functionally validate specific noncoding sequences and compare functionality between species is to use an *in vitro* expression system like the luciferase vector system. There are a lot of important variables that need to be considered for a successful *in vitro* study: what sequence to use as the driving promoter, what cell to express the vector, what kind of stimulation is needed to to mimic the *in vitro* environment? Furthermore, if there are cofactors needed to express a certain gene, are they expressed in the cell line of choice or do they need to be added? Finally, how does

one control for all of the experimental system conditions? One method of controlling for transfection efficiency is the use of a co-transfected control vector. This vector would ideally be expressed in the cell at a low, consistent amount that can then be used to compare to the experimental vector as a means of normalization. However in testing the effectiveness of *Renilla* luciferase vector as a control vector, it was determined that the 'control' vector was not expressed at a low, consistent level and was not only affected by experimental condition, but actually *affected the experimental outcome*. Therefore, it would not be an appropriate control for the experiment and instead the use of increased replicates and normalization of all experimental luciferase vector expression to a promoterless luciferase vector expression values were used.

In this study the sequences to use were based on previously published promoter bashing experiments for three seminal plasma genes: *TGM4, SEMG1,* and *SEMG2.* These genes were chosen due to the evidence of rapid evolution in the coding sequence in species that have promiscuous mating systems, possible pseudogenization in species with low levels of sperm competition, and differing protein abundance in seminal plasma between human and chimpanzee. The proximal promoter region of *TGM4*, *SEMG1*, and *SEMG2* were compared across seven species: six hominoids (human, chimpanzee, bonobo, gorilla, orangutan, and gibbon) and one Old World monkey (macaque). After initial optimizations of the experimental system, the human promoter region of *TGM4* did not drive the expression of luciferase greater than an empty luciferase vector. Unfortunately, even with modifying the promoter region used to instead using the *exact* region used in previously published work, this promoter would not drive expression of the luciferase gene in this system.

Expression of the semenogelins (even though *SEMG1* is expressed lower than the promoterless vector) showed different levels of expression between duplicated genes. Although the initial hypotheses of mating systems affecting expression was not supported, the results led to another interesting question: how do genes differentiate in their regulatory sequences after gene duplication? While this seems like a very straightforward question, there is not a described method to answer *this* question. So, thinking outside the proverbial box and mix-n-matching a few different approaches into one was a necessity. First, phylogenetic footprinting was used to determine what functional elements could be predicted in the promoter region based on conservation between sequences. Using this approach provides more focused results than just using TFBSs prediction software alone as it requires both the presence of a TFBS consensus sequence and the conservation of said site between species. In addition to extant sequences, ancestral sequences can also be used in the footprinting; which leads to the combination of phylogenetic footprinting results with DDC (the duplication-degeneration-complementation model of evolution post-duplication). The combination of these two methods is useful in order to get a more robust insight into the evolution of duplicated regions. This approach allowed the prediction of TFBSs that may be important in the differential expression of *SEMG1* and *SEMG2* stemming from their *initial* duplication/divergence, as well as differences between an Old World monkey *SEMG2* and hominoid *SEMG2*. The results, while only a prediction, can further be used to understand the expression differences through functional studies. Using a reporter vector (like that described above), an inserted sequence can be modified using site directed

mutagenesis to remove or add a binding site and then can be tested for its ability to drive expression.

Using seminal plasma genes to address the two big questions in evolutionary biology (what makes species the same, and what makes them different) we have found that the hominoid seminal plasma coding gene sequences are largely conserved yet patterns of change can be observed in genes with a certain expression pattern or function. Additionally, using a novel approach to studying the evolution of regulatory elements after gene duplication has identified several potential transcription factor-binding sites, which could help explain expression differences observed in a recently duplicated seminal plasma gene. Understanding these differences and attempting to identify when changes occur can lead to a better understanding of the evolution of primate biology.

REFERENCES

Carroll SB (2005) Evolution at two levels: on genes and form. *PLoS Biology* 3(7):e245

Dean AM (2010) The future of molecular evolution. *EMBO reports* 11(6):409

Haygood R, Fedrigo O, Hanson B, Yokoyama K-D, Wray GA (2007) Promoter regions of many neural- and nutrition-related genes have experienced positive selection during human evolution. *Nature Genetics* 39(9):1140-144

King MC, Wilson AC (1975) Evolution at two levels in humans and chimpanzees. Science 188:107-116

Prüfer K, Munch K, Hellmann I, Akagi K, Miller JR, Walenz B, Koren S, Sutton G, Kodira C, Winer R, Knight JR, Mullikin JC, Meader SJ, Ponting CP, Lunter G, Higashino S, Hobolth A, Dutheil J, Karakoç, Alkan C, Sajjadian S, Catacchio CR, Ventura M, Marques-Bonet T, Eichler EE, André C, Atencia R, Mugisha L, Junhold J, Patterson N, Siebauer M, Good JM, Fischer A, Ptak SE, Lachmann M, Symer DE, Mailund T, Schierup MH, Andrés AM, Kelso J, Pääbo S (2012) The bonobo genome compared with the chimpanzee and human genomes. *Nature* 486:527-531

Wong WSW, Neilson R (2004) Detecting selection in noncoding regions of nucleotide sequences. *Genetics* 167:949-958

Appendix 1: Custom Perl scripts used in Chapter 1

Script to randomly pick genes from the genome

```
#!/usr/bin/perl - w

$geneseqs = $ARGV[0];
$outfile = "randomgenename.out2";
#assigning a number to each of the gene seq names, which are the lines in the file

open (geneseqs, $geneseqs) || die "Find no input\n";
$c=1;
        while (<geneseqs>){
          $line = $_; chomp($line);
          $genename{$c} = $line;
          $c = $c+1;
}

#randomly chose 700 numbers between 1 and 18305


open (OUT, ">$outfile");
$d=1;
        until ($d == 700) {
          $pick = int(rand 17634)+1;
          print OUT "$genename{$pick}\n";
          $d = $d+1;
}

close (geneseqs);
close (OUT);
```

Script to make multi-species alignments

```
#!/usr/bin/perl - w

$humangenes = $ARGV[0];
$chimpgenes = $ARGV [1];
$gorillagenes = $ARGV [2];
$oranggenes = $ARGV [3];
$gibbongenes = $ARGV [4];
$macaquegenes = $ARGV [5];

open (Chimp, $chimpgenes) || die "Find no input\n";
        while (<Chimp>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Chimpanzee"}=$seq{$name}{"Chimpanzee"}.$line;}
}
close (Chimp);

open (Gorilla, $gorillagenes) || die "Find no input\n";
        while (<Gorilla>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Gor"}=$seq{$name}{"Gor"}.$line;}
}
close (Gorilla);

open (Orang, $oranggenes) || die "Find no input\n";
        while (<Orang>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Oran"}=$seq{$name}{"Oran"}.$line;}
}
close (Orang);
```

```
open (Gibbon, $gibbongenes) || die "Find no input\n";
        while (<Gibbon>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Gib"}=$seq{$name}{"Gib"}.$line;}
}
close (Gibbon);

open (Macaque, $macaquegenes) || die "Find no input\n";
        while (<Gorilla>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Mac"}=$seq{$name}{"Mac"}.$line;}
}
close (Macaque);

open (Human, $humangenes) || die "Find no input\n";
        while (<Human>){
          $line=$_; chomp ($line);
          if ($line=~/^>/){$name=$';}
          else {$seq{$name}{"Hum"}=$seq{$name}{"Hum"}.$line;}
        $outfile = $name.".upmfa" || die "could not make outfile\n";
        open (OUT, ">$outfile");
        print OUT
">Human\n$seq{$name}{'Hum'}\n>Chimp\n$seq{$name}{'Chimpanzee'}\n>Gorilla\n$seq
{$name}{'Gor'}\n>Orang\n$seq{$name}{'Oran'}\n>Gibbon\n$seq{$name}{'Gib'}\n>Macaq
ue\n$seq{$name}{'Mac'}\n";

}
close (Human);
```

Script to filter alignments based on if non-human sequence had 70% of human length

```
#!/usr/bin/perl -w

foreach $infile (@ARGV) {
	$outfile = $infile.".70";
	open (OUT, ">$outfile");

	open (IN, $infile);
	while (<IN>) {
	  $line = $_; chomp ($line); $line=~s/\r//g;
	  if ($line=~/^>/){$spp=$';}
	  else {$seq{$spp}=$line;}
	}

	foreach $spp (keys %seq) {
	  $ungap{$spp} = $seq{$spp};
		$ungap{$spp} =~ s/-//g;
	  $length{$spp} = length ($ungap{$spp});
	  print "$spp\t$length{$spp}\n";
	}

	$HC = $length{'Chimp'} / $length{'Human'};
	$HG = $length{'Gorilla'} / $length{'Human'};
	$HO = $length{'Orang'} / $length{'Human'};
	$Hgi = $length{'Gibbon'} / $length{'Human'};
	$HM = $length{'Macaque'} / $length{'Human'};

	print OUT ">Human\n$seq{'Human'}\n";

	if ($HC >= .7) {print OUT ">Chimp\n$seq{'Chimp'}\n";}
	if ($HG >= .7) {print OUT ">Gorilla\n$seq{'Gorilla'}\n";}
	if ($HO >= .7) {print OUT ">Orang\n$seq{'Orang'}\n";}
```

```
        if ($Hgi >= .7) {print OUT ">Gibbon\n$seq{'Gibbon'}\n";}
        if ($HM >= .7) {print OUT ">Macaque\n$seq{'Macaque'}\n";}
}
```

Script used to run PAML with a uniform model and subsequently parse the output

```
#!/usr/bin/perl -w  run as: perl HCGOSM_PAMLer.pl *.seq.70

$outfile = "HCGOSM_uniform.paml.out";
open (OUT, ">$outfile")|| die "no make outifle\n";
print OUT "Gene\tlnL\ttree_w\n";

foreach $infile (@ARGV) {
$infile=~/(\w+)\.upmfa\.70/;$core=$1;

        open (CTL, ">codeml.ctl")||die "no make ctl file\n";
        print CTL "\nseqfile = $infile\ntreefile = HCGOSMtree.txt\noutfile = $core.out1\n\n";
        print CTL "noisy = 9\nverbose = 0\nrunmode = 0\n\nseqtype = 1\nCodonFreq =
2\nclock = 0\nmodel = 0\n\n";
        print CTL "icode = 0\n\nfix_kappa = 0\nkappa = 2\nfix_omega = 0\nomega = 0\n";
        print CTL "fix_alpha = 1\nalpha = 0\nMalpha = 0\n\n";
        print CTL "getSE = 0\nRateAncestor = 1\n\nfix_blength = 0\nmethod = 0\n";
        close (CTL);
        system ("/home/seamanm/Desktop/paml44/bin/codeml");
        open (TMP, "$core.out1")||die "no paml outfile found\n";
        while (<TMP>){
          $line=$_;chomp($line);
          if ($line =~ /^lnL\(\S+\s+\d+\s+\S+\s+\d+\)\S\s+(\S+)/){$lnL{$core}=$1;}
          if ($line =~ /^omega\s+\(\S+\)\s\S\s+(\S+)/){$treew{$core}=$1;}
        }
        print OUT "$core\t$lnL{$core}\t$treew{$core}\n";
        close (TMP);
        #close while loop

} #close foreach loop

close (OUT);
```

Script to run PAML for the free model and subsequently parse the output

```
#!/usr/bin/perl -w  run as: perl HCGOSM_PAMLer.pl *.seq.70

$outfile = "HCGOSM_free.paml.out";
open (OUT, ">$outfile")|| die "no make outifle\n";
print OUT
"Gene\tlnL\tHML_w\tCML_w\tGML_w\tOML_w\tSML_w\tMML_w\tHCML_w\tGOML_w\tO
SML_w\tHCng_w\tHC_dN\tHC_dS\tHGng_w\tHG_dN\tHG_dS\tHOng_w\tHO_dN\tHO_dS
\tHSng_w\tHS_dN\tHS_dS\tHMng_w\tHM_dN\tHM_dS\tCGng_w\tCG_dN\tCG_dS\tCOng
_w\tCO_dN\tCO_dS\tCSng_w\tCS_dN\tCS_dS\tCMng_w\tCM_dN\tCM_dS\tGOng_w\tGO
_dN\tGO_dS\tGSng_w\tGS_dN\tGS_dS\tGMng_w\tGM_dN\tGM_dS\tOSng_w\tOS_dN\tO
S_dS\tOMng_w\tOM_dN\tOM_dS\tSMng_w\tSM_dN\tSM_dS\n";

foreach $infile (@ARGV) {
$infile=~/(\w+)\.upmfa\.70/;$core=$1;

        open (CTL, ">codeml.ctl")||die "no make ctl file\n";
        print CTL "\nseqfile = $infile\ntreefile = HCGOSMtree.txt\noutfile = $core.out2\n\n";
        print CTL "noisy = 9\nverbose = 0\nrunmode = 0\n\nseqtype = 1\nCodonFreq =
2\nclock = 0\nmodel = 1\n\n";
        print CTL "icode = 0\n\nfix_kappa = 0\nkappa = 2\nfix_omega = 0\nomega = 0\n";
        print CTL "fix_alpha = 1\nalpha = 0\nMalpha = 0\n\n";
        print CTL "getSE = 0\nRateAncestor = 1\n\nfix_blength = 0\nmethod = 0\n";
        close (CTL);
        system ("/home/seamanm/Desktop/paml44/bin/codeml");
        open (TMP, "$core.out2")||die "no paml outfile found\n";
        while (<TMP>){
          $line=$_;chomp($line);
        #ML_PARSE
          if ($line =~ /^lnL\(\S+\s+\d+\s+\S+\s+\d+\)\S\s+(\S+)/){$lnL{$core}=$1;}
          if ($line =~ /^\s+7\.\.8\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$Ogi_ML{$core}=$1;
$Ogi_MLdN{$core}=$2;}
          if ($line =~ /^\s+8\.\.9\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$GO_ML{$core}=$1;
```

```
$GO_MLdN{$core}=$2;}
        if ($line =~ /^\s+9\.\.10\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$HC_ML{$core}=$1;
$HC_MLdN{$core}=$2;}
        if ($line =~ /^\s+10\.\.1\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$H_ML{$core}=$1;
$H_MLdN{$core}=$2;}
        if ($line =~ /^\s+10\.\.2\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$C_ML{$core}=$1;
$C_MLdN{$core}=$2;}
        if ($line =~ /^\s+9\.\.3\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$G_ML{$core}=$1;
$G_MLdN{$core}=$2;}
        if ($line =~ /^\s+8\.\.4\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$O_ML{$core}=$1;
$O_MLdN{$core}=$2;}
        if ($line =~ /^\s+7\.\.5\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$gi_ML{$core}=$1;
$gi_MLdN{$core}=$2;}
        if ($line =~ /^\s+7\.\.6\s+\S+\s+\S+\s+\S+\s+(\S+)\s+(\S+)/) {$M_ML{$core}=$1;
$M_MLdN{$core}=$2;}

      #NG_PARSE
        if ($line =~ /^Chimp\s+(\S+)\s+\((\S+)\s+(\S+)\)/)
{$HC{$core}=$1;$HC_dN{$core}=$2;$HC_dS{$core}=$3;}
        if ($line =~ /^Gorilla\s+(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)/)
{$HG{$core}=$1;$HG_dN{$core}=$2;$HG_dS{$core}=$3;$CG{$core}=$4;$CG_dN{$cor
e}=$5;$CG_dS{$core}=$6;}
        if ($line =~
/^Orang\s+(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)/
)
{$HO{$core}=$1;$HO_dN{$core}=$2;$HO_dS{$core}=$3;$CO{$core}=$4;$CO_dN{$cor
e}=$5;$CO_dS{$core}=$6;$GO{$core}=$7;$GO_dN{$core}=$8;$GO_dS{$core}=$9;}
        if ($line =~
/^Gibbon\s+(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)
\s*(\S+)\s+\((\S+)\s+(\S+)\)/)
{$HS{$core}=$1;$HS_dN{$core}=$2;$HS_dS{$core}=$3;$CS{$core}=$4;$CS_dN{$core}
=$5;$CS_dS{$core}=$6;$GS{$core}=$7;$GS_dN{$core}=$8;$GS_dS{$core}=$9;$OS{$c
ore}=$10;$OS_dN{$core}=$11;$OS_dS{$core}=$12;}
```

```
        if ($line =~
/^Macaque\s+(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+
)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)\s*(\S+)\s+\((\S+)\s+(\S+)\)/)
{$HM{$core}=$1;$HM_dN{$core}=$2;$HM_dS{$core}=$3;$CM{$core}=$4;$CM_dN{$cor
e}=$5;$CM_dS{$core}=$6;$GM{$core}=$7;$GM_dN{$core}=$8;$GM_dS{$core}=$9;$O
M{$core}=$10;$OM_dN{$core}=$11;$OM_dS{$core}=$12;$SM{$core}=$13;$SM_dN{$c
ore}=$14;$SM_dS{$core}=$15;}
 }


        if ($Ogi_MLdN{$core}=~ /0.0000/){$Ogi_ML{$core} = '0.0000';}
        if ($GO_MLdN{$core}=~ /0.0000/){$GO_ML{$core} = '0.0000';}
        if ($HC_MLdN{$core}=~ /0.0000/){$HC_ML{$core} = '0.0000';}
        if ($H_MLdN{$core}=~ /0.0000/){$H_ML{$core} = '0.0000';}
        if ($C_MLdN{$core}=~ /0.0000/){$C_ML{$core} = '0.0000';}
        if ($G_MLdN{$core}=~ /0.0000/){$G_ML{$core} = '0.0000';}
        if ($O_MLdN{$core}=~ /0.0000/){$O_ML{$core} = '0.0000';}
        if ($gi_MLdN{$core}=~ /0.0000/){$gi_ML{$core} = '0.0000';}
        if ($M_MLdN{$core}=~ /0.0000/){$M_ML{$core} = '0.0000';}


        if ($HC_dN{$core} =~ /0.0000/){$HC{$core} = '0.0000';}
        if ($HG_dN{$core} =~ /0.0000/){$HG{$core} = '0.0000';}
        if ($HO_dN{$core} =~ /0.0000/){$HO{$core} = '0.0000';}
        if ($HS_dN{$core} =~ /0.0000/){$HS{$core} = '0.0000';}
        if ($HM_dN{$core} =~ /0.0000/){$HM{$core} = '0.0000';}
        if ($CG_dN{$core} =~ /0.0000/){$CG{$core} = '0.0000';}
        if ($CO_dN{$core} =~ /0.0000/){$CO{$core} = '0.0000';}
        if ($CS_dN{$core} =~ /0.0000/){$CS{$core} = '0.0000';}
        if ($CM_dN{$core} =~ /0.0000/){$CM{$core} = '0.0000';}
        if ($GO_dN{$core} =~ /0.0000/){$GO{$core} = '0.0000';}
        if ($GS_dN{$core} =~ /0.0000/){$GS{$core} = '0.0000';}
        if ($GM_dN{$core} =~ /0.0000/){$GM{$core} = '0.0000';}
```

```
        if ($OS_dN{$core} =~ /0.0000/){$OS{$core} = '0.0000';}
        if ($OM_dN{$core} =~ /0.0000/){$OM{$core} = '0.0000';}
        if ($SM_dN{$core} =~ /0.0000/){$SM{$core} = '0.0000';}



    print OUT
"$core\t$lnL{$core}\t$H_ML{$core}\t$C_ML{$core}\t$G_ML{$core}\t$O_ML{$core}\t$gi_
ML{$core}\t$M_ML{$core}\t$HC_ML{$core}\t$GO_ML{$core}\t$Ogi_ML{$core}\t$HC{$co
re}\t$HC_dN{$core}\t$HC_dS{$core}\t$HG{$core}\t$HG_dN{$core}\t$HG_dS{$core}\t$H
O{$core}\t$HO_dN{$core}\t$HO_dS{$core}\t$HS{$core}\t$HS_dN{$core}\t$HS_dS{$core
}\t$HM{$core}\t$HM_dN{$core}\t$HM_dS{$core}\t$CG{$core}\t$CG_dN{$core}\t$CG_dS
{$core}\t$CO{$core}\t$CO_dN{$core}\t$CO_dS{$core}\t$CS{$core}\t$CS_dN{$core}\t$C
S_dS{$core}\t$CM{$core}\t$CM_dN{$core}\t$CM_dS{$core}\t$GO{$core}\t$GO_dN{$cor
e}\t$GO_dS{$core}\t$GS{$core}\t$GS_dN{$core}\t$GS_dS{$core}\t$GM{$core}\t$GM_d
N{$core}\t$GM_dS{$core}\t$OS{$core}\t$OS_dN{$core}\t$OS_dS{$core}\t$OM{$core}\t$
OM_dN{$core}\t$OM_dS{$core}\t$SM{$core}\t$SM_dN{$core}\t$SM_dS{$core}\n";
    close (TMP);
    #close while loop

} #close foreach loop

close (OUT);
```

Script used to run PAML for branch models and subsequently parse the output

```
#!/usr/bin/perl -w  run as: perl HCGOSM_PAMLer.pl *.seq.70

$outfile = "HCGOSM_OS_free.paml.out";
open (OUT, ">$outfile")|| die "no make outifle\n";
print OUT "Gene\tlnL\tbranch_w\ttree_w\n";

foreach $infile (@ARGV) {
$infile=~/(\w+)\.upmfa\.70/;$core=$1;

        open (CTL, ">codeml.ctl")||die "no make ctl file\n";
        print CTL "\nseqfile = $infile\ntreefile = HCGOSMtree.txt\noutfile =
$core.out20\n\n";
        print CTL "noisy = 9\nverbose = 0\nrunmode = 0\n\nseqtype = 1\nCodonFreq =
2\nclock = 0\nmodel = 2\n\n";
        print CTL "icode = 0\n\nfix_kappa = 0\nkappa = 2\nfix_omega = 0\nomega = 0\n";
        print CTL "fix_alpha = 1\nalpha = 0\nMalpha = 0\n\n";
        print CTL "getSE = 0\nRateAncestor = 1\n\nfix_blength = 0\nmethod = 0\n";
        close (CTL);
        system ("/home/seamanm/Desktop/paml44/bin/codeml");
        open (TMP, "$core.out20")||die "no paml outfile found\n";
        while (<TMP>){
          $line=$_;chomp($line);
          if ($line =~ /^lnL\(\S+\s+\d+\s+\S+\s+\d+\)\S\s+(\S+)/){$lnL{$core}=$1;}
          if ($line =~
/^w\s\(\S+\)\s\S+\s\S+\s+(\S+)\s(\S+)/){$treew{$core}=$1;$branchw{$core}=$2;}
          if ($line =~ /\s+7\.\.8\s+\S+\s+\S+\s+\S+\s+\S+\s+\S+\s+(\S+)/){$dNbranch{$core}=$1;}
        }

          if ($dNbranch{$core} =~ /0.0000/){$branchw{$core}= '0.0000';}

        print OUT "$core\t$lnL{$core}\t$branchw{$core}\t$treew{$core}\n";
```

```
        close (TMP);
        #close while loop

} #close foreach loop

close (OUT);
```

Script to calculate Tau

Written by Dr. Michael I. Jensen-Seaman

```
#!/usr/bin/perl -w

$infile=$ARGV[0];
$annfile=$ARGV[1];
$gnffile=$ARGV[2];
$outfile=$infile.".tau";

open (ANN, "$annfile")||die "no open annotation file\n";
while (<ANN>){
        $line=$_;chomp ($line);
        unless ($line=~/^#/){
          @data=split /\t/, $line;
          $id=$data[0];$descr{$id}=$data[13];$symbol{$id}=$data[14];
          }
        }
close (ANN);

open (GNF, "$gnffile")||die "no open gnf annotation file\n";
while (<GNF>){
        $line=$_;chomp ($line);
        unless ($line=~/^#/){
          @data=split /\t/, $line;
          $id=$data[0];$descr{$id}=$data[7];$symbol{$id}=$data[6];
          }
        }
close (GNF);



open (IN, "$infile")|| die "no open infile\n";
```

```
open (OUT, ">$outfile")|| die "no create outfile\n";
print OUT "ID\tTau\n";

while (<IN>){
        $line=$_;chomp ($line);
        unless ($line=~/^Chip/){
          @data=split /\t/, $line;
          $id=$data[0];$max{$id}=$data[85]; ### change if not full 84 tissues ###
          foreach $tissue (1..84){ ### change if not full 84 tissues ###
                    $v{$tissue}{$id}=(1-($data[$tissue]/$max{$id}));
                    $vtotal{$id}=$vtotal{$id}+$v{$tissue}{$id}; $chksum{$id}=$chksum{$id}+1;
          #print OUT "$id\t$max{$id}\n";
          }
          $tau{$id}=$vtotal{$id}/$chksum{$id};
          print OUT "$id\t$symbol{$id}\t$tau{$id}\n";
        }
}




close (IN);close(OUT);
```

Script used to calculate average Tau

(for genes with more than one entry in database)

Written by Dr. Michael I. Jensen-Seaman

```
#!/usr/bin/perl -w

$infile=$ARGV[0];
$outfile=$infile.".ave";

open (IN, "$infile")|| die "no open infile\n";
open (OUT, ">$outfile")|| die "no create outfile\n";
print OUT "Symbol\tTau\n";

while (<IN>){
        $line=$_;chomp ($line);
        unless ($line=~/^ID/){
          @data=split /\t/, $line;
          $id=$data[0];$symbol{$id}=$data[1];
          unless ($symbol{$id}=~/\//){
                    push @{$taus{$symbol{$id}}}, $data[2];
          }
        }
}
close (IN);

foreach $symbol (keys %taus){
        foreach $value (@{$taus{$symbol}}){$sumvalues{$symbol} =
$sumvalues{$symbol} + $value}
        $number_values{$symbol} = scalar (@{$taus{$symbol}});
        $avevalue{$symbol} = $sumvalues{$symbol}/$number_values{$symbol};
        print OUT "$symbol\t$avevalue{$symbol}\n";
        }

close(OUT);
```

Script used to parse Tau data

```
#!/usr/bin/perl -w

$taufile = $ARGV[0]; #indicate TauValues in command line
#$genename_seminal = $ARGV[1]; #indicate file with seminal gene names
$genename_random = $ARGV[1]; #indicate file with random gene names
#$outfile1 = "TauOut_Seminal.txt";
$outfile2 = "TauOut_Random.txt";

open (TAU, "$taufile");
while (<TAU>) {
        $line = $_; chomp ($line);
        @data = split /\t/, $line;
          $symbol = $data[0];
          $tau{$symbol} = $data[1];
}

#open (OUT1, ">$outfile1");

#open (SEM, "$genename_seminal");
#while (<SEM>) {
        #$line = $_; chomp ($line);
        #$genename = $line;
        #print OUT1 " $genename\t$tau{$genename}\n";
#}

open (OUT2, ">$outfile2");

open (RAN, $genename_random);
while (<RAN>) {
        $line = $_; chomp ($line);
        $randomgenename = $line;
        print OUT2 " $randomgenename\t$tau{$randomgenename}\n";
```

```
}
```

Appendix 2: Data from chapter 2

Seminal uniform estimates of ω, *Ka,* and *Ks*

Gene	tree_w	Ka	Ks
A1BG	0.33426	0.0682	0.204
a4GALT	0.09809	0.031	0.3155
ABP1	0.17234	0.0388	0.2249
ACAT2	0.50645	0.0513	0.1013
ACE	0.10981	0.0333	0.3037
ACE2	0.66947	0.096	0.1434
ACLY	0.06161	0.0089	0.1443
ACO1	0.13829	0.0144	0.1039
ACP5	0.11253	0.0221	0.1961
ACPP	0.73724	0.0522	0.0708
ACR	0.40141	0.0769	0.1916
ACRBP	0.41611	0.0717	0.1724
ACRV1	0.42613	0.0873	0.205
ACTN1	0.0318	0.0077	0.2425
ACTN4	0.00599	0.0026	0.4381
ACTR1A	0	0	0.1522
ACYP1	0.3842	0.0372	0.0967
ADAM10	0.07671	0.006	0.0777
ADAM7	0.51589	0.0608	0.1179
ADAMTS1	0.08923	0.0153	0.1711
ADAMTSL1	0.15136	0.0177	0.1167
AGA	0.47452	0.0478	0.1008
AGR2	0.23294	0.0144	0.0617
AGRN	0.13581	0.0436	0.3213
AGT	0.23471	0.0582	0.2481
AHCY	0.20319	0.058	0.2856
AKR1A1	0.11113	0.0105	0.0941
AKR1B1	0.11948	0.0172	0.1436
AKR7A2	0.1908	0.057	0.299
ALAD	0.24398	0.0329	0.1346
ALB	0.38549	0.052	0.1349
ALCAM	0.08863	0.0089	0.1
ALDH1A1	0.09454	0.0114	0.1209
ALDH7A1	0.16655	0.0213	0.1278
ALDH9A1	0.18802	0.0236	0.1253
ALDOA	0.02534	0.0054	0.2137
ALDOC	0.09505	0.0094	0.0989
AMBP	0.16497	0.0292	0.1773
ANG	1.26483	0.1571	0.1242
ANPEP	0.21071	0.0443	0.2102
ANTXR2	0.15789	0.0172	0.1087
ANXA1	0.07163	0.0073	0.1019
ANXA11	0.61009	0.3073	0.5037
ANXA2	0.00787	0.0013	0.1647
ANXA3	0.21532	0.0291	0.1354
ANXA4	0.16539	0.014	0.0848
ANXA5	0.15992	0.009	0.0563
ANXA6	0.20573	0.0425	0.2067
ANXA7	0.21453	0.0171	0.0799
APCS	0.66684	0.0833	0.125
APEH	0.08984	0.0084	0.0932
APLP2	0.13033	0.0176	0.135
apoa1BP	0.25795	0.0291	0.1128
APOA2	0.50302	0.0777	0.1545
APOB	0.50294	0.051	0.1015
APOD	1.85478	0.1371	0.0739
APOE	0.21988	0.0833	0.3789
APOH	0.28839	0.0395	0.137
APP	0.17444	0.0246	0.141
ARF1	0	0	0.2302
ARF6	0	0	0.0569
ARHGDIA	0.26962	0.0308	0.1144
ARSA	0.22162	0.0422	0.1905

Gene	tree_w	Ka	Ks
ASAH1	0.41078	0.0536	0.1306
ASRGL1	0.28671	0.0419	0.1463
ATRN	0.26264	0.0411	0.1566
AZGP1	0.42468	0.0812	0.1912
B2M	0.51482	0.0596	0.1157
B4GALT1	0.2536	0.0488	0.1924
B4GALT4	0.33034	0.0375	0.1135
BAIAP2	0.0372	0.013	0.3496
BASP1	0.19262	0.0193	0.1002
BCAN	0.19515	0.0266	0.1364
BGN	0.02656	0.0089	0.3337
BPIL1	0.2419	0.0416	0.172
BPNT1	0.18307	0.0189	0.1032
BTD	0.36377	0.0397	0.1091
C19orf10	0.03204	0.0086	0.2677
C1RL	0.28272	0.057	0.2016
C3	0.22609	0.044	0.1944
C9	0.4675	0.0739	0.1581
CA2	0.27904	0.0316	0.1131
CA4	0.61962	0.1208	0.195
CA6	0.24573	0.0592	0.241
CAB39	0.03366	0.0015	0.0443
CAB39L	0.0312	0.003	0.0974
CACNA2D1	0.06728	0.007	0.1038
CACYBP	0.16147	0.0134	0.0827
CALR	0.02978	0.0044	0.148
CAMP	1.17322	0.1246	0.1062
CANT1	0.10605	0.0456	0.43
CAP1	0.19238	0.019	0.0989
CAPG	0.07453	0.0117	0.1569
CAPN1	0.02918	0.0087	0.2996
CAPNS1	0.06818	0.0161	0.2364
CAPZA1	0.08727	0.005	0.0574
CAPZA2	0.05711	0.0033	0.0572
CAPZB	0.46787	0.1497	0.32
CAT	0.25119	0.0319	0.1271
CCT2	0.00897	0.0009	0.0949
CCT3	0.24102	0.0495	0.2056
CCT4	0.041	0.0035	0.0841
CCT5	0.0113	0.0016	0.1381
CCT7	0.05102	0.0063	0.1237
CCT8	0.07093	0.0068	0.0953
CD109	0.36155	0.0448	0.1238
CD14	0.43576	0.0473	0.1086
CD151	0.08282	0.0231	0.2786
CD38	0.84752	0.0681	0.0803
CD44	0.45853	0.0504	0.1099
CD47	0.1187	0.0105	0.0883
CD59	2.49128	0.2234	0.0897
CD63	0.08642	0.0079	0.0916
CD81	0.01699	0.0072	0.4263
CD9	0.08598	0.0126	0.1467
CDC42	0.09607	0.0022	0.0225
CDH1	0.19729	0.0339	0.1721
CFB	0.3508	0.0488	0.1392
CFL1	0.00954	0.0025	0.2668
CKB	0.02772	0.0062	0.2252
CLIC1	0.2248	0.0218	0.0971
CLN5	0.46382	0.0546	0.1178
CLSTN1	0.05783	0.0134	0.2326
CLTC	0.01865	0.0011	0.0613
CLU	0.2118	0.041	0.1936

Gene	tree_w	Ka	Ks
CNDP2	0.38803	0.8795	2.2665
CNP	0.09662	0.0142	0.1466
CNTN3	0.13329	0.018	0.1353
CNTNAP2	0.13809	0.0314	0.2272
col12A1	0.1314	0.0143	0.1085
COL18A1	0.28163	0.0619	0.2197
COL6A1	0.15215	0.0632	0.4154
COL6A2	0.17475	0.0808	0.4625
COL9A1	0.31564	0.0324	0.1028
COLEC12	0.06913	0.0109	0.1573
COMP	0.12853	0.0343	0.2666
COPB2	0.09465	0.0068	0.0721
CP	0.28965	0.0273	0.0943
CPAMD8	0.18279	0.0396	0.2169
CPD	0.28376	0.0172	0.0606
CPE	0.1066	0.0113	0.1056
CPM	0.23619	0.0255	0.1078
CPO	0.44663	0.0914	0.2046
CPVL	0.47714	0.0516	0.1082
CPZ	0.0753	0.0158	0.2097
CREG1	0.14957	0.0252	0.1684
CRISP1	0.60043	0.105	0.1749
Crisp2	0.49591	0.0598	0.1206
CRISP3	0.43931	0.059	0.1343
CRTAC1	0.08009	0.0112	0.1395
CRYZ	0.33434	0.0496	0.1485
CST1	0.4454	0.2108	0.4732
CST3	0.07408	0.0173	0.2337
CST6	0.14608	0.0298	0.2043
CTBS	0.33236	0.0414	0.1245
CTSB	0.09991	0.0272	0.2722
CTSD	0.07036	0.0346	0.4914
CTSF	0.26689	0.0489	0.1831
CTSH	0.17724	0.0306	0.1725
CTSO	0.42717	0.0358	0.0839
CTSZ	0.23084	0.0578	0.2505
CUL3	0.03312	0.0023	0.0705
CYB561	0.34622	0.1505	0.4346
CYB5R2	0.2849	0.0444	0.1559
DAG1	0.21846	0.023	0.1053
DBI	0.3187	0.046	0.1442
DCD	0.78102	0.0812	0.104
DCXR	0.23412	0.0535	0.2285
DDAH1	0.07909	0.0087	0.1095
DDB1	0.023	0.0025	0.1089
DDR1	0.04061	0.0054	0.1336
DDT	0.14877	0.0333	0.224
DEFB129	0.69522	0.0536	0.0772
DNAJB9	0.41566	0.0352	0.0846
DNAJC3	0.05636	0.0065	0.1147
DNASE1	0.18122	0.0452	0.2495
DNASE2	0.33377	0.0548	0.1641
DPEP3	0.38552	0.0551	0.143
DPP4	0.27757	0.0179	0.0645
DPP7	0.11549	0.0412	0.3565
DSC2	0.36703	0.0424	0.1154
DSC3	0.25095	0.0303	0.1205
ECM1	0.54571	0.0491	0.09
EDIL3	0.09572	0.0088	0.092
EEF1A1	0	0	0.092
EEF1G	0.17534	0.0207	0.118
EEF2	0.00178	0.001	0.5629

Gene	tree_w	Ka	Ks
EFEMP1	0.11517	0.0068	0.0592
EFHD2	0.04856	0.0307	0.6323
EGF	0.5994	0.053	0.0884
ELSPBP1	0.14843	0.026	0.1751
ENO1	0.01082	0.0021	0.1969
ENPP3	0.29381	0.0341	0.116
ENPP5	0.33018	0.026	0.0787
EPHA5	0.15929	0.0133	0.0837
ESD	0.12855	0.012	0.0931
EXTL2	0.22022	0.0142	0.0647
F11R	0.35622	0.0318	0.0892
FAM12A	0.89891	0.1	0.1112
FAM12B	0.56441	0.0395	0.07
fam3B	0.72136	0.0687	0.0952
FAM3C	0.0976	0.0061	0.0625
FASN	0.1235	0.0517	0.4186
FBLN2	0.12755	0.019	0.1492
FBP1	0.07692	0.0169	0.2201
FCGBP	0.19151	0.0318	0.166
FDPS	0.24122	0.0288	0.1195
FH	0.10285	0.0128	0.1244
FKBP4	0.23325	0.0277	0.1188
FLNB	0.05836	0.0089	0.1524
FMOD	0.04614	0.0091	0.1975
FN1	0.1145	0.0135	0.1176
FOLH1	0.3166	0.0327	0.1034
FSTL1	0.03158	0.003	0.0965
FTH1	0.06923	0.0078	0.1122
FUCA1	0.25481	0.0374	0.1466
FUCA2	0.22975	0.0214	0.0933
FUT3	0.16557	0.0927	0.5599
GAA	0.12394	0.0376	0.303
GALC	0.23822	0.0237	0.0993
GALNS	0.12852	0.0441	0.3429
GALNT6	0.11878	0.0147	0.1237
GALNT7	0.14096	0.0081	0.0578
GANAB	0.21498	0.0177	0.0825
GAPDH	0.0398	0.008	0.2013
GAPDHS	0.21675	0.0375	0.1731
GAS6	0.11006	0.0398	0.3616
GBA	0.57864	0.1306	0.2256
GC	0.37888	0.0399	0.1054
GCHFR	0.18092	0.0218	0.1206
GDF15	0.39784	0.0713	0.1792
GDI2	0.06813	0.0087	0.128
GFRA2	0.03267	0.0071	0.218
GGH	0.46332	0.054	0.1165
GGT1	0.11826	0.0386	0.3265
GLA	0.32047	0.0248	0.0775
GLB1	0.44713	0.0538	0.1204
GLB1L	0.47739	0.0342	0.0716
GLG1	0.04455	0.0055	0.1232
GLO1	0.14205	0.0196	0.138
GM2A	0.4432	0.0593	0.1339
GMPPA	0.09519	0.0105	0.1101
GNAI3	0	0	0.0751
GNB1	0.01164	0.0014	0.121
GNB2	0.03504	0.0063	0.1787
GNB2L1	0	0	0.1383
GNG12	0.13522	0.013	0.0961
GNMT	0.06685	0.0153	0.2294
GNPDA1	0.04066	0.0048	0.1187

Gene	tree_w	Ka	Ks
GNPTG	0.12664	0.0497	0.3926
GNS	0.13572	0.0147	0.108
GOT1	0.10364	0.0154	0.1482
GP2	0.42542	0.0612	0.1439
GPC1	0.05502	0.0239	0.4342
GPC4	0.17128	0.0127	0.0744
GPD1L	0.09575	0.0153	0.1594
GPI	0.09336	0.0184	0.1976
GPR115	0.40563	0.0623	0.1536
GPR56	0.19109	0.0378	0.1979
GPR64	0.39159	0.0227	0.0579
GPRC5C	0.09742	0.0281	0.2885
GPX3	0.17703	0.0267	0.1508
GRHPR	0.22933	0.0377	0.1643
GRN	0.37234	0.0506	0.1358
GSN	0.10021	0.0193	0.1921
GSR	0.22362	0.0491	0.2194
GSS	0.23469	0.0189	0.0806
GSTM3	0.10633	0.0158	0.1486
GSTO1	0.27514	0.026	0.0944
GSTP1	0.11791	0.0287	0.2433
GSTT1	0.25068	0.0307	0.1224
GSTZ1	0.33622	0.0393	0.1168
GUSB	0.27561	0.0727	0.2638
HDHD2	0.25007	0.0196	0.0783
HEBP2	0.17335	0.022	0.1269
HEXA	0.20408	0.0213	0.1043
HEXB	0.4545	0.0504	0.1109
HINT1	0.09701	0.0117	0.1207
HIST2H2BE	0	0	0.297
HPRT1	0.29012	0.035	0.1207
HPX	0.67457	0.1034	0.1532
HRSP12	0.22527	0.0256	0.1137
HSPA1L	0.03881	0.0472	1.2174
HSPA4	0.06868	0.006	0.0877
HSPA5	0.0487	0.0055	0.1139
HSPA8	0	0	0.1623
HSPB1	0.05552	0.0176	0.3162
HSPG2	0.4074	0.276	0.6775
Hyou1	0.12987	0.0148	0.1143
IDE	0.0866	0.0078	0.0897
IDH1	0.265	0.0411	0.1551
IDI1	0.28544	0.0504	0.1764
IDS	0.29901	0.0275	0.092
IDUA	0.28007	0.0663	0.2369
IGF2R	0.22362	0.033	0.1475
IGFBP2	0.027	0.0052	0.1918
IGFBP5	0.06919	0.0089	0.1284
IGHG2	0.28039	0.097	0.3458
IGHG4	0.19341	0.0716	0.3703
IGJ	1.05716	0.0642	0.0607
IGKC	2.36478	0.2409	0.1019
IGLV1-40	0.56706	0.1145	0.202
IL1R1	0.35872	0.0359	0.1
IL1RAP	0.06479	0.0078	0.1201
IL1RL1	0.55601	0.1906	0.3428
IL6ST	0.19931	0.0172	0.0861
IMPA1	0.34041	0.0314	0.0924
INHBB	0.04703	0.0078	0.1666
IQGAP1	0.05349	0.0049	0.0924
IQGAP2	0.18891	0.0131	0.0692
ITIH5	0.21116	0.0463	0.2193

Gene	tree_w	Ka	Ks
KAL1	0.20081	0.0221	0.1102
KIF5B	0.11556	0.0156	0.1354
KLK11	0.27337	0.055	0.201
KLK2	0.41834	0.0498	0.119
KLK3	0.39957	0.1085	0.2716
KPNB1	0.02703	0.0027	0.0997
KRT1	0.11737	0.0166	0.1414
KRT10	0.20231	0.0349	0.1724
KRT5	0.06082	0.0153	0.2516
KRT8	0.19706	0.0667	0.3385
KRT9	0.4345	0.056	0.129
LAMA5	0.13514	0.0445	0.329
LAMB2	0.28588	0.0375	0.1312
LAMC1	0.09255	0.0133	0.1433
LAMP1	0.15986	0.0366	0.2288
LAMP2	0.46213	0.0262	0.0567
LAP3	0.38199	0.0922	0.2415
LCN1	0.32753	0.106	0.3238
LCN2	0.41134	0.0734	0.1784
LCP1	0.02083	0.0023	0.1102
LDHA	0.09163	0.008	0.0877
LDHB	0	0	0.1125
LDHC	0.18715	0.0196	0.1049
LDLR	0.13874	0.0368	0.2653
LEFTY2	0.06355	0.039	0.6142
LGALS3	0.59968	0.0608	0.1015
LGALS3BP	0.17687	0.0567	0.3208
LGMN	0.17889	0.0421	0.2353
LIFR	0.21051	0.0228	0.1083
LIPA	0.52468	0.0674	0.1285
LIPG	0.21196	0.0365	0.1722
LIPI	0.66784	0.0765	0.1146
LMAN2	0.03762	0.0059	0.156
LNPEP	0.34041	0.0295	0.0867
LPL	0.08979	0.0153	0.1702
LRG1	0.28021	0.0586	0.2092
LSAMP	0.04607	0.0029	0.062
LTA4H	0.19132	0.0121	0.0634
LTF	0.54832	0.1212	0.221
LYZ	0.77421	0.0803	0.1037
LZTFL1	0.31176	0.0139	0.0446
MAMDC2	0.11294	0.0115	0.1015
MAN2A1	0.21517	0.0201	0.0932
MAN2B1	0.14342	0.0256	0.1787
MAN2B2	0.25926	0.0813	0.3134
MANBA	0.2677	0.0294	0.1098
MARCKS	0.13143	0.0191	0.1457
MATN2	0.19117	0.0219	0.1147
MDH1	0.12758	0.0107	0.0841
MDH2	0.08792	0.0153	0.1743
MFAP4	0.03403	0.0066	0.1951
MGAM	0.21447	0.0341	0.1588
MINPP1	0.30424	0.0392	0.129
MLPH	0.52134	0.1408	0.2701
MME	0.07672	0.0094	0.1225
MMP14	0.08387	0.0086	0.1021
MMP2	0.05326	0.0115	0.2156
MMP7	0.295	0.043	0.1457
MPI	0.17907	0.017	0.0948
MPST	0.13639	0.0532	0.3903
MSLN	0.41431	0.1216	0.2934
MSMB	1.45178	0.1655	0.114

Gene	tree_w	Ka	Ks
MUC5B	0.37182	0.1075	0.2891
MUC6	0.33656	0.0705	0.2094
MYH9	0.01165	0.0035	0.304
MYO1C	0.06255	0.0199	0.3189
NAGA	0.15037	0.0265	0.1765
NAGLU	0.08384	0.0175	0.209
NAPA	0.0001	0	0.141
NBL1	0.08402	0.014	0.1666
NCSTN	0.21163	0.0258	0.1217
NELL1	0.22725	0.0243	0.1068
NEO1	0.14864	0.0134	0.0903
NEU1	0.14015	0.0206	0.147
NIF3L1	0.37359	0.0393	0.1052
NME3	0.02462	0.0072	0.2912
NP	0.37191	0.0365	0.0982
NPC2	0.07267	0.0097	0.1337
NPEPPS	0.11108	0.0052	0.0466
NRCAM	0.1105	0.0107	0.0971
NRP1	0.1187	0.0124	0.1048
NUCB1	0.12083	0.0256	0.2122
NUCB2	0.49462	0.0611	0.1235
NUTF2	0.24164	0.0541	0.2238
ODZ2	0.02107	0.0028	0.1351
OLFM1	0.02472	0.0068	0.2765
OLFM4	0.36665	0.0537	0.1466
ORM1	0.34271	0.0888	0.2591
ORM2	0.39559	0.1099	0.2779
OS9	0.12269	0.0139	0.1133
P4HB	0.08835	0.0178	0.2018
PACSIN2	0.13757	0.0579	0.4212
PAEP	0.61304	0.1131	0.1845
PAICS	0.27061	0.0265	0.0979
PAM	0.28683	0.0204	0.0711
Park7	0.1005	0.0078	0.0775
PCMT1	0.12522	0.0088	0.0699
PDCD6	0.14806	0.0352	0.238
PDCD6IP	0.03412	0.0027	0.0802
PDGFA	0.28039	0.0647	0.2308
PDIA3	0.14971	0.0173	0.1158
PEBP4	0.38835	0.0702	0.1809
PFAS	0.20845	0.0304	0.1459
PFKP	0.06371	0.0216	0.3383
PFN1	0.29469	0.0249	0.0846
PFN2	0.31537	0.0048	0.0151
PGAM2	0.02754	0.0064	0.2325
PGC	0.15509	0.0358	0.2307
PGCP	0.37912	0.0256	0.0676
PGD	0.13151	0.0253	0.1924
PGK1	0.20731	0.0158	0.0763
PGK2	0.20829	0.0201	0.0963
PGLS	0.09575	0.0188	0.1968
PGM1	0.10201	0.012	0.1172
PGM2	0.3495	0.1098	0.3143
PHGDH	0.08515	0.0123	0.1441
PI15	0.10346	0.011	0.1063
PIGR	0.47638	0.0876	0.1838
PIP	2.33674	0.253	0.1083
PITPNA	0.08676	0.0093	0.1077
PKM2	0.16829	0.0229	0.1362
PLA1A	0.40009	0.0618	0.1545
pla2g2A	0.41423	0.087	0.21
PLA2G7	0.36576	0.038	0.1038

Gene	tree_w	Ka	Ks
PLOD2	0.12028	0.013	0.1077
PLOD3	0.10437	0.0262	0.2514
PLXNB2	0.06133	0.0294	0.4799
PODXL2	0.27153	0.0275	0.1012
PPAP2A	0.25775	0.0136	0.0528
PPIA	0.04806	0.0056	0.1155
PPIB	0.034	0.0044	0.1295
PPIC	0.22018	0.0332	0.1508
PPP1CC	0	0	0.0586
PPP1R7	0.05014	0.0051	0.102
PPP2CA	0.04184	0.0044	0.1042
PPP2R4	0.34304	0.0694	0.2023
PPP5C	0.03747	0.0076	0.2039
PPT1	0.12499	0.0163	0.1302
PRCP	0.4072	0.0515	0.1265
PRDX1	0.1014	0.0078	0.0768
PRDX2	0.12405	0.025	0.2013
PRDX4	0.33071	0.0215	0.0651
PRDX5	0.3221	0.0321	0.0997
PRDX6	0.08072	0.0089	0.1099
PRKACA	0.21771	0.0496	0.2278
PRKAR1A	0.02182	0.0025	0.1154
PRKAR2A	0.26782	0.0336	0.1255
PRKCSH	0.11368	0.0286	0.252
PROM2	0.25088	0.0684	0.2725
PROS1	0.36304	0.0366	0.1009
PRSS22	0.25859	0.0496	0.1919
PRSS8	0.28973	0.0625	0.2157
PSAP	0.11398	0.0149	0.1309
PSAT1	0.14332	0.0171	0.1195
PSCA	0.12498	0.047	0.3758
PSMA1	0.05462	0.0081	0.1479
PSMA2	0.19882	0.0182	0.0914
PSMA3	0.22828	0.0448	0.1963
PSMA4	0.02917	0.0035	0.1187
PSMA5	0	0	0.0624
PSMA6	0.15024	0.0136	0.0908
PSMA7	0.06726	0.0096	0.1434
PSMB1	0.12317	0.0144	0.1173
PSMB2	0.16208	0.0225	0.1386
PSMB4	0.08328	0.0092	0.1105
PSMB5	0.06972	0.0073	0.1047
PSMB6	0.08442	0.0105	0.1242
PSMB7	0.07857	0.0106	0.1346
PSMB8	0.40269	0.0413	0.1025
PSMD14	0	0	0.0315
PSMD2	0.05075	0.0049	0.0969
PSME4	0.09526	0.0084	0.0887
PTGDS	0.12775	0.0365	0.2857
PTN	0.05059	0.0057	0.1126
PTPRD	0.0833	0.0093	0.1114
PTPRF	0.04714	0.0097	0.2053
PTPRJ	0.43859	0.0706	0.161
PTPRS	0.05222	0.0167	0.3191
PURA	0.06875	0.0036	0.0526
PYGB	0.11028	0.051	0.4623
QPCT	0.24935	0.0286	0.1145
QSCN6	0.28271	0.0402	0.1422
RAB10	0	0	0.0283
RAB11B	0	0	0.392
RAB13	0	0	0.1558
RAB14	0	0	0.064

Gene	tree_w	Ka	Ks
Rab18	0.0552	0.004	0.0733
RAB1A	0.07614	0.0047	0.0612
RAB1B	0.07787	0.0182	0.2342
RAB27A	0.15118	0.0156	0.1029
RAB27B	0.21051	0.0152	0.0722
RAB2A	0.0001	0	0.0221
RAB3B	0.02735	0.0043	0.1554
RAB3D	0.04423	0.0098	0.2222
RAB5B	0.25884	0.0331	0.1279
RAB5C	0.09729	0.0099	0.1014
RAC1	0.12088	0.007	0.0577
RAD23B	0.13207	0.0142	0.1078
RALA	0.33887	0.0592	0.1746
RALB	0.08639	0.008	0.0932
RAP1B	0	0	0.0788
RBP4	0.02341	0.0042	0.1804
RDX	0.1668	0.0238	0.1426
RELN	0.09263	0.0113	0.1218
RHOA	0	0	0.0419
RNASE1	0.3914	0.0684	0.1747
RNASE4	0.23967	0.0365	0.1524
RNASET2	0.23948	0.0577	0.2411
RPLP0	0.04414	0.003	0.0669
RRBP1	0.13849	0.0288	0.208
RTN4RL1	0.07028	0.0339	0.4826
RUVBL1	0	0	0.101
RUVBL2	0.00916	0.0027	0.2947
s100A11	0.09238	0.0141	0.1531
SCGB2A1	0.50319	0.1086	0.2158
SCPEP1	0.28463	0.0314	0.1102
SDC1	0.42477	0.0612	0.1441
SDCBP	0.14582	0.0153	0.105
SDCBP2	0.17189	0.0378	0.2201
SDK2	0.04119	0.0094	0.2271
SELENBP1	0.11919	0.0232	0.1949
SEMA3C	0.1026	0.0098	0.0955
SEMA3F	0.09798	0.0173	0.1768
SEMA7A	0.11662	0.0236	0.2021
SEMG1	0.90477	0.1874	0.2071
SEMG2	1.07914	0.15	0.139
SEPP1	0.71077	0.0633	0.0891
SERPINA1	0.4603	0.0723	0.157
SERPINA3	0.69942	0.1373	0.1963
SERPINA4	0.31022	0.0472	0.1523
SERPINA5	0.21902	0.0582	0.2657
SERPINA6	0.35446	0.053	0.1495
SERPINB5	0.15915	0.0152	0.0957
SERPINB6	0.14886	0.0469	0.3149
SERPINC1	0.37296	0.0615	0.165
SERPINF1	0.13839	0.0433	0.3127
SERPING1	0.35049	0.0537	0.1533
SERPINI1	0.24428	0.0226	0.0923
sez6L2	0.11038	0.0148	0.1342
SFN	0.01088	0.0032	0.2915
SH3BGRL2	0.05585	0.0042	0.076
SI	0.27066	0.0349	0.1289
SIL1	0.22735	0.0475	0.2089
SLC15A2	0.29309	0.0223	0.076
SLC1A1	0.09929	0.0154	0.1552
SLC35F2	0.18336	0.0242	0.132
SLC44A4	0.17158	0.0289	0.1684
SLIT2	0.09964	0.0136	0.136

Gene	tree_w	Ka	Ks
SLPI	0.55658	0.1019	0.1831
SMOC2	0.08184	0.012	0.1471
SMPD1	0.23664	0.0315	0.133
smpdl3A	0.34902	0.0391	0.1121
SMPDL3B	0.43209	0.077	0.1783
SMS	0.23779	0.0367	0.1542
SOD1	0.59912	0.0769	0.1284
SOD3	0.07039	0.0315	0.4473
SORD	0.28128	0.0529	0.188
SORL1	0.10077	0.015	0.1492
SORT1	0.14231	0.014	0.0982
SPACA3	0.65389	0.0892	0.1364
SPINK2	1.33875	0.1708	0.1276
SPINT1	0.27985	0.0477	0.1704
SPINT3	1.11091	0.106	0.0954
SPOCK3	0.11295	0.0129	0.1145
SPON2	0.11153	0.0256	0.2292
ST14	0.09418	0.0307	0.3263
STEAP2	0.11769	0.0105	0.089
STXBP2	0.06415	0.0183	0.2852
SYT1	0.02594	0.0024	0.0907
SYT7	0.06	0.0118	0.1967
TAGLN2	0.05075	0.007	0.1381
TALDO1	0.12716	0.0172	0.1351
TCP1	0.03	0.0032	0.107
TEX101	0.75291	0.0806	0.107
TF	0.54147	0.0872	0.161
TFPI2	0.55887	0.0526	0.094
TFRC	0.21664	0.0434	0.2002
TGFB1	0.01709	0.0035	0.2025
TGFB3	0.01365	0.0011	0.0792
TGFBR3	0.18951	0.0197	0.104
TGM4	0.38754	0.0541	0.1395
THBS1	0.04402	0.0066	0.1496
THBS2	0.06881	0.0198	0.2874
THBS4	0.13337	0.0179	0.1341
TIMP1	0.81715	0.0557	0.0682
TIMP2	0.03019	0.008	0.2647
TIMP3	0.02181	0.0039	0.1773
TKT	0.03005	0.0069	0.2312
TMC5	0.40918	0.0556	0.1359
TMEFF2	0.08682	0.0054	0.0617
TMEM8	0.11682	0.0417	0.3571
tmpRSS2	0.50285	0.1037	0.2063
TNFSF10	0.3777	0.0384	0.1017
TOLLIP	0.02961	0.0126	0.4244
tor1B	0.08296	0.0095	0.115
TP53I3	0.22876	0.0268	0.1171
TPI1	0.08996	0.0132	0.1471
TPP2	0.12797	0.0184	0.1441
TPT1	0.31717	0.0197	0.0621
TSG101	0.0311	0.0024	0.076
TSN	0	0	0.0646
TSNAX	0.09848	0.0095	0.0966
TSTA3	0.1166	0.0242	0.2078
TTR	0.59375	0.0644	0.1085
TUBB1	0.07015	0.0131	0.1874
TWSG1	0.02561	0.002	0.0792
TXN	0.34466	0.02	0.0581
UBE2L3	0.1222	0.0126	0.1028
UBE2N	0.0001	0	0.0376
UGCGL1	0.1394	0.0145	0.1039

Gene	tree_w	Ka	Ks
UGDH	0.04163	0.0037	0.09
USP14	0.09211	0.0058	0.0629
VAMP2	0	0	0.0848
VAMP8	0	0	0.1315
VAT1	0.16604	0.0311	0.1875
VCL	0.07167	0.0055	0.0774
VCP	0.02398	0.0023	0.0973
VPS28	0.05097	0.0282	0.553
VTN	0.46352	0.0724	0.1561
VWA1	0.08623	0.025	0.2899
VWF	0.16405	0.0249	0.1518

Gene	tree_w	Ka	Ks
WFDC2	0.20458	0.0487	0.2382
WFDC8	0.63099	0.1005	0.1593
WFDC9	1.00331	0.0995	0.0991
XPNPEP1	0.02849	0.0031	0.1074
YWHAB	0	0	0.1029
YWHAE	0.09136	0.0037	0.0409
YWHAG	0	0	0.2309
YWHAQ	0.33806	0.0224	0.0663
YWHAZ	0	0	0.0222
ZPBP	0.34036	0.0435	0.1279

Control estimates of *ω, Ka,* and *Ks*

Gene	tree_w	Ka	Ks
ABCB11	0.28618	0.0377	0.1318
ABCD3	0.13009	0.0188	0.1445
ABHD10	0.2221	0.023	0.1035
ABHD4	0.06569	0.0103	0.1563
ACCN1	0.24264	0.0504	0.2079
ACOT12	0.2554	0.0366	0.1433
ACSM1	0.53826	0.0717	0.1332
ADAM29	0.44471	0.0826	0.1856
ADAM9	0.16305	0.016	0.0981
ADAMTS8	0.10182	0.0136	0.1333
ADAT2	0.22183	0.0181	0.0815
ADH1A	0.40953	0.1178	0.2878
ADNP2	0.1646	0.0206	0.125
ADRA1B	0.09743	0.023	0.2357
AGAP10	0.87447	0.1641	0.1877
AGGF1	0.31754	0.0276	0.0868
AGPAT2	0.07626	0.0358	0.469
AHSA1	0.13916	0.0076	0.0545
ALDH1A3	0.11748	0.0175	0.1488
ALKBH3	0.11509	0.0101	0.0881
ALOX15	0.28034	0.0717	0.2558
AMBN	1.29269	0.0816	0.0631
ANGEL2	0.14992	0.0102	0.0684
ANKRD52	0.16149	0.0147	0.0909
ANO1	0.05996	0.0174	0.2899
APC2	0.08569	0.033	0.3854
APOBEC1	0.35525	0.0483	0.1361
ARCN1	0.05611	0.0046	0.0826
ARHGAP19	0.16643	0.0172	0.1032
ARHGAP4	0.24802	0.1016	0.4097
ARHGEF25	0.32586	0.0209	0.0641
ARL6IP1	0.11307	0.0098	0.0864
ARV1	0.31252	0.0276	0.0885
ASB1	0.02141	0.0042	0.1981
ASCC3	0.11789	0.0096	0.0811
ASH2L	0.07034	0.0069	0.0974
ASPH	0.31762	0.0332	0.1046
ATAD2	0.23109	0.0195	0.0843
ATAD5	0.5056	0.0522	0.1032
ATG16L1	0.10018	0.0111	0.1107
ATP10D	0.31096	0.033	0.1062
ATP5H	0.35319	0.0327	0.0925
B4GALT5	0.0594	0.0048	0.08
BCCIP	0.7671	0.0518	0.0675
BCL9L	0.10357	0.0145	0.1399
BET1	0.30585	0.0118	0.0385
BLNK	0.25319	0.0353	0.1395
BROX	0.11335	0.0089	0.0781
C10orf11	0.39057	0.0356	0.0913
C11orf20	0.34281	0.1315	0.3837
C11orf40	1.55366	0.2002	0.1288
C11orf80	0.60189	0.0702	0.1166
C11orf84	0.37879	0.2302	0.6076
C12orf5	0.53333	0.0675	0.1265

Gene	tree_w	Ka	Ks
C14orf180	0.61768	0.158	0.2558
C14orf181	0.97191	0.0388	0.0399
C17orf51	0.82216	0.0949	0.1154
C19orf47	0.12431	0.0199	0.1597
C19orf68	0.16196	0.0517	0.3193
C1orf101	0.73027	0.1062	0.1454
C1orf187	0.22563	0.0352	0.1562
C1orf27	0.33672	0.0222	0.0659
C1orf43	0.09663	0.0078	0.0803
C1QTNF7	0.14347	0.0138	0.096
C20orf160	0.33617	0.0864	0.2569
C21orf59	0.05525	0.0095	0.1727
C22orf41	0.07235	0.0105	0.1456
C4orf31	0.12253	0.0155	0.1262
C4orf33	0.46533	0.0501	0.1077
C4orf7	1.64355	0.1593	0.0969
C7orf60	0.04471	0.0035	0.0784
C8orf39	999	0.0413	0
C8orf40	0.0001	0	0.0799
C9orf142	0.34087	0.0429	0.1258
C9orf46	0.05665	0.0077	0.1357
C9orf9	0.1529	0.045	0.2942
CA10	0.01332	0.0015	0.1132
CA5A	0.4998	0.0295	0.059
CACNG6	0.33835	0.0533	0.1575
CAPN11	0.3139	0.0634	0.202
CAPN7	0.10233	0.01	0.0975
CAPS2	0.3361	0.0562	0.1673
CARD11	0.07595	0.0263	0.346
CASP8	0.42606	0.0482	0.1131
CAV1	0.03265	0.005	0.1529
CCDC115	0.21616	0.0331	0.1533
CCDC132	0.07944	0.0084	0.1058
CCDC157	0.37409	0.0539	0.1441
CCDC36	0.75733	0.0585	0.0772
CCDC68	0.65398	0.0419	0.064
CCDC69	0.40889	0.0371	0.0908
CCDC73	0.73278	0.0655	0.0893
CCDC82	0.62107	0.0624	0.1004
CCL24	0.35182	0.0967	0.2748
CCNB1	0.25128	0.0132	0.0527
CCRL1	0.39503	0.0284	0.0718
CD2AP	0.24962	0.0267	0.1071
CD300C	0.7195	0.1239	0.1723
CD69	0.44299	0.0612	0.1382
CDC20	0.06302	0.0057	0.0904
CDC23	0.09586	0.0074	0.0776
CDC37	0.00621	0.0023	0.3689
CDCA2	0.46008	0.0596	0.1294
CDCA3	0.40356	0.024	0.0594
CDK13	0.10513	0.006	0.0568
CDK9	0.01091	0.0023	0.2129
CDT1	0.15736	0.0618	0.3925

Gene	tree_w	Ka	Ks
CEACAM6	0.7904	0.3141	0.3975
CEBPZ	0.38003	0.0374	0.0984
CENPT	0.77714	0.0842	0.1083
CEP78	0.3478	0.0335	0.0962
CES5A	0.48386	0.0723	0.1494
CHL1	0.19809	0.0293	0.1479
CHM	0.2921	0.0212	0.0726
CHMP5	0.0001	0	0.1039
CHRDL2	0.1641	0.0388	0.2362
CHST2	0.07547	0.0134	0.1775
CHST4	0.28245	0.0437	0.1549
CISH	0.3206	0.0376	0.1172
CLCN4	0.05529	0.0105	0.1902
CLEC4E	0.58328	0.0752	0.1289
CLK4	0.13393	0.0099	0.0742
CMBL	0.31914	0.0318	0.0997
CNPY1	0.62828	0.0273	0.0435
CNTFR	0.09218	0.0127	0.1374
CNTN6	0.19901	0.0229	0.1148
COL20A1	0.22552	0.0387	0.1714
COL5A2	0.08985	0.0081	0.0907
COPS4	0.09887	0.0075	0.0757
COQ3	0.63308	0.0576	0.0909
CORO1C	0.04779	0.0042	0.0887
COX5B	0.74972	0.0715	0.0953
CPA5	0.16552	0.0363	0.2194
CPB2	0.51219	0.0576	0.1125
CPT1B	0.13443	0.0214	0.1589
CWC22	0.22459	0.0224	0.0998
CXCR5	0.08145	0.0178	0.2183
CYLC1	0.94067	0.0894	0.0951
CYP3A5	0.54142	0.0671	0.124
CYP4F11	0.23863	0.0621	0.2604
CYTH1	0.00665	0.0011	0.1707
DACT2	0.27172	0.0587	0.2159
DARC	0.60104	0.0737	0.1225
DBX1	0.194	0.0496	0.2557
DCAF12L2	0.1266	0.0583	0.4604
DCAF4L1	0.17259	0.0222	0.1289
DCAF5	0.12757	0.0136	0.1069
DCAF7	0.01161	0.0013	0.1144
DCTN6	0.02566	0.0026	0.1006
DDB2	0.10933	0.0122	0.1118
DDHD2	0.31257	0.0191	0.0611
DDTL	0.62793	0.1328	0.2114
DEF8	0.08634	0.0263	0.3044
DEFB103A	0.08913	0.0157	0.1764
DEFB110	1.19831	0.0644	0.0537
DENND4B	0.17505	0.0187	0.1069
DERL1	0.0566	0.0037	0.0646
DGAT1	0.25792	0.0604	0.2343
DHRS7	0.33835	0.0259	0.0765
DHTKD1	0.21395	0.0341	0.1596

Gene	tree_w	Ka	Ks
DIRC2	0.10554	0.0085	0.0808
DLEC1	0.32377	0.0434	0.1342
DLX6	0.27729	0.0082	0.0295
DMGDH	0.20438	0.021	0.1026
DNAI2	0.15138	0.0407	0.2686
DNAJC17	0.12622	0.02	0.1584
DNAJC24	0.16564	0.0237	0.143
DNAJC30	0.37881	0.0708	0.1868
DNAJC5G	0.90695	0.1114	0.1229
DRAP1	0.12032	0.0211	0.1752
DSCR3	0.07754	0.0174	0.2243
DUSP1	0.0001	0	0.1662
EBI3	0.23925	0.0538	0.2247
ECEL1	0.0406	0.0132	0.3245
EFS	0.29914	0.0346	0.1157
EIF2C2	0.02379	0.0042	0.1783
EIF2C4	0.0001	0	0.0505
ELF4	0.23113	0.0287	0.124
ENOPH1	0.10166	0.0079	0.0773
EPB41L1	0.07384	0.0104	0.1411
EPB49	0.01706	0.0023	0.1374
EPHB3	0.02051	0.0032	0.1547
EPSTI1	0.57515	0.0656	0.114
EPT1	0.15899	0.0117	0.0737
ERC1	0.04897	0.006	0.1226
ERCC3	0.05756	0.0094	0.1641
EXD1	0.55544	0.0468	0.0843
EXPH5	0.57323	0.0657	0.1146
FAAH2	0.37276	0.0413	0.1109
FAM103A1	0.03079	0.0037	0.1209
FAM111A	1.28121	0.0892	0.0696
FAM120A	0.23679	0.0249	0.1052
FAM126B	0.21272	0.0249	0.117
FAM131A	0.09811	0.0132	0.1343
FAM165B	0.28081	0.0389	0.1386
FAM167A	0.12596	0.022	0.1749
FAM55B	0.44134	0.0423	0.0958
FAM64A	0.63812	0.076	0.1191
FANCG	0.71818	0.1148	0.1599
FBL	0.1293	0.0204	0.1574
FBXL12	0.02168	0.0055	0.2542
FBXO22	0.22695	0.0191	0.0842
FCRL2	0.71925	0.1065	0.148
FGF2	0.27381	0.019	0.0694
FGGY	0.17813	0.0176	0.099
FKRP	0.05172	0.0183	0.3543
FLT3	0.28362	0.0293	0.1033
FMO6P	0.35202	0.0967	0.2748
FOLR2	0.11806	0.0247	0.2096
FOSB	0.02275	0.0014	0.0611
FTSJ2	0.27228	0.0439	0.1614
FXYD3	0.58545	0.0891	0.1521
FZR1	0.01962	0.007	0.3588

Gene	tree_w	Ka	Ks
CEACAM6	0.7904	0.3141	0.3975
CEBPZ	0.38003	0.0374	0.0984
CENPT	0.77714	0.0842	0.1083
CEP78	0.3478	0.0335	0.0962
CES5A	0.48386	0.0723	0.1494
CHL1	0.19809	0.0293	0.1479
CHM	0.2921	0.0212	0.0726
CHMP5	0.0001	0	0.1039
CHRDL2	0.1641	0.0388	0.2362
CHST2	0.07547	0.0134	0.1775
CHST4	0.28245	0.0437	0.1549
CISH	0.3206	0.0376	0.1172
CLCN4	0.05529	0.0105	0.1902
CLEC4E	0.58328	0.0752	0.1289
CLK4	0.13393	0.0099	0.0742
CMBL	0.31914	0.0318	0.0997
CNPY1	0.62828	0.0273	0.0435
CNTFR	0.09218	0.0127	0.1374
CNTN6	0.19901	0.0229	0.1148
COL20A1	0.22552	0.0387	0.1714
COL5A2	0.08985	0.0081	0.0907
COPS4	0.09887	0.0075	0.0757
COQ3	0.63308	0.0576	0.0909
CORO1C	0.04779	0.0042	0.0887
COX5B	0.74972	0.0715	0.0953
CPA5	0.16552	0.0363	0.2194
CPB2	0.51219	0.0576	0.1125
CPT1B	0.13443	0.0214	0.1589
CWC22	0.22459	0.0224	0.0998
CXCR5	0.08145	0.0178	0.2183
CYLC1	0.94067	0.0894	0.0951
CYP3A5	0.54142	0.0671	0.124
CYP4F11	0.23863	0.0621	0.2604
CYTH1	0.00665	0.0011	0.1707
DACT2	0.27172	0.0587	0.2159
DARC	0.60104	0.0737	0.1225
DBX1	0.194	0.0496	0.2557
DCAF12L2	0.1266	0.0583	0.4604
DCAF4L1	0.17259	0.0222	0.1289
DCAF5	0.12757	0.0136	0.1069
DCAF7	0.01161	0.0013	0.1144
DCTN6	0.02566	0.0026	0.1006
DDB2	0.10933	0.0122	0.1118
DDHD2	0.31257	0.0191	0.0611
DDTL	0.62793	0.1328	0.2114
DEF8	0.08634	0.0263	0.3044
DEFB103A	0.08913	0.0157	0.1764
DEFB110	1.19831	0.0644	0.0537
DENND4B	0.17505	0.0187	0.1069
DERL1	0.0566	0.0037	0.0646
DGAT1	0.25792	0.0604	0.2343
DHRS7	0.33835	0.0259	0.0765
DHTKD1	0.21395	0.0341	0.1596

Gene	tree_w	Ka	Ks
DIRC2	0.10554	0.0085	0.0808
DLEC1	0.32377	0.0434	0.1342
DLX6	0.27729	0.0082	0.0295
DMGDH	0.20438	0.021	0.1026
DNAI2	0.15138	0.0407	0.2686
DNAJC17	0.12622	0.02	0.1584
DNAJC24	0.16564	0.0237	0.143
DNAJC30	0.37881	0.0708	0.1868
DNAJC5G	0.90695	0.1114	0.1229
DRAP1	0.12032	0.0211	0.1752
DSCR3	0.07754	0.0174	0.2243
DUSP1	0.0001	0	0.1662
EBI3	0.23925	0.0538	0.2247
ECEL1	0.0406	0.0132	0.3245
EFS	0.29914	0.0346	0.1157
EIF2C2	0.02379	0.0042	0.1783
EIF2C4	0.0001	0	0.0505
ELF4	0.23113	0.0287	0.124
ENOPH1	0.10166	0.0079	0.0773
EPB41L1	0.07384	0.0104	0.1411
EPB49	0.01706	0.0023	0.1374
EPHB3	0.02051	0.0032	0.1547
EPSTI1	0.57515	0.0656	0.114
EPT1	0.15899	0.0117	0.0737
ERC1	0.04897	0.006	0.1226
ERCC3	0.05756	0.0094	0.1641
EXD1	0.55544	0.0468	0.0843
EXPH5	0.57323	0.0657	0.1146
FAAH2	0.37276	0.0413	0.1109
FAM103A1	0.03079	0.0037	0.1209
FAM111A	1.28121	0.0892	0.0696
FAM120A	0.23679	0.0249	0.1052
FAM126B	0.21272	0.0249	0.117
FAM131A	0.09811	0.0132	0.1343
FAM165B	0.28081	0.0389	0.1386
FAM167A	0.12596	0.022	0.1749
FAM55B	0.44134	0.0423	0.0958
FAM64A	0.63812	0.076	0.1191
FANCG	0.71818	0.1148	0.1599
FBL	0.1293	0.0204	0.1574
FBXL12	0.02168	0.0055	0.2542
FBXO22	0.22695	0.0191	0.0842
FCRL2	0.71925	0.1065	0.148
FGF2	0.27381	0.019	0.0694
FGGY	0.17813	0.0176	0.099
FKRP	0.05172	0.0183	0.3543
FLT3	0.28362	0.0293	0.1033
FMO6P	0.35202	0.0967	0.2748
FOLR2	0.11806	0.0247	0.2096
FOSB	0.02275	0.0014	0.0611
FTSJ2	0.27228	0.0439	0.1614
FXYD3	0.58545	0.0891	0.1521
FZR1	0.01962	0.007	0.3588

Gene	tree_w	Ka	Ks
MBLAC2	0.06274	0.0068	0.1089
MBNL2	0.08903	0.003	0.0341
MBTPS2	0.05409	0.0058	0.1077
MDM4	0.13548	0.0067	0.0498
ME2	0.05195	0.0056	0.1069
MED19	0.03658	0.004	0.1103
MED7	0.0001	0	0.0727
MEGF10	0.07245	0.0105	0.1454
METAP1D	0.31651	0.0177	0.0558
METTL6	0.40283	0.037	0.0918
MFSD6L	0.45263	0.0751	0.1659
MIER1	0.03199	0.0031	0.0962
MLLT6	0.07658	0.006	0.0777
MLXIPL	0.21341	0.01	0.0468
MOAP1	0.2101	0.0216	0.1026
MOCS3	0.29627	0.0353	0.1193
MPHOSPH9	0.35669	0.0295	0.0826
MPV17L	0.49477	0.1092	0.2206
MPZL2	0.15926	0.0139	0.0873
MRGPRD	0.40455	0.1095	0.2706
MRGPRE	0.08977	0.0368	0.4098
MRPL20	0.26008	0.1014	0.3901
MRPL21	0.29047	0.0544	0.1872
MRPL43	0.36544	0.0832	0.2276
MRPL55	0.45772	0.0876	0.1915
MS4A7	0.49329	0.0609	0.1234
MSL2	0.04331	0.0026	0.0591
MSRB2	0.2631	0.0529	0.2012
MTG1	0.29918	0.0481	0.1608
MTIF3	0.84182	0.0981	0.1165
MYL6B	0.11479	0.0631	0.5498
NCKAP1L	0.14652	0.0158	0.1076
NCOR2	0.06662	0.0198	0.2969
NDP	0.03482	0.0035	0.1019
NDUFA6	0.2592	0.0434	0.1674
NLGN3	0.02587	0.0017	0.0666
NPFF	1.32221	0.0939	0.071
NPFFR1	0.11288	0.0289	0.2558
NPY1R	0.0435	0.0038	0.0883
NPY5R	0.06886	0.0061	0.0893
NR1D2	0.0573	0.0061	0.1057
NR1I3	0.23094	0.0222	0.0963
NR2C2	0.03019	0.0032	0.1048
NSUN3	0.32474	0.0228	0.0702
NT5M	0.16816	0.0146	0.087
NUDCD1	0.24199	0.0191	0.0791
NUP88	0.31658	0.0383	0.121
NXT1	0.0001	0	0.1557
OAS1	1.0655	0.1074	0.1008
OAZ2	0.05829	0.0027	0.0458
OLA1	0.10932	0.0048	0.0441
OR10G3	0.462	0.0675	0.1461
OR13J1	0.38906	0.1156	0.2972
OR14A2	0.79819	0.058	0.0727
OR1A2	0.87692	0.0588	0.0671
PRPF4B	0.06779	0.0081	0.1199
PRRC1	0.24139	0.023	0.0954

Gene	tree_w	Ka	Ks
OR1N2	0.57511	0.0401	0.0698
OR2J3	0.45275	0.0657	0.1452
OR51F2	0.74253	0.0291	0.0392
OR5AS1	0.41454	0.0486	0.1173
OR5H6	0.53688	0.0775	0.1443
OR6M1	0.50467	0.0706	0.1398
OR6X1	0.52466	0.0627	0.1195
ORC2	0.15016	0.0124	0.0828
OVOL2	0.04459	0.0129	0.2889
PADI1	0.20957	0.0453	0.2164
PAFAH1B1	0.19401	0.0153	0.0788
PAX9	0.03506	0.0064	0.1817
PCDH7	0.04162	0.0046	0.1106
PCDHA1	0.29576	0.0518	0.1752
PCDHA3	0.17195	0.031	0.18
PCDHB5	0.27942	0.0611	0.2188
PDK3	0.04152	0.0025	0.0594
PDZD7	0.13174	0.036	0.2733
PER3	0.51372	0.0674	0.1312
PFDN6	0.05592	0.004	0.0707
PGAM1	0.03469	0.0035	0.1015
PIAS1	0.00964	0.0007	0.0765
PIGA	0.58822	0.0376	0.0639
PINX1	0.41847	0.0548	0.1309
PIP4K2C	0.14508	0.0155	0.1067
PITPNM1	0.08239	0.0196	0.2373
PLAU	0.35402	0.056	0.1581
PLB1	0.31859	0.0503	0.1579
PLCB1	0.09634	0.0075	0.0779
PLCH2	0.11674	0.0376	0.3217
PLEKHA5	0.20914	0.0086	0.0411
PLEKHB2	0.16318	0.0228	0.1396
PLK2	0.09085	0.0068	0.0748
PLP1	0.07234	0.0018	0.0244
PLS3	0.03425	0.0023	0.0665
PLXDC2	0.13644	0.0193	0.1415
PM20D2	0.24738	0.0284	0.1148
PMFBP1	0.53977	0.0563	0.1043
PNKP	0.13825	0.0409	0.2962
PNLIPRP3	0.61214	0.0437	0.0714
PNMA1	0.13351	0.0104	0.0778
PNPLA7	0.24036	0.0497	0.2067
PNPT1	0.19903	0.0201	0.101
POFUT2	0.08607	0.0164	0.1909
POGK	0.07697	0.0099	0.1286
POLR2F	0.07162	0.0075	0.1044
POU2F2	0.09881	0.0121	0.1223
PPIG	0.32185	0.032	0.0995
PPM1E	0.28141	0.0148	0.0525
PPM1K	0.12621	0.008	0.0631
PPP1R12A	0.11377	0.0086	0.0756
PPP2R2C	0.01826	0.0047	0.2557
PRKCD	0.02783	0.0058	0.2085
PRKRIP1	0.13991	0.0227	0.162
PRMT6	0.02662	0.0046	0.1722
SHPRH	0.15954	0.0185	0.1159
SIPA1	0.06162	0.0127	0.2065

Gene	tree_w	Ka	Ks
PRRG1	0.11671	0.0072	0.062
PRSS55	0.40917	0.0904	0.2209
PSMD4	0.02592	0.0025	0.0976
PSMD9	0.13632	0.024	0.1762
PTPRCAP	0.22203	0.0442	0.199
PTTG2	0.8162	0.1055	0.1292
PYGO2	0.14517	0.0082	0.0564
RAB17	0.31202	0.0747	0.2394
RABEP1	0.09904	0.0112	0.1135
RABGGTA	0.18157	0.0164	0.0905
RAD21L1	0.66225	0.042	0.0633
RAE1	0.03208	0.0052	0.161
RALGDS	0.10056	0.0234	0.2331
RAP1GAP2	0.07865	0.0185	0.2353
RBBP6	0.14204	0.0142	0.1001
RBBP7	0.16826	0.01	0.0597
RBCK1	0.04825	0.0058	0.1194
RBM7	0.1533	0.0198	0.1293
RBP7	0.54877	0.0474	0.0864
RC3H1	0.13467	0.0087	0.0646
RCN2	0.12665	0.0124	0.098
RD3	0.10484	0.0302	0.2883
RESP18	1.03761	0.0902	0.0869
RFX7	0.15548	0.0121	0.078
RGS18	0.37106	0.024	0.0648
RGS8	0.08965	0.0067	0.0742
RHOB	0.00865	0.004	0.4671
RNF11	0.0001	0	0.0447
RNF208	0.02538	0.0051	0.2011
RNF216	0.16529	0.0167	0.1013
RNF34	0.15787	0.0149	0.0944
ROBO4	0.32214	0.0437	0.1358
ROR2	0.04994	0.0129	0.2588
RPL23A	0.34186	0.0865	0.2531
RPL26	0.19832	0.0273	0.1375
RPS12	0.144	0.0215	0.149
RPS23	0.0001	0	0.1298
RTN4RL2	0.10758	0.0316	0.2933
S100A4	0.0001	0	0.1474
S1PR3	0.07308	0.0155	0.2114
SCG3	0.1282	0.0152	0.1186
SCN1B	0.04253	0.0113	0.2662
SCT	0.2481	0.0145	0.0585
SDAD1	0.34749	0.0485	0.1394
SDC2	0.1843	0.0171	0.0926
SDHA	0.22614	0.0439	0.1941
SDSL	0.19743	0.0471	0.2385
SEC13	0.11993	0.0152	0.1271
SEC14L5	0.07534	0.021	0.2785
SECTM1	0.50986	0.0658	0.129
SEMA4B	0.13293	0.0196	0.1472
SEMA6B	0.04865	0.0126	0.2597
SFRP1	0.0472	0.0169	0.3584
SH3D21	0.54033	0.0724	0.134
SHMT2	0.14247	0.0141	0.0992

Gene	tree_w	Ka	Ks
SIX6	0.0515	0.0071	0.1373
SLC16A8	0.08908	0.0209	0.2348
SLC22A17	0.02267	0.0026	0.1126
SLC24A4	0.07227	0.0117	0.1622
SLC25A23	0.0302	0.0048	0.1598
SLC31A1	0.27658	0.0154	0.0556
SLC35C1	0.0749	0.0247	0.3303
SLC45A2	0.27837	0.0352	0.1265
SLC4A4	0.11363	0.0076	0.0666
SLC5A3	0.10763	0.0065	0.0607
SLC6A4	0.07005	0.0121	0.1723
SLC7A14	0.05471	0.008	0.1456
SLIT1	0.06266	0.0137	0.2191
SMC2	0.09617	0.0101	0.1055
SMC5	0.24785	0.0209	0.0845
SMPD3	0.03518	0.0085	0.2426
SMR3B	0.71114	0.1409	0.1981
SNRPA1	0.0001	0	0.0739
SOAT2	0.21479	0.0384	0.179
SOCS4	0.08137	0.0081	0.0996
SPIB	0.06607	0.005	0.0757
SPTB	0.09327	0.02	0.2148
SQSTM1	0.14793	0.0419	0.2831
SREK1	0.09477	0.0058	0.0607
STAT5B	0.03661	0.0055	0.1515
STH	0.95266	0.0982	0.103
STUB1	0.0001	0	0.3835
STX2	0.13497	0.0136	0.101
SULF2	0.06703	0.0154	0.2305
SUMF1	0.29505	0.0334	0.1133
SUSD3	0.24717	0.046	0.186
SUV39H1	0.0001	0	0.1129
SV2B	0.02962	0.0041	0.1368
SYNJ2BP	0.34558	0.0177	0.0512
SYNPO2L	0.38996	0.0421	0.108
TAC4	0.86078	0.0889	0.1033
TACR2	0.1945	0.0335	0.1721
TAGLN	0.01342	0.0021	0.1576
TBC1D17	0.05219	0.0125	0.2402
TBC1D9	0.0128	0.0015	0.119
TBCB	0.04941	0.0109	0.2216
TBR1	0.00823	0.0007	0.0838
TBRG1	0.33208	0.0199	0.0598
TBXA2R	0.06219	0.0245	0.394
TEKT5	0.14052	0.0494	0.3514
TFEC	0.38492	0.0253	0.0658
TGM1	0.07911	0.0161	0.2036
THY1	0.03844	0.0079	0.2053
TIAF1	1.56927	0.097	0.0618
TJP2	0.1903	0.0257	0.1349
TMC8	0.16858	0.0359	0.2129
TMCC3	0.06746	0.0084	0.1252
TMED4	0.06661	0.012	0.1798
TMEM105	1.0875	0.0828	0.0762
TMEM106B	0.09353	0.0081	0.0867

Gene	tree_w	Ka	Ks
TMEM121	0.01478	0.0048	0.325
TMEM139	1.34675	0.0721	0.0536
TMEM178	0.17408	0.0198	0.1139
TMEM179	0.1174	0.0289	0.2463
TMEM18	0.16057	0.0184	0.1147
TMEM194A	0.36685	0.0234	0.0639
TMEM208	0.06763	0.0055	0.0812
TMEM232	0.40741	0.044	0.1079
TMEM38B	0.20856	0.0256	0.1227
TMEM42	0.07808	0.0058	0.0739
TMEM43	0.10472	0.0253	0.2414
TMEM61	0.35218	0.077	0.2187
TMEM92	0.56742	0.0726	0.128
TNFAIP8L3	0.18326	0.0301	0.1645
TNFSF9	0.26866	0.0385	0.1433
TNIP3	0.55937	0.085	0.1519
TNS3	0.16329	0.0351	0.2147
TOP3A	0.2615	0.0363	0.1389
TRAIP	0.38503	0.035	0.0909
TRIM39	0.1087	0.0084	0.0769
TSPAN15	0.064	0.0122	0.191
TSPAN8	1.69742	0.1882	0.1109
TSSK2	0.10263	0.0223	0.2177
TSSK4	0.5521	0.0701	0.127
TTC29	0.57975	0.0362	0.0624
TTF1	0.5884	0.0796	0.1353
TTLL9	0.20965	0.0491	0.234
TTYH1	0.0886	0.0162	0.1829
TUBB	0.16238	0.026	0.1599
TXNDC11	0.31256	0.034	0.1087
UBLCP1	0.02682	0.0027	0.1007
UGT1A3	0.39584	0.0477	0.1206
UNC13C	0.14659	0.0174	0.1184
UPF2	0.07336	0.0059	0.0801
USP1	0.21049	0.0144	0.0684
USP18	0.39733	0.0685	0.1723
USP26	0.90656	0.0873	0.0963
USP7	0.01015	0.0008	0.0822
VCX2	0.63864	0.205	0.321
VPREB1	0.47646	0.0698	0.1466
VPS13D	0.12546	0.0124	0.0986
VPS52	0.07923	0.0077	0.0973
VSIG1	0.59697	0.0414	0.0694
WDFY2	0.09537	0.0074	0.0772
WDR33	0.06752	0.0048	0.0718
WDR5B	0.20814	0.0227	0.1089
WDR63	0.39106	0.0318	0.0814
WDR74	0.26369	0.0282	0.107
WFDC11	0.61073	0.1043	0.1708
WFDC6	1.10794	0.0743	0.0671
WISP3	0.2632	0.0224	0.0853
WSB2	0.09507	0.0081	0.0855
YLPM1	0.13547	0.0089	0.0657
YTHDC1	0.03828	0.0024	0.0622
ZBP1	0.81373	0.1181	0.1452
ZBTB38	0.17502	0.0173	0.0989
ZC3H12D	0.19087	0.043	0.2254
ZC3H13	0.13398	0.013	0.0967

Gene	tree_w	Ka	Ks
ZC4H2	0.0001	0	0.0608
ZCCHC17	0.02179	0.002	0.0916
ZFP37	0.87814	0.0479	0.0545
ZFP57	0.41787	0.0458	0.1095
ZFP64	0.05215	0.0103	0.1967
ZFYVE20	0.20531	0.0197	0.0959
ZMYND17	0.43223	0.0393	0.0909
ZNF117	0.60373	0.216	0.3579
ZNF157	0.34854	0.0248	0.0712
ZNF192	0.46068	0.0284	0.0616
ZNF20	0.46875	0.0413	0.088
ZNF235	0.32765	0.0342	0.1045
ZNF275	0.07994	0.0195	0.2444
ZNF30	0.47462	0.0661	0.1393
ZNF302	0.49188	0.0888	0.1805
ZNF324B	0.19381	0.0594	0.3063
ZNF335	0.13374	0.0192	0.1434
ZNF528	0.35099	0.0464	0.1322
ZNF540	0.44193	0.0359	0.0811
ZNF561	0.65825	0.1985	0.3015
ZNF569	0.14679	0.0141	0.0961
ZNF570	0.08974	0.0071	0.0792
ZNF574	0.05399	0.0063	0.1162
ZNF575	0.26699	0.0382	0.1432
ZNF592	0.12998	0.013	0.1
ZNF625	0.18908	0.0179	0.0948
ZNF652	0.21862	0.0154	0.0703
ZNRD1	0.20302	0.0148	0.0729

Seminal estimates of pairwise *ω*, *Ka*, and *Ks*

Gene	CH_*ω*	CH_*Ka*	CH_*Ks*	GH_*ω*	GH_*Ka*	GH_*Ks*	GC_*ω*	GC_*Ka*	GC_*Ks*
A1BG	0.3239	0.0092	0.0285	0.2656	0.0111	0.0418	0.1947	0.0055	0.0284
a4GALT	0.2318	0.0059	0.0254	0.1243	0.0038	0.0309	0.3326	0.0086	0.0258
ABP1	0.1464	0.0049	0.0334	0.3217	0.0078	0.0242	0.1921	0.0052	0.027
ACAT2	0.5148	0.0032	0.0062	0.4128	0.0058	0.014	0.9992	0.0069	0.0069
ACE	0.2448	0.0073	0.03	0.1412	0.0044	0.031	0.227	0.0084	0.0369
ACE2	0.4483	0.0045	0.01						
ACLY	0.1509	0.0036	0.0237	0.0806	0.0008	0.0098	0.0919	0.0016	0.0178
ACO1	0.0345	0.0005	0.0143	0.0412	0.001	0.024	0.0846	0.0015	0.0175
ACP5	0.2053	0.0087	0.0426	0.3344	0.0041	0.0124	0.1416	0.0052	0.037
ACPP	0.4027	0.0042	0.0104	0.0753	0.0011	0.0139	0.5047	0.0053	0.0104
ACR	0.3695	0.013	0.0352	0.2336	0.0097	0.0414	0.2409	0.0141	0.0585
ACRBP	0.2206	0.004	0.0183	0.3084	0.0065	0.0211	0.726	0.0057	0.0078
ACRV1	1.0706	0.0116	0.0109	0.5052	0.0173	0.0343	0.5325	0.0121	0.0227
ACTN1	0	0	0.0229	0.0416	0.0005	0.0114	0.0223	0.0005	0.0212
ACTN4	0	0	0.0266	0	0	0.0273	0	0	0.0325
ACTR1A	0	0	0.0148	0	0	0.0185	0	0	0.0185
ACYP1	0	0	0	0	0	0.0216	0	0	0.0216
ADAM10	0	0	0.0061	0.225	0.0024	0.0108	0.2816	0.0024	0.0086
ADAM7	0.4806	0.008	0.0165	0.585	0.0089	0.0153	0.4057	0.0107	0.0265
ADAMTS1	0.0341	0.0005	0.0132	0.0549	0.0018	0.0331	0.057	0.0014	0.0239
ADAMTSL1	0.2254	0.0023	0.01	0.1709	0.0025	0.0147	0.1624	0.0023	0.0139
AGA	0.1262	0.0026	0.0202	0.3969	0.0064	0.0161	0.3161	0.0064	0.0202
AGR2	0	0.0026	0	0	0.005	0	0	0.0026	0
AGRN	0.2105	0.0051	0.0244	0.1791	0.0056	0.031	0.2412	0.0078	0.0325
AGT	0.1102	0.0056	0.0505	0.0476	0.0019	0.039	0.2255	0.0037	0.0165
AHCY	0	0	0.013	0	0	0.0398	0	0	0.0467
AKR1A1	0.1081	0.0014	0.0126	0.1067	0.0015	0.0139	0.3222	0.0015	0.0046
AKR1B1	0.8814	0.0041	0.0047	0.2956	0.0014	0.0047	0.2953	0.0028	0.0095
AKR7A2	0.3306	0.0075	0.0227	0.1322	0.0025	0.0188	0.2053	0.0062	0.0304
ALAD	0.1477	0.0038	0.0256	0.5224	0.0078	0.015	0.2468	0.0065	0.0264
ALB	0.4767	0.0053	0.0111	0.3334	0.005	0.0149	0.3747	0.006	0.0161
ALCAM	0.0268	0.0007	0.0278	0.0741	0.0015	0.0201	0.0329	0.0007	0.0227
ALDH1A1	0	0	0.0199	0.0513	0.0009	0.0171	0.0439	0.0009	0.0199
ALDH7A1	0.1595	0.0025	0.0154	0.1035	0.0031	0.0296	0.1728	0.0051	0.0296
ALDH9A1	0.1606	0.0017	0.0106	0.1593	0.0043	0.0269	0.2674	0.0043	0.016
ALDOA	0	0	0.0162	0.0295	0.0011	0.0369	0.027	0.0011	0.0404
ALDOC	0.3387	0.0012	0.0036	0	0	0.0109	0.169	0.0012	0.0073
AMBP	0.2353	0.0038	0.0161	0.4191	0.005	0.012	0.5241	0.0063	0.012
ANG	0.3211	0.003	0.0094	0.3235	0.0031	0.0094	0	0.0061	0
ANPEP	0.2683	0.0068	0.0253	0.4635	0.0093	0.0201	0.4709	0.0077	0.0164
ANTXR2	0.1962	0.0027	0.0139	0.5174	0.008	0.0154	0.6593	0.008	0.0121
ANXA1	0	0	0.021	0.0601	0.0013	0.021	0.05	0.0013	0.0252
ANXA11	0	0	0.0094	0.2537	0.0045	0.0177	0.2005	0.0032	0.0159
ANXA2	0	0	0.0343	0	0	0.0331	0	0	0.0387
ANXA3	0.1841	0.0068	0.0367	0.0845	0.0027	0.0319	0.0978	0.0041	0.0414
ANXA4	0.1035	0.0014	0.0132	0.1238	0.0027	0.0221	0.0384	0.0014	0.0357
ANXA5	0	0	0.0087	0.1048	0.0014	0.0131	0.1048	0.0014	0.0131
ANXA6	0.2587	0.0039	0.015	0.12	0.0026	0.0216	0.092	0.0026	0.0282
ANXA7	0.9834	0.0027	0.0028	1.2925	0.0045	0.0034	0.4821	0.0033	0.0069
APCS	0.6304	0.0079	0.0126	0.7894	0.0099	0.0126	0.7914	0.01	0.0126
APEH	0.1625	0.0006	0.0037	0.1942	0.0018	0.0093	0.0922	0.0012	0.013
APLP2	0.1907	0.0023	0.0119	0.071	0.0017	0.0239	0.1786	0.0028	0.0159
apoa1BP	0.3404	0.0031	0.0092	0.4034	0.0096	0.0238	0.5639	0.008	0.0142
APOA2	1.2973	0.018	0.0139	0	0	0.0278	1.2973	0.018	0.0139
APOB	0.4805	0.0063	0.0131	0.5067	0.0081	0.016	0.4612	0.0078	0.017
APOD	0.4595	0.007	0.0152	1.2501	0.0094	0.0075	0.9361	0.007	0.0075
APOE	0.8281	0.0328	0.0396	0.6962	0.0144	0.0206	0.7614	0.0269	0.0353
APOH	0.1502	0.0025	0.0168	0.2904	0.0033	0.0112	0.1926	0.0033	0.0169
APP	0.0488	0.0006	0.0115	0.073	0.0011	0.0154	0.0365	0.0006	0.0154
ARF1	0	0	0.0325	0	0	0.025	0	0	0.0421
ARF6	0	0	0	0	0	0.0162	0	0	0.0162
ARHGDIA	0.2147	0.0039	0.0184	0.1785	0.004	0.0222	0.2024	0.0053	0.026
ARSA	0.5192	0.0128	0.0246	0.2452	0.0099	0.0402	0.5747	0.0224	0.0389
ASAH1	0.4523	0.0064	0.0141	0.9064	0.0096	0.0106	0.4211	0.0075	0.0177
ASRGL1	0.8384	0.0073	0.0087						
ATRN	0.5897	0.0242	0.0411	0.1129	0.0021	0.0183	0.1523	0.0024	0.0158
AZGP1	0.0586	0.0015	0.0249	0.2203	0.0044	0.0199	0.2344	0.0058	0.0249
B2M	0	0.0036	0	0	0	0	0	0.0036	0
B4GALT1	0.4457	0.009	0.0203	0.1477	0.0045	0.0305	0.2956	0.009	0.0306
B4GALT4	0	0.0089	0	0.4408	0.0114	0.0259	0.2936	0.0076	0.0259
BAIAP2	0.0552	0.0016	0.0287	0.1016	0.0024	0.0234	0.0304	0.0008	0.026
BASP1	0.1069	0.002	0.0183	0.1542	0.0045	0.0289	0.1031	0.0022	0.0216
BCAN	0.1044	0.0015	0.0143	0.1744	0.0025	0.0142	0.099	0.002	0.0201
BGN	0.0448	0.0012	0.0268	0.0941	0.0036	0.0383	0.07	0.0024	0.0344
BPIL1	0.2811	0.003	0.0107	0.2471	0.006	0.0245	0.1983	0.0071	0.0356
BPNT1	0	0	0.0044	0	0	0.0044	0	0	0.0089
BTD	0.1945	0.0032	0.0163	0.4115	0.0056	0.0136	0.4894	0.004	0.0081
C19orf10	0	0	0.0437						
C1RL	0.3118	0.0054	0.0174	0.3097	0.0091	0.0293	0.5206	0.0091	0.0174
C3	0.2919	0.0067	0.023						
C9	0.6772	0.0054	0.008	0.285	0.0069	0.0242	0.2211	0.006	0.0272
CA2	0	0.005	0	0.3761	0.0088	0.0233	0.45	0.0105	0.0234
CA4	1.2871	0.0057	0.0044	0.9691	0.0129	0.0133	0.8838	0.0157	0.0178
CA6	0.2643	0.01	0.0379	0.2191	0.0125	0.0572	0.0752	0.0047	0.0623
CAB39	0	0	0.0046	0	0	0.014	0	0	0.0187
CAB39L	0	0	0.0091	0	0	0.0235	0	0	0.014
CACNA2D1	0.0965	0.0008	0.0082	0.0285	0.0008	0.0295	0	0	0.031
CACYBP	0	0	0	1.4062	0.0095	0.0067	1.4062	0.0095	0.0067
CALR	0	0	0.0039	0.1029	0.002	0.0196	0.129	0.002	0.0157

Gene	OH_*ω*	OH_*Ka*	OH_*Ks*	OC_*ω*	OC_*Ka*	OC_*Ks*	OG_*ω*	OG_*Ka*	OG_*Ks*
A1BG	0.3887	0.0281	0.0722	0.4173	0.0243	0.0581	0.3691	0.0214	0.0581
a4GALT	0.2038	0.0102	0.0501	0.305	0.0151	0.0496	0.1636	0.009	0.055
ABP1	0.2273	0.0119	0.0522	0.1871	0.0092	0.0494	0.2243	0.0113	0.0503
ACAT2	0.2837	0.0112	0.0393	0.34	0.0117	0.0344	0.1231	0.0035	0.0281
ACE	0.1029	0.0079	0.0769	0.1358	0.0117	0.0861	0.1162	0.009	0.0772
ACE2	0.7953	0.0673	0.0846	0.6616	0.0448	0.0677			
ACLY	0.0474	0.002	0.0432	0.0821	0.0043	0.052	0.0586	0.0021	0.0361
ACO1	0.117	0.004	0.0338	0.1634	0.0045	0.0272	0.1501	0.0052	0.0346
ACP5	0.2343	0.0104	0.0443	0.1559	0.0114	0.0731	0.1558	0.0062	0.0399
ACPP	0.2069	0.0073	0.0354	0.3278	0.011	0.0336	0.237	0.0084	0.0356
ACR	0.3522	0.0168	0.0476	0.3467	0.0194	0.0559	0.2308	0.0168	0.0726
ACRBP	0.3483	0.0244	0.07	0.3972	0.0233	0.0587	0.3728	0.0234	0.0627
ACRV1	0.2764	0.0212	0.0766	0.3014	0.0194	0.0643	0.3859	0.0258	0.0669
ACTN1	0.0736	0.0045	0.0611	0.0598	0.0045	0.0752	0.0791	0.005	0.063
ACTN4	0.0056	0.0005	0.085	0.0061	0.0005	0.0777	0.0067	0.0005	0.0723
ACTR1A	0	0	0.0451	0	0	0.0451	0	0	0.0413
ACYP1	0	0	0.0633	0	0	0.0633	0	0	0.0438
ADAM10	0.0254	0.0006	0.0226	0.028	0.0006	0.0205	0.1159	0.003	0.0261
ADAM7	0.257	0.0122	0.0476	0.2287	0.014	0.061	0.2544	0.0134	0.0528
ADAMTS1	0.1106	0.0073	0.0657	0.1337	0.0077	0.0577	0.1239	0.0082	0.0663
ADAMTSL1	0.2112	0.0076	0.0361	0.2137	0.0074	0.0344	0.1556	0.006	0.0386
AGA	0.7638	0.0155	0.0202	0.6336	0.0154	0.0244	0.8274	0.0168	0.0202
AGR2	0.9384	0.0076	0.0081	0.6252	0.0053	0.0084	0.9379	0.0076	0.0081
AGRN	0.1841	0.0135	0.0735	0.1887	0.015	0.0795	0.2152	0.0157	0.073
AGT	0.1768	0.0131	0.0738	0.2102	0.013	0.0621	0.2041	0.0103	0.0504
AHCY	0.0479	0.0031	0.0639	0.0479	0.0031	0.0639	0.0359	0.0031	0.0852
AKR1A1	0.1844	0.0055	0.0297	0.2694	0.0069	0.0255	0.2275	0.0074	0.0327
AKR1B1	0.1299	0.0069	0.053	0.1428	0.0083	0.0579	0.0867	0.0042	0.0484
AKR7A2	0.2994	0.0201	0.067	0.3	0.0226	0.0753	0.2819	0.02	0.0711
ALAD	0.1823	0.0088	0.0485	0.1447	0.0076	0.0523	0.186	0.0078	0.042
ALB	0.1469	0.0071	0.0482	0.194	0.0096	0.0494	0.1365	0.0067	0.0494
ALCAM	0.1074	0.003	0.0278	0.063	0.0022	0.0355	0.0657	0.0015	0.0227
ALDH1A1	0.1394	0.0044	0.0315	0.1275	0.0044	0.0344	0.1115	0.0035	0.0315
ALDH7A1	0.1741	0.0082	0.0473	0.1566	0.0074	0.0473	0.126	0.0072	0.0569
ALDH9A1	0.113	0.0043	0.0379	0.1594	0.0043	0.0268	0.1059	0.0034	0.0323
ALDOA	0.0201	0.0011	0.053	0.0189	0.0011	0.0564	0.0318	0.0022	0.0686
ALDOC	0.0874	0.0049	0.0565	0.0938	0.0049	0.0526	0.0817	0.0049	0.0604
AMBP	0.1236	0.005	0.0406	0.0926	0.0038	0.0408	0.1777	0.005	0.0282
ANG	0.96	0.0323	0.0337	1.4846	0.0355	0.0239	1.4957	0.0358	0.0239
ANPEP	0.2998	0.0141	0.047	0.3446	0.0141	0.0409	0.4517	0.0164	0.0363
ANTXR2	0.023	0.0009	0.0396	0.0588	0.0018	0.0309	0.2234	0.008	0.0357
ANXA1	0.0297	0.0013	0.0425	0.0269	0.0013	0.0469	0.0662	0.0025	0.0382
ANXA11	0.1333	0.004	0.0298	0.2235	0.0042	0.0189	0.185	0.005	0.0271
ANXA2	0.0223	0.0012	0.0546	0	0	0.0701	0.0192	0.0012	0.0633
ANXA3	0.2218	0.0081	0.0366	0.1701	0.0095	0.0558	0.131	0.0054	0.0413
ANXA4	0.1547	0.0027	0.0177	0.0439	0.0014	0.0312	0.0681	0.0027	0.0403
ANXA5	0.0523	0.0014	0.0264	0.0523	0.0014	0.0264	0.0892	0.0028	0.0309
ANXA6	0.0936	0.0039	0.0416	0.0889	0.0039	0.0438	0.0623	0.0026	0.0416
ANXA7	0.2434	0.0055	0.0225	0.1795	0.0046	0.0254	0.3204	0.0056	0.0174
APCS	0.3789	0.0221	0.0583	0.3799	0.0221	0.0582	0.345	0.0201	0.0581
APEH	0.1165	0.0024	0.0207	0.0737	0.0018	0.0246	0.0636	0.0018	0.0285
APLP2	0.0801	0.0034	0.0423	0.1252	0.0045	0.0362	0.0882	0.0028	0.0321
apoa1BP	0.2504	0.0105	0.0418	0.3371	0.0105	0.0311	0.3335	0.0125	0.0375
APOA2	0.2486	0.0182	0.0732	0.5461	0.032	0.0587	0.2486	0.0182	0.0732
APOB	0.3437	0.0115	0.0336	0.3495	0.0118	0.0337	0.3288	0.012	0.0365
APOD	2.1924	0.0332	0.0152	2.0325	0.0308	0.0152	4.4672	0.0335	0.0075
APOE	0.6363	0.0158	0.0249	0.7513	0.0308	0.041	0.7669	0.0158	0.0206
APOH	0.2215	0.0115	0.0517	0.1886	0.0115	0.0607	0.2211	0.0115	0.0518
APP	0.0119	0.0006	0.0471	0	0	0.0431	0.0144	0.0006	0.0391
ARF1	0	0	0.0579	0	0	0.0579	0	0	0.0687
ARF6	0	0	0	0	0	0	0	0	0.0162
ARHGDIA	0.1397	0.0079	0.0566	0.1516	0.0092	0.0608	0.188	0.0092	0.0492
ARSA	0.1273	0.0062	0.0489	0.3425	0.0178	0.0519	0.1271	0.0062	0.0491
ASAH1	0.4677	0.015	0.0321	0.2717	0.0107	0.0393	0.489	0.0139	0.0284
ASRGL1	0.1751	0.0102	0.0584	0.2508	0.0146	0.0584			
ATRN	0.0944	0.0038	0.04	0.4786	0.0264	0.0551	0.0902	0.0032	0.0358
AZGP1	0.2929	0.014	0.0477	0.2116	0.0118	0.0556	0.4417	0.0177	0.0401
B2M	1.2772	0.0147	0.0115	1.5983	0.0184	0.0115	1.2772	0.0147	0.0115
B4GALT1	0.1324	0.0045	0.034	0.3327	0.009	0.0272	0.1013	0.0045	0.0445
B4GALT4	0.9899	0.0127	0.0128	0.6922	0.0089	0.0128	0.3775	0.0114	0.0303
BAIAP2	0.0439	0.0032	0.0723	0.0211	0.0016	0.0751	0.0316	0.0024	0.0751
BASP1	0.1752	0.0098	0.0561	0.1581	0.0079	0.0497	0.2564	0.0112	0.0437
BCAN	0.2028	0.0076	0.0372	0.1767	0.0073	0.0414	0.2184	0.0073	0.0334
BGN	0.054	0.0036	0.0667	0.0385	0.0024	0.0625	0.1142	0.0048	0.0422
BPIL1	0.4277	0.0152	0.0355	0.3029	0.0142	0.0468	0.2733	0.0152	0.0556
BPNT1	0	0	0.0225	0	0	0.0225	0	0	0.027
BTD	0.2069	0.0128	0.0618	0.199	0.0112	0.0562	0.2562	0.0136	0.0532
C19orf10	0.035	0.003	0.0865	0.0372	0.0036	0.0966			
C1RL	0.1478	0.0118	0.0795	0.1769	0.0118	0.0664	0.1997	0.0146	0.0731
C3	0.2915	0.0148	0.0507	0.3803	0.0167	0.044			
C9	0.5554	0.0275	0.0495	0.4871	0.0283	0.058	0.3136	0.0226	0.072
CA2	0.5962	0.0101	0.0169	0.6937	0.0118	0.017	0.4991	0.0132	0.0264
CA4	1.2642	0.037	0.0293	1.1754	0.0399	0.034	0.7227	0.0363	0.0502
CA6	0.355	0.0275	0.0775	0.265	0.0231	0.0873	0.199	0.0189	0.0952
CAB39	0.0668	0.0012	0.0187	0.0533	0.0012	0.0234	0.0893	0.0012	0.014
CAB39L	0	0	0.0563	0	0	0.0466	0	0	0.0527
CACNA2D1	0.0227	0.0008	0.0349	0	0	0.0406	0	0	0.0388
CACYBP	0	0	0.0135	0	0	0.0135	0.4645	0.0095	0.0204
CALR	0	0	0.0398	0	0	0.0357	0.046	0.002	0.0439

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
A1BG	0.4968	0.0509	0.1024	0.563	0.0473	0.0839	0.5774	0.0485	0.084	0.5089	0.0521	0.1024
a4GALT												
ABP1	0.2296	0.0135	0.059	0.1842	0.0107	0.058	0.2434	0.0126	0.0518	0.2041	0.0104	0.0508
ACAT2	0.6475	0.0225	0.0347	0.8356	0.0236	0.0282	0.7181	0.0151	0.021	0.5245	0.0182	0.0346
ACE	0.2026	0.0134	0.0662	0.2231	0.0176	0.0787	0.2191	0.0134	0.0613	0.1582	0.0134	0.0848
ACE2	0.2287	0.0102	0.0445	0.2491	0.0101	0.0405				0.8274	0.0706	0.0853
ACLY	0.0253	0.0016	0.0633	0.0631	0.0046	0.0728	0.0315	0.0017	0.0526	0.0197	0.0013	0.0656
ACO1	0.1709	0.0049	0.0289	0.2431	0.0054	0.0224	0.2081	0.0062	0.0297	0.2884	0.0069	0.024
ACP5	0.0802	0.0055	0.0687	0.0745	0.007	0.0937	0.0215	0.0014	0.0641	0.1142	0.0076	0.0665
ACPP	0.4184	0.012	0.0287	0.5904	0.0158	0.0268	0.6133	0.0132	0.0215	0.1902	0.0076	0.0399
ACR	0.3811	0.0267	0.0701	0.3561	0.0308	0.0866	0.3452	0.0284	0.0823	0.3652	0.0221	0.0606
ACRBP	0.354	0.0364	0.1029	0.3787	0.0356	0.0939	0.3718	0.0339	0.0912	0.4636	0.0489	0.1056
ACRV1	0.5306	0.0268	0.0505	0.5642	0.0285	0.0505	0.5371	0.0314	0.0586	0.4019	0.0211	0.0526
ACTN1	0.0095	0.0005	0.0502	0.0078	0.0005	0.0606	0.0189	0.001	0.0503	0.0645	0.005	0.0775
ACTN4	0.0247	0.0024	0.0957	0.0257	0.0024	0.0919	0.0246	0.0024	0.0981	0.0256	0.0028	0.111
ACTR1A	0	0	0.0568	0	0	0.0568	0	0	0.0529	0	0	0.0607
ACYP1	0	0	0.0633	0	0	0.0633	0	0	0.0216	0	0	0.031
ADAM10	0	0	0.0205	0	0	0.0184	0.1116	0.0024	0.0217	0.0214	0.0006	0.0267
ADAM7	0.4687	0.0151	0.0323	0.3594	0.0163	0.0453	0.4965	0.0159	0.032	0.2927	0.0143	0.0487
ADAMTS1	0.0672	0.0041	0.0607	0.0858	0.0045	0.0529	0.084	0.005	0.0597	0.1035	0.0086	0.0834
ADAMTSL1	0.1568	0.0053	0.0338	0.1606	0.0053	0.033	0.1166	0.004	0.0346	0.1755	0.0071	0.0404
AGA	0.4319	0.0141	0.0327	0.3821	0.0141	0.037	0.4711	0.0154	0.0328	0.5847	0.0167	0.0286
AGR2	0.1029	0.0025	0.0245	0	0	0.0255	0.1028	0.0025	0.0245	0.311	0.005	0.0162
AGRN	0.1912	0.0155	0.081	0.2121	0.0173	0.0813	0.2095	0.0179	0.0856	0.1865	0.017	0.0911
AGT	0.2217	0.0173	0.0781	0.2762	0.0187	0.0678	0.2675	0.015	0.0561	0.245	0.0187	0.0765
AHCY	0.671	0.0489	0.0728	0.67	0.0488	0.0729	0.5604	0.0489	0.0872	0.4887	0.0478	0.0978
AKR1A1	0.029	0.0014	0.0472	0.0803	0.0027	0.0341	0.0703	0.003	0.0423	0.0797	0.0041	0.0516
AKR1B1	0.1144	0.0055	0.048	0.1299	0.0069	0.053	0.0965	0.0042	0.0435	0.0565	0.0041	0.073
AKR7A2	0.2724	0.0232	0.0853	0.2388	0.0245	0.1028	0.2544	0.0206	0.0811	0.3092	0.0336	0.1088
ALAD	0.2559	0.0114	0.0445	0.1806	0.0101	0.056	0.388	0.0118	0.0303	0.1343	0.0076	0.0563
ALB	0.2158	0.0121	0.056	0.2303	0.0132	0.0572	0.204	0.0114	0.0558	0.1817	0.0121	0.0666
ALCAM	0.0782	0.003	0.0382	0.0549	0.0022	0.0407	0.0452	0.0015	0.033	0.0839	0.003	0.0356
ALDH1A1	0.0502	0.0026	0.0523	0.0533	0.0026	0.0493	0.0712	0.0035	0.0493	0.1073	0.0053	0.0491
ALDH7A1	0.1922	0.0091	0.0472	0.1788	0.0099	0.0554	0.0912	0.0061	0.0674	0.156	0.0091	0.0581
ALDH9A1	0.1189	0.0069	0.0577	0.1319	0.0069	0.0521	0.1562	0.0095	0.0606	0.1492	0.0095	0.0634
ALDOA	0.0132	0.0011	0.0808	0.0126	0.0011	0.0844	0.0252	0.0022	0.0866	0.0357	0.0021	0.0598
ALDOC												
AMBP	0.1482	0.0098	0.0662	0.118	0.0085	0.0717	0.1479	0.0098	0.0663	0.0846	0.0056	0.0661
ANG												
ANPEP	0.4813	0.0187	0.039	0.5283	0.0174	0.033	0.6739	0.0211	0.0313	0.3423	0.0179	0.0524
ANTXR2	0.0712	0.0037	0.0526	0.0859	0.0037	0.0436	0.2218	0.0105	0.0474	0.0479	0.0028	0.0586
ANXA1	0.05	0.0013	0.0252	0.0427	0.0013	0.0295	0.1204	0.0025	0.021	0.0595	0.0025	0.0425
ANXA11	0.9291	0.2941	0.3166	0.9473	0.4181	0.4414	0.9108	0.2926	0.3212	0.9072	0.3808	0.4198
ANXA2	0	0	0.0525	0	0	0.0617	0	0	0.0571	0	0	0.0302
ANXA3	0.213	0.0109	0.0509	0.1344	0.0095	0.0705	0.1459	0.0081	0.0557	0.1863	0.0095	0.0509
ANXA4	0.1018	0.0027	0.0269	0.1013	0.0041	0.0407	0.1216	0.0055	0.0453	0.1524	0.0055	0.0361
ANXA5	0.1245	0.0055	0.0445	0.1245	0.0055	0.0445	0.1408	0.0069	0.0492	0.1966	0.0069	0.0353
ANXA6	0.0659	0.0026	0.0393	0.0624	0.0026	0.0415	0.0296	0.0013	0.0438	0.0624	0.0026	0.0415
ANXA7	0.1834	0.0073	0.0398	0.1727	0.0064	0.037	0.2821	0.0089	0.0317	0.2585	0.0073	0.0283
APCS	1.0113	0.0386	0.0382	1.2219	0.0386	0.0316	0.9595	0.0366	0.0381	0.5436	0.0242	0.0445
APEH	0.0503	0.0018	0.0361	0.0302	0.0012	0.04	0.0263	0.0012	0.046	0.0452	0.0018	0.0404
APLP2	0.08	0.0049	0.0609	0.1015	0.0062	0.0611	0.0755	0.0042	0.0561	0.0827	0.0042	0.051
apoa1BP	0.1932	0.011	0.0569	0.2338	0.011	0.047	0.2102	0.0112	0.0533	0.0368	0.0017	0.0472
APOA2	1.4898	0.0414	0.0278	4.3356	0.0603	0.0139	1.4898	0.0414	0.0278	1.0802	0.0464	0.043
APOB	0.3747	0.0152	0.0406	0.3791	0.0155	0.0409	0.3545	0.0152	0.0427	0.3158	0.0136	0.0429
APOD	1.2942	0.0345	0.0266	1.4604	0.0333	0.0228	2.3952	0.036	0.015	1.7905	0.0406	0.0227
APOE	0.4834	0.035	0.0724	0.6484	0.054	0.0833	0.516	0.035	0.0679	0.5278	0.0335	0.0635
APOH	0.1273	0.0089	0.0699	0.1271	0.0089	0.0699	0.0699	0.0049	0.07	0.1741	0.0134	0.0768
APP	0.0468	0.002	0.0421	0.0334	0.0014	0.0421	0.0654	0.002	0.0301	0.0369	0.0014	0.0381
ARF1	0	0	0.0579	0	0	0.0754	0	0	0.0687	0	0	0.0495
ARF6	0	0	0.0244	0	0	0.0244	0	0	0.0411	0	0	0.0244
ARHGDIA												
ARSA	0.146	0.0073	0.0499	0.3297	0.0165	0.05	0.2656	0.0158	0.0597	0.2663	0.0083	0.0313
ASAH1	0.2391	0.0139	0.0581	0.1463	0.0096	0.0656	0.2357	0.0128	0.0544	0.1558	0.0096	0.0617
ASRGL1	0.214	0.0176	0.0822	0.2501	0.0206	0.0822				0.2081	0.0161	0.0774
ATRN	0.1581	0.0097	0.0616	0.3994	0.03	0.075	0.166	0.0093	0.0563	0.1902	0.0096	0.0507
AZGP1	0.4892	0.0395	0.0808	0.4456	0.0372	0.0835	0.596	0.0433	0.0727	0.4534	0.0327	0.0721
B2M	0.3085	0.0154	0.05	0.3085	0.0154	0.05	0.3085	0.0154	0.05	0.2456	0.0154	0.0628
B4GALT1	0.3225	0.0224	0.0693	0.3713	0.0273	0.0734	0.2759	0.0224	0.0811	0.2871	0.0199	0.0694
B4GALT4	0.2427	0.0127	0.0525	0.1697	0.0089	0.0524	0.1618	0.0115	0.0707	0.266	0.0127	0.0479
BAIAP2	0.0294	0.0026	0.0875	0.0196	0.0017	0.0875	0.0195	0.0017	0.0875	0.0148	0.0017	0.1159
BASP1	0.0775	0.0042	0.0548	0.0387	0.0021	0.0548	0.0498	0.0024	0.049	0.3176	0.0085	0.0268
BCAN	0.1811	0.0072	0.0398	0.1542	0.007	0.0453	0.1927	0.007	0.0362	0.2022	0.0083	0.0412
BGN	0.0777	0.0036	0.0464	0.0478	0.0024	0.0503	0.0522	0.0024	0.0461	0.0826	0.0048	0.0583
BPIL1	0.3161	0.0164	0.0519	0.2814	0.0164	0.0583	0.2897	0.0197	0.0681	0.3131	0.0153	0.0489
BPNT1	0.5394	0.0145	0.027	0.5394	0.0145	0.027	0.461	0.0145	0.0315	0.4611	0.0145	0.0315
BTD	0.2256	0.0108	0.048	0.1988	0.0089	0.0445	0.2654	0.0109	0.041	0.221	0.0138	0.0625
C19orf10	0.046	0.0026	0.0563	0	0	0.0712				0.1304	0.0061	0.0466
C1RL	0.2778	0.0192	0.069	0.3557	0.0201	0.0565	0.3678	0.022	0.0597	0.1789	0.0136	0.0763
C3	0.3391	0.0204	0.06	0.4277	0.0226	0.0529				0.2956	0.0206	0.0698
C9	0.4532	0.0265	0.0585	0.445	0.0273	0.0614	0.2652	0.0217	0.0819	0.2304	0.0195	0.0846
CA2	0.1672	0.0067	0.0402	0.1248	0.005	0.0403	0.0974	0.0052	0.0539	0.2179	0.0101	0.0463
CA4	0.3732	0.0349	0.0937	0.4006	0.0386	0.0965	0.3697	0.0365	0.0986	0.3074	0.0312	0.1015
CA6	0.229	0.0143	0.0626	0.0988	0.0071	0.0723	0.0185	0.0016	0.0843	0.3229	0.0217	0.0671
CAB39	0.0668	0.0012	0.0187	0.0533	0.0012	0.0234	0.0532	0.0012	0.0234	0	0	0.0187
CAB39L	0	0	0.0612	0	0	0.0612	0	0	0.0678	0	0	0.0323
CACNA2D1	0.1037	0.0041	0.0399	0.0726	0.0033	0.0459	0.0773	0.0035	0.046	0.0865	0.0033	0.0387
CACYBP	0.069	0.0019	0.0273	0.069	0.0019	0.0273	0.3323	0.0114	0.0342	0.069	0.0019	0.0273
CALR	0.0167	0.001	0.0606	0.0179	0.001	0.0564	0.0538	0.003	0.0564	0.0146	0.001	0.0691

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
A1BG												
a4GALT	0.1918	0.0218	0.1138	0.2206	0.0244	0.1105	0.1693	0.018	0.1066	0.2162	0.0251	0.116
ABP1	0.2995	0.0263	0.0879	0.2438	0.0236	0.0969	0.2607	0.0239	0.0918	0.2015	0.021	0.1041
ACAT2	0.3293	0.0273	0.083	0.3457	0.0263	0.0759	0.3225	0.0192	0.0594	0.3171	0.023	0.0725
ACE	0.0945	0.0109	0.1149	0.1027	0.0136	0.1324	0.0836	0.0102	0.1219	0.0832	0.0119	0.1431
ACE2	0.2788	0.019	0.0681	0.3473	0.0207	0.0597				0.557	0.0456	0.0818
ACLY	0.0541	0.004	0.0736	0.0888	0.0072	0.0813	0.0509	0.0033	0.0639	0.0448	0.0037	0.0829
ACO1	0.0535	0.0044	0.0832	0.065	0.0049	0.0761	0.0707	0.0057	0.0805	0.0848	0.0067	0.0788
ACP5	0.1118	0.0097	0.0866	0.1317	0.0123	0.0933	0.0675	0.0055	0.0819	0.12	0.0118	0.0981
ACPP	0.6247	0.0287	0.0459	0.7365	0.0325	0.0441	0.6497	0.03	0.0462	0.5001	0.0286	0.0573
ACR	0.3105	0.0332	0.1069	0.3198	0.0379	0.1185	0.2899	0.0344	0.1186	0.2648	0.0274	0.1036
ACRBP	0.2598	0.0217	0.0835	0.2788	0.0209	0.0748	0.2576	0.0201	0.0779	0.3709	0.0238	0.0643
ACRV1	0.3716	0.0407	0.1096	0.3556	0.039	0.1096	0.3745	0.0415	0.1108	0.2423	0.0357	0.1474
ACTN1	0.0357	0.0031	0.0861	0.0311	0.0031	0.0988	0.0404	0.0036	0.0881	0.0709	0.0076	0.1072
ACTN4	0	0	0.1244	0	0	0.1166	0	0	0.1139	0.004	0.0005	0.119
ACTR1A	0	0	0.0973	0	0	0.0973	0	0	0.0849	0	0	0.0972
ACYP1	0.3775	0.0311	0.0823	0.3775	0.0311	0.0823	0.4432	0.0305	0.0688	0.4531	0.0334	0.0736
ADAM10	0.0659	0.0029	0.0436	0.0693	0.0029	0.0414	0.1181	0.0055	0.0462	0.0633	0.0034	0.0544
ADAM7	0.346	0.029	0.0839	0.3293	0.0308	0.0934	0.3146	0.028	0.089	0.3345	0.029	0.0867
ADAMTS1	0.047	0.0045	0.0965	0.0536	0.005	0.0931	0.0543	0.0055	0.1008	0.0812	0.0091	0.1118
ADAMTSL1	0.1189	0.0073	0.0616	0.1214	0.0076	0.0624	0.0948	0.0063	0.0666	0.1327	0.0102	0.0767
AGA	0.3926	0.0239	0.0608	0.3626	0.0239	0.0658	0.3921	0.0239	0.0609	0.4525	0.0254	0.0561
AGR2	0.0667	0.0051	0.0758	0.0333	0.0026	0.079	0.0667	0.0051	0.0758	0.1134	0.0076	0.0669
AGRN	0.1593	0.0207	0.1301	0.1619	0.0221	0.1363	0.1529	0.0205	0.1339	0.1584	0.0238	0.1504
AGT	0.2791	0.0389	0.1393	0.2922	0.0389	0.133	0.2927	0.0371	0.1268	0.2405	0.035	0.1456
AHCY	0.1337	0.0133	0.0999	0.1243	0.0133	0.1074	0.1388	0.0133	0.0962	0.1077	0.0123	0.1144
AKR1A1	0.045	0.0027	0.0608	0.0866	0.0041	0.0474	0.026	0.0015	0.057	0.0841	0.0055	0.0652
AKR1B1	0.1229	0.0096	0.0785	0.1321	0.011	0.0836	0.1137	0.0084	0.074	0.0881	0.0083	0.0938
AKR7A2	0.2369	0.0214	0.0905	0.1994	0.0214	0.1075	0.2368	0.0214	0.0905	0.2481	0.0303	0.1222
ALAD	0.2371	0.0184	0.0777	0.2	0.0171	0.0857	0.2461	0.0177	0.072	0.1773	0.0146	0.0821
ALB	0.3526	0.0303	0.0859	0.3354	0.0292	0.0871	0.3693	0.0296	0.0801	0.3917	0.0325	0.083
ALCAM	0.0778	0.0052	0.0673	0.0641	0.0045	0.0699	0.0603	0.0037	0.0619	0.081	0.0052	0.0646
ALDH1A1	0.0686	0.0053	0.0768	0.0659	0.0053	0.0798	0.0572	0.0044	0.0767	0.0839	0.0062	0.0734
ALDH7A1	0.1336	0.0074	0.0554	0.1292	0.0082	0.0637	0.0627	0.0051	0.0817	0.0865	0.0058	0.0665
ALDH9A1	0.0956	0.0077	0.0807	0.1031	0.0077	0.0749	0.1278	0.0103	0.0807	0.1379	0.0103	0.0748
ALDOA	0.0215	0.0021	0.0991	0.0208	0.0021	0.1028	0.0299	0.0033	0.1093	0.0323	0.0032	0.0991
ALDOC	0.0293	0.0025	0.0842	0.0461	0.0037	0.0802	0.0279	0.0025	0.0883	0.1136	0.0087	0.0762
AMBP	0.1505	0.0157	0.1041	0.1501	0.0158	0.105	0.184	0.0178	0.0968	0.163	0.0149	0.0916
ANG	1.2386	0.1235	0.0997	1.275	0.1272	0.0997	1.2855	0.1284	0.0999	1.1019	0.1287	0.1168
ANPEP	0.2044	0.0213	0.1042	0.2099	0.021	0.1003	0.2304	0.022	0.0954	0.18	0.0206	0.1142
ANTXR2	0.1128	0.0057	0.0507	0.1497	0.0067	0.0445	0.2681	0.013	0.0486	0.094	0.0048	0.0506
ANXA1	0.0619	0.0044	0.0715	0.0582	0.0044	0.0761	0.085	0.0057	0.067	0.0797	0.0057	0.0714
ANXA11	0.178	0.0143	0.0804	0.0742	0.0064	0.0857	0.1761	0.0152	0.0861	0.0641	0.006	0.0932
ANXA2	0	0	0.0999	0	0	0.1181	0	0	0.1092	0.0142	0.0012	0.086
ANXA3	0.1943	0.0136	0.07	0.187	0.015	0.0801	0.1803	0.0109	0.0603	0.1943	0.0136	0.07
ANXA4	0.1223	0.0055	0.0449	0.0833	0.0041	0.0494	0.0937	0.0055	0.0587	0.1015	0.0055	0.0542
ANXA5												
ANXA6	0.3058	0.0394	0.1287	0.3123	0.0394	0.1261	0.284	0.038	0.1338	0.2896	0.0384	0.1324
ANXA7	0.1168	0.0064	0.0547	0.0947	0.0055	0.0578	0.1563	0.0078	0.0499	0.1234	0.0064	0.0517
APCS	0.448	0.0448	0.1	0.4835	0.0448	0.0927	0.4284	0.0427	0.0998	0.2844	0.0303	0.1066
APEH	0.1097	0.0054	0.0495	0.0902	0.0048	0.0534	0.0811	0.0048	0.0594	0.1011	0.0054	0.0539
APLP2	0.0659	0.0074	0.1117	0.0829	0.0088	0.1062	0.0693	0.0068	0.0983	0.0885	0.0085	0.096
apoa1BP	0.3073	0.0189	0.0617	0.3663	0.019	0.0518	0.3038	0.0177	0.0583	0.2603	0.0122	0.047
APOA2	0.3665	0.0319	0.0871	0.6963	0.0506	0.0727	0.3665	0.0319	0.0871	0.3508	0.0368	0.105
APOB	0.3423	0.025	0.0729	0.3369	0.0247	0.0734	0.3241	0.0248	0.0766	0.3005	0.0234	0.078
APOD	0.9882	0.0685	0.0693	1.1558	0.0729	0.0631	1.3468	0.0736	0.0546	1.5228	0.0833	0.0547
APOE	0.2635	0.029	0.11	0.318	0.0447	0.1407	0.2429	0.029	0.1193	0.2399	0.0275	0.1147
APOH	0.2737	0.0211	0.0771	0.2584	0.0217	0.0841	0.2795	0.0214	0.0766	0.403	0.0237	0.0588
APP	0.2136	0.0224	0.105	0.2081	0.0219	0.105	0.2329	0.0224	0.0963	0.1997	0.0219	0.1094
ARF1	0	0	0.0751	0	0	0.0578	0	0	0.0775	0	0	0.0665
ARF6	0	0	0.0161	0	0	0.0161	0	0	0.0326	0	0	0.0161
ARHGDIA	0.3079	0.0206	0.0668	0.3467	0.0219	0.0631	0.3473	0.0206	0.0593	0.3457	0.0225	0.0652
ARSA	0.143	0.0156	0.1089	0.2584	0.0267	0.1035	0.1778	0.0224	0.1259	0.1655	0.0157	0.0948
ASAH1	0.4154	0.033	0.0794	0.3535	0.0308	0.0871	0.4218	0.0319	0.0756	0.3847	0.0319	0.083
ASRGL1	0.2028	0.0176	0.0869	0.2543	0.0221	0.0869				0.1606	0.0132	0.082
ATRN	0.0776	0.0055	0.0705	0.3352	0.0278	0.0829	0.1001	0.0067	0.0673	0.0941	0.006	0.0637
AZGP1	0.3553	0.0373	0.105	0.3247	0.035	0.1078	0.3717	0.0381	0.1024	0.3119	0.0343	0.11
B2M	0.3834	0.0372	0.0971	0.4222	0.0411	0.0972	0.3834	0.0372	0.0971	0.4434	0.0373	0.0841
B4GALT1	0.2147	0.0205	0.0955	0.2481	0.0228	0.0919	0.2069	0.0205	0.0991	0.1833	0.0165	0.0899
B4GALT4	0.1411	0.014	0.0993	0.1025	0.0102	0.0992	0.1289	0.0153	0.1187	0.176	0.0166	0.0943
BAIAP2	0.0699	0.0096	0.137	0.0623	0.008	0.1279	0.0685	0.0088	0.1279	0.0605	0.0096	0.1584
BASP1	0.095	0.0079	0.0827	0.0774	0.0059	0.076	0.1135	0.0067	0.059	0.1979	0.0098	0.0497
BCAN	0.1626	0.0158	0.0971	0.1532	0.0156	0.1018	0.1697	0.0156	0.0916	0.1546	0.0163	0.1052
BGN	0.0307	0.0036	0.1177	0.0198	0.0024	0.1219	0.0192	0.0024	0.1257	0.037	0.0048	0.1307
BPIL1	0.2733	0.0183	0.0669	0.2326	0.0183	0.0786	0.2124	0.0193	0.0909	0.2507	0.0183	0.0729
BPNT1	0.0561	0.0033	0.0586	0.0561	0.0033	0.0586	0.0513	0.0033	0.0642	0.0472	0.0033	0.0698
BTD	0.2516	0.019	0.0755	0.2287	0.0173	0.0758	0.2737	0.0182	0.0665	0.2617	0.0215	0.0821
C19orf10	0.0199	0.003	0.1502	0.0186	0.003	0.1605				0.0427	0.0072	0.1689
C1RL	0.2823	0.0281	0.0994	0.3038	0.0271	0.0891	0.3361	0.03	0.0893	0.2823	0.0305	0.1081
C3	0.1945	0.0218	0.1118	0.2639	0.0276	0.1045				0.1821	0.021	0.1151
C9	0.6693	0.0416	0.0622	0.6363	0.0432	0.068	0.4694	0.0391	0.0834	0.4183	0.0359	0.0858
CA2	0.1225	0.0101	0.0825	0.1425	0.0118	0.0828	0.1339	0.0123	0.0919	0.1512	0.0135	0.0892
CA4	0.8131	0.0715	0.0879	0.8003	0.0745	0.0931	0.8046	0.0746	0.0928	0.7645	0.0714	0.0933
CA6	0.3192	0.0349	0.1092	0.2414	0.0275	0.114	0.1552	0.0221	0.1424	0.3208	0.0364	0.1136
CAB39	0.033	0.0012	0.0378	0.0292	0.0012	0.0426	0.0292	0.0012	0.0427	0	0	0.0378
CAB39L	0.0251	0.0025	0.1016	0.0251	0.0025	0.1016	0.0248	0.0026	0.1042	0.0314	0.0025	0.081
CACNA2D1	0.0514	0.0031	0.0594	0.0397	0.0026	0.066	0.0415	0.0028	0.0675	0.0428	0.0026	0.0614
CACYBP	0.0336	0.0019	0.0559	0.0336	0.0019	0.0559	0.1797	0.0114	0.0632	0.0336	0.0019	0.0559
CALR	0.0083	0.001	0.122	0.0086	0.001	0.1174	0.024	0.003	0.1266	0.0077	0.001	0.1312

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
A1BG			
a4GALT			
ABP1	0.2421	0.0225	0.093
ACAT2	0.4008	0.0307	0.0765
ACE	0.1244	0.0158	0.1269
ACE2	0.3421	0.0216	0.0631
ACLY	0.0325	0.0029	0.0884
ACO1	0.0931	0.0077	0.0824
ACP5	0.0655	0.0069	0.1054
ACPP	0.6305	0.0321	0.0508
ACR	0.2794	0.0334	0.1194
ACRBP	0.3637	0.0392	0.1079
ACRV1	0.3361	0.0467	0.1391
ACTN1	0.0411	0.0036	0.0866
ACTN4	0.0197	0.0028	0.1437
ACTR1A	0	0	0.1013
ACYP1	0.3778	0.0311	0.0823
ADAM10	0.055	0.0029	0.0522
ADAM7	0.4725	0.0331	0.0701
ADAMTS1	0.0508	0.005	0.0981
ADAMTSL1	0.1279	0.0085	0.0662
AGA	0.3355	0.0238	0.0711
AGR2	0.0377	0.0025	0.0669
AGRN	0.1819	0.0255	0.1403
AGT	0.2173	0.0326	0.1501
AHCY	0.5014	0.0565	0.1127
AKR1A1	0.021	0.0014	0.0651
AKR1B1	0.0776	0.0069	0.0887
AKR7A2	0.282	0.0352	0.1247
ALAD	0.2201	0.0171	0.0779
ALB	0.38	0.0325	0.0856
ALCAM	0.0884	0.0052	0.0592
ALDH1A1	0.069	0.0061	0.0891
ALDH7A1	0.1145	0.0082	0.072
ALDH9A1	0.1393	0.0129	0.0928
ALDOA	0.0282	0.0032	0.1136
ALDOC			
AMBP	0.1469	0.0185	0.1261
ANG			
ANPEP	0.2178	0.0201	0.0921
ANTXR2	0.1425	0.0079	0.0551
ANXA1	0.0506	0.0032	0.0625
ANXA11	0.7969	0.2975	0.3734
ANXA2	0	0	0.0853
ANXA3	0.1811	0.0136	0.0751
ANXA4	0.1515	0.0083	0.0546
ANXA5			
ANXA6	0.3344	0.038	0.1137
ANXA7	0.1001	0.0064	0.0638
APCS	0.5713	0.0407	0.0713
APEH	0.0737	0.0049	0.0658
APLP2	0.0844	0.0088	0.1043
apoa1BP	0.1785	0.011	0.0616
APOA2	0.1031	0.009	0.0871
APOB	0.2887	0.0231	0.08
APOD	1.0677	0.0756	0.0708
APOE	0.3645	0.0477	0.131
APOH	0.3276	0.023	0.0703
APP	0.2341	0.0233	0.0997
ARF1	0	0	0.0841
ARF6	0	0	0.0243
ARHGDIA			
ARSA	0.1534	0.0137	0.0895
ASAH1	0.2933	0.0277	0.0944
ASRGL1	0.2435	0.0236	0.0968
ATRN	0.1453	0.0122	0.084
AZGP1	0.4268	0.0526	0.1233
B2M	0.3802	0.0392	0.1031
B4GALT1	0.2739	0.0323	0.1178
B4GALT4	0.0861	0.0089	0.1034
BAIAP2	0.0541	0.0086	0.1591
BASP1	0.1164	0.0064	0.0548
BCAN	0.1637	0.0155	0.0948
BGN	0.0206	0.0024	0.1173
BPIL1	0.2296	0.0209	0.0908
BPNT1	0.2473	0.02	0.0808
BTD	0.2566	0.0178	0.0695
C19orf10	0.0214	0.003	0.1399
C1RL	0.3669	0.029	0.0791
C3	0.1862	0.0201	0.108
C9	0.3557	0.0327	0.0919
CA2	0.0989	0.0101	0.102
CA4	0.7025	0.0665	0.0947
CA6	0.2123	0.0231	0.1087
CAB39	0	0	0.0378
CAB39L	0.0335	0.0025	0.076
CACNA2D1	0.1246	0.0064	0.0512
CACYBP	0.0674	0.0038	0.0559
CALR	0.0196	0.0025	0.129

Gene	CH_ω	CH_Ka	CH_Ks	GH_ω	GH_Ka	GH_Ks	GC_ω	GC_Ka	GC_Ks
CAMP	0.161	0.0026	0.0163	0.9702	0.0079	0.0081	1.2983	0.0105	0.0081
CANT1	0.2743	0.0066	0.0242	0.0586	0.0033	0.0566	0.1212	0.0055	0.0457
CAP1	0.9465	0.0056	0.0059	0.5507	0.0065	0.0118	0.1572	0.0019	0.0118
CAPG	0.0795	0.0013	0.016	0.2395	0.0038	0.0159	0.106	0.0025	0.024
CAPN1	0.0474	0.0012	0.0259	0.0397	0.0018	0.0465	0.0152	0.0006	0.0403
CAPNS1	0.2708	0.007	0.0257	0.1144	0.0057	0.0496	0.2743	0.0086	0.0312
CAPZA1	0	0	0.0165	0.1384	0.002	0.0143	0.0685	0.002	0.0288
CAPZA2	0.1839	0.003	0.0163	0	0	0.0218	0.1839	0.003	0.0163
CAPZB	0.0594	0.0014	0.0244	0.1491	0.0029	0.0194	0.0594	0.0014	0.0244
CAT	0.1468	0.0025	0.0168	0.1295	0.0033	0.0255	0.1761	0.0025	0.0141
CCT2	0	0	0.0052	0	0	0.0052	0	0	0.0104
CCT3	0.0774	0.0008	0.0104	0.4427	0.0407	0.092	0.4519	0.0416	0.092
CCT4	0	0	0.0075	0.1096	0.0009	0.0081	0.1645	0.0009	0.0054
CCT5	0	0	0.0054	0	0	0.0162	0	0	0.0162
CCT7	0	0	0.0128	0.0351	0.0008	0.0232	0.0529	0.0008	0.0154
CCT8	0.4664	0.0024	0.0051	0	0	0.0208	0.1154	0.0024	0.0208
CD109	0.2838	0.0042	0.0149	0.2631	0.0043	0.0162	0.3546	0.0053	0.0151
CD14	0.5301	0.0087	0.0163	0.5707	0.0037	0.0065	0.456	0.0074	0.0163
CD151	0	0	0.0221	0	0	0.022	0	0	0.0109
CD38	0.2863	0.0043	0.0151	0.1702	0.0043	0.0254	0.188	0.0058	0.0306
CD44	0.3659	0.0065	0.0177	0.4723	0.0065	0.0137	0.2734	0.0065	0.0237
CD47	0.4818	0.0043	0.0089	0.1629	0.0014	0.0085	0.3188	0.0029	0.009
CD59	0	0.0139	0	0	0.0356	0	3.5291	0.0393	0.0111
CD63	0	0.0019	0	0	0	0.0059	0.3149	0.0019	0.0059
CD81	0	0	0.0303	0	0	0.0203	0	0	0.0342
CD9	0.1451	0.0019	0.0131	0	0	0	0.2919	0.0021	0.0072
CDC42	0	0	0.0059						
CDH1	0.056	0.0015	0.0268	0.0316	0.001	0.0317	0.0932	0.0025	0.0269
CFB	0.4057	0.0056	0.0139	0.3909	0.0063	0.0162	0.5643	0.0092	0.0163
CFL1	0	0	0.0089	0	0	0.0574	0	0	0.0475
CKB	0	0	0.011	0	0	0.0098	0	0	0.0148
CLIC1	0	0	0.035	0.0795	0.0018	0.0231	0.0797	0.0018	0.0231
CLN5	0.4799	0.0086	0.0179	0.5631	0.0105	0.0187	0.4689	0.0065	0.014
CLSTN1	0.0747	0.0018	0.0238	0.0494	0.0018	0.0359	0.0455	0.0018	0.039
CLTC	0	0	0.0088	0	0	0.0106	0	0	0.007
CLU	0.3355	0.0069	0.0207	0.2197	0.0052	0.0237	0.3528	0.0052	0.0147
CNDP2	0.1692	0.0046	0.0273	0.1659	0.0055	0.0334	0.1161	0.0046	0.0398
CNP	0	0	0.0065	0.2171	0.0021	0.0097	0.6542	0.0021	0.0032
CNTN3	0.0518	0.0013	0.0247	0.1034	0.003	0.029	0.059	0.0017	0.029
CNTNAP2	0.0645	0.002	0.0302	0.2852	0.0163	0.0573	0.3319	0.0176	0.0529
col12A1	0.0718	0.001	0.0141	0.0819	0.0015	0.0177	0.1129	0.0016	0.0141
COL18A1	0.2064	0.0082	0.0397	0.4707	0.0204	0.0433	0.3893	0.0184	0.0472
COL6A1	0.1694	0.0039	0.0232	0.0534	0.0017	0.0327	0.0535	0.0017	0.0327
COL6A2	0.0339	0.0013	0.0388	0.0679	0.0026	0.0387	0.0481	0.0022	0.0456
COL9A1	0.5901	0.004	0.0067	0.9684	0.0089	0.0092	0.9363	0.01	0.0107
COLEC12	0.0691	0.0018	0.0255	0.0746	0.0024	0.0315	0.0469	0.0018	0.0376
COMP	0.5379	0.013	0.0242						
COPB2	0.1752	0.0014	0.0082	0.2928	0.0014	0.0049	0.1456	0.0019	0.0131
CP	0.1556	0.002	0.0129	0.3421	0.0045	0.0132	0.2536	0.0041	0.0161
CPAMD8	0.1896	0.0061	0.0323						
CPD	0.2694	0.0036	0.0135						
CPE	0.043	0.0009	0.0213	0.1005	0.0018	0.0182	0.0604	0.0009	0.0152
CPM	0.3865	0.0039	0.0101	0.0715	0.0019	0.0273	0.0633	0.0019	0.0308
CPO	1.5005	0.0058	0.0039	0.2975	0.0047	0.0157	0.6988	0.0082	0.0117
CPVL	0.7789	0.0073	0.0094	0.3483	0.0055	0.0157	0.3863	0.0073	0.0189
CPZ	0.1832	0.0101	0.055	0.1012	0.008	0.0786	0.1651	0.0125	0.0756
CREG1	0.0881	0.0021	0.0235	0.1761	0.0041	0.0235	0	0.0021	0
CRISP1	0.4099	0.0052	0.0126	0.2026	0.0052	0.0254	0.2695	0.0104	0.0384
Crisp2	0.2789	0.0031	0.0111	0.2782	0.0046	0.0167	0.2786	0.0015	0.0055
CRISP3	0.2776	0.0053	0.019	0.1837	0.007	0.0383	0.1174	0.0053	0.0449
CRTAC1	0.1132	0.0041	0.036	0.0688	0.002	0.0297	0.1467	0.0034	0.0233
CRYZ	0.0727	0.0041	0.0558	0.3164	0.0207	0.0656	0.3195	0.0166	0.0518
CST1	0.5387	0.0222	0.0412						
CST3									
CST6	0	0.003	0	0.2466	0.0091	0.0368	0.3295	0.0121	0.0368
CTBS	0.2366	0.0045	0.0191	0.3962	0.0045	0.0114	0.2191	0.0068	0.031
CTSB	0.0482	0.0026	0.0532	0.0292	0.0013	0.0443	0.0265	0.0013	0.0489
CTSD	0.1517	0.0055	0.036	0.0552	0.0022	0.0394	0.066	0.0033	0.0495
CTSF	0.3264	0.0083	0.0255	0.4515	0.0102	0.0225	1.0586	0.0148	0.014
CTSH	0.0562	0.0013	0.0237	0.1398	0.0053	0.0382	0.2843	0.004	0.0141
CTSO	0.075	0.0014	0.0181	0.5046	0.0068	0.0135	0.2401	0.0055	0.0227
CTSZ	0	0	0.0187	0.1321	0.0044	0.033	0.1321	0.0044	0.033
CUL3	0	0	0.0119	0.0935	0.0006	0.0059	0.056	0.0006	0.0099
CYB561	0.2866	0.0062	0.0215	0.2682	0.0046	0.0173	0.3603	0.0015	0.0043
CYB5R2	0.4224	0.0112	0.0264	0.4811	0.0127	0.0265	1.0615	0.0111	0.0105
DAG1	0.4179	0.003	0.0072	0.3042	0.0035	0.0116	0.0944	0.0015	0.016
DBI	0.1542	0.0034	0.0222	0.1534	0.0035	0.023	0	0	0.023
DCD	0.3666	0.0038	0.0105	0	0	0.0106	0	0.0039	0
DCXR	0.8536	0.0132	0.0155	0.5845	0.0152	0.0261	0.0913	0.0019	0.0207
DDAH1	0.3177	0.0015	0.0049	0	0.0016	0	0.6348	0.0031	0.0049
DDB1	0	0	0.0089	0	0	0.0188	0	0	0.0204
DDR1	0	0	0.0115	0.0683	0.0005	0.0071	0.0378	0.0005	0.0129
DDT	0	0	0.0108						
DEFB129	0	0	0	0	0.0024	0	0	0.0024	0
DNAJB9	0.2592	0.0019	0.0073	0.2596	0.0019	0.0073	0.2587	0.0038	0.0147
DNAJC3	0.0697	0.0008	0.0122	0.0701	0.0009	0.0123	0	0	0.0123
DNASE1	0.4299	0.0063	0.0147	0.192	0.0047	0.0246	0.1186	0.0047	0.0398
DNASE2	0.2526	0.0049	0.0195	0.53	0.0062	0.0116	0.1967	0.0062	0.0314
DPEP3	0.179	0.0027	0.0152	0.6149	0.0107	0.0174	0.6468	0.0082	0.0127

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
CAMP	0.6951	0.0347	0.05	0.6417	0.032	0.0499	0.9024	0.0375	0.0415
CANT1	0.0662	0.0056	0.0845	0.0877	0.0067	0.0766	0.0465	0.0045	0.0963
CAP1	0.451	0.0121	0.0269	0.313	0.0065	0.0208	0.3124	0.0084	0.0268
CAPG	0.1399	0.0051	0.0364	0.0854	0.0038	0.0447	0.0857	0.0038	0.0446
CAPN1	0.0264	0.0018	0.0698	0.01	0.0006	0.0613	0.0181	0.0012	0.0677
CAPNS1	0.063	0.0041	0.0659	0.0788	0.0056	0.0706	0.0684	0.0057	0.083
CAPZA1	0.1353	0.003	0.0221	0.0765	0.003	0.0391	0.0917	0.002	0.0215
CAPZA2	0	0	0.0273	0.1374	0.003	0.0218	0	0	0.0273
CAPZB	0.0843	0.0029	0.0344	0.0325	0.0014	0.0445	0	0	0.0445
CAT	0.1657	0.0066	0.0398	0.2186	0.0074	0.034	0.2041	0.0079	0.0386
CCT2	0	0	0.0289	0	0	0.0289	0	0	0.0342
CCT3	0.0202	0.0008	0.0398	0.0404	0.0016	0.0398	0.3689	0.0416	0.1127
CCT4	0	0	0.0381	0	0	0.0355	0.0248	0.0009	0.0359
CCT5	0.0366	0.0016	0.0439	0.0392	0.0016	0.0411	0.0307	0.0016	0.0524
CCT7	0.1206	0.0041	0.0337	0.1577	0.0041	0.0258	0.0894	0.0033	0.0364
CCT8	0	0	0.0288	0.0833	0.0024	0.0288	0	0	0.045
CD109	0.2542	0.0082	0.0322	0.2823	0.0088	0.0312	0.2391	0.0093	0.0388
CD14	0.4306	0.0099	0.023	0.4139	0.0137	0.033	0.3782	0.0087	0.0229
CD151	0.1415	0.0088	0.0622	0.1562	0.0088	0.0563	0.1564	0.0088	0.0563
CD38	0.4758	0.0145	0.0305	0.446	0.016	0.0358	0.502	0.0167	0.0332
CD44	0.3307	0.0118	0.0357	0.2824	0.0124	0.0439	0.2692	0.0118	0.0439
CD47	0.0916	0.0028	0.03	0.1349	0.0043	0.0319	0.0534	0.0014	0.026
CD59	0.8662	0.039	0.045	1.1996	0.0538	0.0448	1.5333	0.0693	0.0452
CD63	0.1026	0.0037	0.0361	0.0513	0.0019	0.0361	0.1242	0.0037	0.0301
CD81	0	0	0.0746	0	0	0.0963	0	0	0.0848
CD9	0.0811	0.0042	0.0517	0.0312	0.0021	0.0672	0.0811	0.0042	0.0522
CDC42	0	0	0.0119	0	0	0.0059			
CDH1	0.1079	0.0081	0.0747	0.1292	0.0093	0.0722	0.124	0.0091	0.0731
CFB	0.2668	0.0113	0.0424	0.3333	0.0142	0.0425	0.3632	0.0163	0.0449
CFL1	0	0	0.0366	0	0	0.0273	0	0	0.0785
CKB	0.0634	0.0016	0.025	0.0526	0.0016	0.0301	0.0536	0.0025	0.0458
CLIC1	0.0527	0.0018	0.0349	0.0393	0.0018	0.0468	0.1058	0.0037	0.0348
CLN5	0.358	0.0129	0.0362	0.3416	0.0086	0.0252	0.6603	0.0092	0.0139
CLSTN1	0.0681	0.0058	0.085	0.0681	0.0058	0.085	0.0681	0.0058	0.085
CLTC	0	0	0.0276	0	0	0.0258	0	0	0.0223
CLU	0.2272	0.0131	0.0576	0.2344	0.0113	0.0483	0.2347	0.0113	0.0482
CNDP2	0.0988	0.0065	0.0655	0.0489	0.0037	0.0754	0.1096	0.0065	0.059
CNP	0.0962	0.0032	0.0329	0.1208	0.0032	0.0262	0.1785	0.0053	0.0296
CNTN3	0.1358	0.0071	0.0522	0.1367	0.0064	0.0469	0.1462	0.0073	0.0499
CNTNAP2	0.1082	0.0072	0.0664	0.1159	0.0078	0.0676	0.2786	0.0225	0.0808
col12A1	0.0693	0.0026	0.0377	0.0822	0.0028	0.0336	0.0648	0.0023	0.0358
COL18A1	0.2568	0.0216	0.0841	0.2375	0.0204	0.0858	0.3579	0.0332	0.0926
COL6A1									
COL6A2	0.0432	0.0029	0.068	0.0322	0.0024	0.0759	0.0472	0.0034	0.0727
COL9A1	0.1988	0.006	0.0301	0.2217	0.007	0.0315	0.3246	0.0121	0.0374
COLEC12	0.1029	0.0047	0.0457	0.0734	0.0041	0.0561	0.113	0.0047	0.0416
COMP	0.2225	0.0053	0.0239	0.3403	0.0137	0.0403			
COPB2	0.1696	0.0033	0.0197	0.102	0.0029	0.0281	0.1547	0.0038	0.0247
CP	0.2642	0.0081	0.0306	0.239	0.0077	0.0321	0.3016	0.0099	0.0327
CPAMD8	0.2041	0.0124	0.0605	0.1688	0.0107	0.0634			
CPD	0.2437	0.0076	0.0312	0.3451	0.0099	0.0286			
CPE	0.0248	0.0009	0.0369	0.0458	0.0018	0.0401	0.0746	0.0028	0.0369
CPM	0.1587	0.0049	0.0308	0.1423	0.0049	0.0343	0.0561	0.0029	0.0521
CPO	0.2065	0.0117	0.0566	0.2911	0.0152	0.0523	0.18	0.0117	0.065
CPVL	0.3075	0.0137	0.0447	0.421	0.0174	0.0414	0.2511	0.0137	0.0547
CPZ	0.1047	0.0079	0.0751	0.3038	0.0135	0.0443	0.0796	0.0069	0.0868
CREG1	0.0343	0.0021	0.0603	0.057	0.0041	0.0727	0.0854	0.0062	0.0729
CRISP1	0.0475	0.0034	0.0722	0.1474	0.0086	0.0584	0.1377	0.0095	0.0688
Crisp2	0.2777	0.0139	0.0502	0.2781	0.0122	0.0438	0.3728	0.0139	0.0374
CRISP3	0.2301	0.0088	0.0383	0.1569	0.007	0.0448	0.1667	0.0053	0.0317
CRTAC1	0.1169	0.0058	0.0498	0.1065	0.0059	0.0553	0.1068	0.0052	0.0484
CRYZ	0.1647	0.0122	0.0741	0.1346	0.0081	0.0603	0.4651	0.0221	0.0476
CST1	0.4947	0.0894	0.1807	0.5639	0.0983	0.1743			
CST3	0	0	0.0559						
CST6	0.0818	0.003	0.0368	0.164	0.006	0.0368	0.2206	0.006	0.0274
CTBS	0.5941	0.0114	0.0192	0.3502	0.0137	0.039	0.44	0.0137	0.0311
CTSB	0.1079	0.0077	0.0717	0.1078	0.0077	0.0717	0.1036	0.0065	0.0627
CTSD	0.0808	0.0065	0.081	0.1166	0.0098	0.0844	0.0742	0.0065	0.0882
CTSF	0.2718	0.0153	0.0563	0.4018	0.0191	0.0474	0.2608	0.0116	0.0444
CTSH	0.1404	0.0125	0.0888	0.1375	0.0102	0.0745	0.1835	0.0147	0.08
CTSO	0.2003	0.0055	0.0272	0.1117	0.0041	0.0366	0.4234	0.0096	0.0226
CTSZ	0.3616	0.0265	0.0733	0.3169	0.0265	0.0836	0.4117	0.028	0.0681
CUL3	0	0	0.0119	0	0	0.0158	0.056	0.0006	0.0099
CYB561	0.2828	0.0124	0.0437	0.3566	0.0108	0.0303	0.4286	0.0093	0.0217
CYB5R2	0.4284	0.016	0.0373	0.4211	0.0111	0.0265	0.4989	0.016	0.032
DAG1	0.3947	0.0126	0.0318	0.2969	0.0109	0.0367	0.3122	0.0115	0.0367
DBI	0.4243	0.0243	0.0572	0.3627	0.0207	0.0572	0.3605	0.0214	0.0594
DCD	1.4741	0.0155	0.0105	0.9172	0.0194	0.0211	0.7297	0.0156	0.0214
DCXR	0.4988	0.0228	0.0458	0.2405	0.0124	0.0515	0.2531	0.0146	0.0575
DDAH1	0.1573	0.0031	0.0197	0.1885	0.0047	0.0247	0.2357	0.0047	0.0198
DDB1	0.0606	0.0019	0.0317	0.0605	0.002	0.0323	0.0456	0.0019	0.0421
DDR1	0.0385	0.0015	0.038	0.0385	0.0015	0.038	0.0494	0.002	0.0395
DDT	0.2797	0.0157	0.056	0.3523	0.0157	0.0444			
DEFB129	0.2917	0.0096	0.0328	0.2917	0.0096	0.0328	0.3655	0.012	0.0327
DNAJB9	0.5181	0.0114	0.0221	0.4516	0.0134	0.0296	0.4524	0.0134	0.0296
DNAJC3	0.0829	0.0027	0.0324	0.0552	0.0018	0.0324	0.0552	0.0018	0.0324
DNASE1	0.2276	0.0175	0.0767	0.1874	0.0175	0.0931	0.1702	0.0159	0.0931
DNASE2	0.4505	0.0123	0.0274	0.3138	0.0124	0.0394	0.3549	0.0111	0.0314
DPEP3	0.222	0.0107	0.0482	0.1984	0.0082	0.0413	0.2646	0.0107	0.0404

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
CAMP	0.9634	0.0319	0.0332	0.8832	0.0292	0.0331	1.288	0.0319	0.0248	2.7827	0.0457	0.0164
CANT1	0.3276	0.0288	0.0878	0.4294	0.0311	0.0724	0.3006	0.0276	0.0917	0.2978	0.0303	0.1016
CAP1	0.2209	0.0121	0.0548	0.1342	0.0065	0.0485	0.1663	0.0088	0.0531	0.1227	0.0056	0.0454
CAPG	0.1032	0.0064	0.0618	0.0826	0.0051	0.0617	0.0727	0.0051	0.0702	0.0579	0.0038	0.066
CAPN1	0.0583	0.0039	0.0662	0.0416	0.0026	0.0618	0.0503	0.0032	0.064	0.0485	0.0032	0.0663
CAPNS1	0.0213	0.0017	0.0807	0.08	0.0069	0.0868	0.0388	0.0035	0.0908	0.0154	0.0017	0.1118
CAPZA1	0.1813	0.003	0.0165	0.0896	0.003	0.0333	0.0918	0.002	0.0215	0.1079	0.003	0.0277
CAPZA2	0	0	0.0163	0.2768	0.003	0.0108	0	0	0.0163	0	0	0.0218
CAPZB	0.5871	0.0871	0.1484	0.5542	0.0855	0.1543	0.6368	0.0871	0.1369	0.5243	0.0871	0.1662
CAT	0.1726	0.0099	0.0575	0.2359	0.0108	0.0456	0.2381	0.0116	0.0489	0.2543	0.0116	0.0456
CCT2	0.0395	0.0008	0.0209	0.0315	0.0008	0.0262	0.0315	0.0008	0.0262	0.0208	0.0008	0.0397
CCT3	0.1139	0.0048	0.0425	0.133	0.0056	0.0425	0.4071	0.0458	0.1126	0.1173	0.004	0.0343
CCT4	0	0	0.0329	0	0	0.0303	0.0324	0.0009	0.0275	0	0	0.0381
CCT5	0	0	0.0393	0	0	0.0362	0	0	0.0456	0.0594	0.0018	0.0301
CCT7	0.0366	0.0016	0.0444	0.0447	0.0016	0.0364	0.0345	0.0016	0.0471	0.0929	0.0049	0.0526
CCT8	0.0434	0.0016	0.0368	0.1088	0.004	0.0368	0.0301	0.0016	0.0532	0.0404	0.0016	0.0396
CD109	0.2592	0.0095	0.0368	0.3115	0.0101	0.0326	0.2575	0.0101	0.0394	0.2771	0.0108	0.0389
CD14	0.7048	0.0162	0.023	0.6064	0.02	0.0329	0.6529	0.0149	0.0229	0.4909	0.0162	0.033
CD151	0.2798	0.0148	0.0531	0.3625	0.0148	0.0409	0.3629	0.0148	0.0409	0.2546	0.0074	0.029
CD38	0.9841	0.0248	0.0252	0.7658	0.0233	0.0305	0.861	0.0263	0.0305	0.8643	0.0219	0.0253
CD44	0.3713	0.0148	0.0398	0.2831	0.0154	0.0543	0.307	0.0154	0.0501	0.2729	0.0148	0.0542
CD47	0.0355	0.0014	0.0388	0.0696	0.0029	0.0412	0	0	0.0394	0.0317	0.0014	0.0434
CD59	2.5306	0.0705	0.0279	2.9591	0.0821	0.0278	2.2825	0.077	0.0337	1.63	0.0727	0.0446
CD63	0.0774	0.0019	0.0239	0	0	0.0239	0.1568	0.0019	0.0119	0.0513	0.0019	0.0361
CD81	0	0	0.1039	0	0	0.1113	0	0	0.1155	0	0	0.0964
CD9	0	0	0.0131	0.1451	0.0019	0.0131	0	0	0.0072	0.0624	0.0042	0.0672
CDC42												
CDH1	0.1036	0.006	0.0581	0.1376	0.0075	0.0548	0.1281	0.007	0.0549	0.1655	0.0121	0.0732
CFB	0.2967	0.0134	0.045	0.3929	0.0166	0.0423	0.3478	0.0166	0.0478	0.1617	0.0089	0.0549
CFL1	0	0	0.0742	0	0	0.0645	0	0	0.1195	0	0	0.0752
CKB	0.1382	0.0046	0.0335	0.1241	0.0046	0.0374	0.0632	0.0016	0.0248	0.1044	0.0048	0.0457
CLIC1	0.1072	0.0024	0.022	0.1075	0.0024	0.0219	0.6523	0.0047	0.0072	0.0803	0.0024	0.0294
CLN5	0.276	0.0162	0.0588	0.2496	0.0119	0.0475	0.4677	0.0132	0.0281	0.3884	0.014	0.0361
CLSTN1	0.0367	0.0032	0.0869	0.0389	0.0032	0.0819	0.036	0.0032	0.0886	0.0697	0.0055	0.0785
CLTC	0.0199	0.0005	0.0259	0.0232	0.0005	0.0222	0.0276	0.0005	0.0187	0.0242	0.0005	0.0213
CLU	0.2413	0.0131	0.0543	0.2515	0.0113	0.045	0.2356	0.0113	0.0481	0.2383	0.0122	0.0512
CNDP2	0.0954	0.0078	0.082	0.0707	0.0067	0.0947	0.106	0.0078	0.0738	0.0677	0.0056	0.0823
CNP	0.0423	0.0021	0.0499	0.049	0.0021	0.0431	0.0907	0.0042	0.0465	0.0592	0.0032	0.0535
CNTN3	0.1263	0.006	0.0475	0.1023	0.0047	0.0461	0.1199	0.0058	0.0483	0.1897	0.0071	0.0373
CNTNAP2	0.0727	0.006	0.0829	0.0772	0.0067	0.0867	0.1669	0.0176	0.1053	0.1159	0.0093	0.0804
col12A1	0.1363	0.0068	0.0499	0.15	0.0072	0.0478	0.1423	0.0067	0.0473	0.1417	0.0064	0.0454
COL18A1												
COL6A1	0.385	0.0578	0.15	0.4101	0.0602	0.1467	0.3699	0.062	0.1676			
COL6A2	0.5571	0.0652	0.117	0.5312	0.0649	0.1222	0.5828	0.065	0.1114	0.5509	0.07	0.1271
COL9A1	0.2437	0.0111	0.0455	0.2744	0.0121	0.044	0.3457	0.0176	0.051	0.2212	0.0108	0.049
COLEC12	0.0303	0.0018	0.0581	0.0182	0.0012	0.0644	0.0369	0.0018	0.0478	0.0734	0.0041	0.0561
COMP	0.1304	0.0073	0.0557	0.2671	0.0186	0.0697				0.1924	0.0094	0.0487
COPB2	0.0967	0.0019	0.0197	0.0509	0.0014	0.0281	0.0964	0.0024	0.0247	0.0802	0.0024	0.0298
CP	0.1179	0.0048	0.041	0.123	0.0052	0.0426	0.1761	0.0066	0.0372	0.1324	0.006	0.0457
CPAMD8	0.2041	0.0157	0.0769	0.188	0.0154	0.082				0.2147	0.0178	0.0831
CPD	0.1949	0.0094	0.0484	0.2571	0.0115	0.0447				0.2142	0.0085	0.0395
CPE	0.1603	0.0064	0.0401	0.17	0.0074	0.0433	0.2064	0.0083	0.0401	0.1375	0.0055	0.0401
CPM	0.1626	0.0044	0.0271	0.2134	0.0066	0.031	0.0861	0.0044	0.0512	0.113	0.0044	0.039
CPO	0.1452	0.007	0.0482	0.2393	0.0105	0.044	0.124	0.007	0.0564	0.3924	0.0093	0.0238
CPVL	0.221	0.0128	0.058	0.285	0.0156	0.0547	0.2085	0.0128	0.0614	0.2698	0.0174	0.0646
CPZ												
CREG1	0.0493	0.0021	0.0418	0.0765	0.0041	0.0541	0.1147	0.0062	0.0542	0.0519	0.0041	0.0796
CRISP1	0.0588	0.0034	0.0584	0.1479	0.0086	0.0583	0.1474	0.0086	0.0584	0.1054	0.0069	0.0653
Crisp2	0.3846	0.0219	0.0569	0.4128	0.0187	0.0453	0.3964	0.0203	0.0512	0.4006	0.0228	0.0568
CRISP3	0.1373	0.0053	0.0384	0.1564	0.007	0.045	0.2775	0.0088	0.0317	0.562	0.007	0.0125
CRTAC1	0.065	0.0044	0.0681	0.0557	0.0044	0.0795	0.0514	0.0038	0.0731	0.0685	0.0055	0.0807
CRYZ	0.2596	0.0205	0.0788	0.2705	0.0163	0.0604	0.5329	0.0278	0.0521	0.6881	0.0204	0.0297
CST1	0.2177	0.0692	0.3178	0.2873	0.0848	0.295				0.3047	0.0755	0.2476
CST3	0.165	0.0125	0.0755							0.337	0.0124	0.0369
CST6	0.1628	0.006	0.037	0.2446	0.0091	0.037	0.2453	0.0091	0.0369	0.0814	0.003	0.037
CTBS	0.1827	0.0057	0.0312	0.1546	0.008	0.0516	0.2257	0.008	0.0353	0.1546	0.008	0.0517
CTSB	0.169	0.0174	0.103	0.1539	0.0174	0.1131	0.1732	0.0162	0.0936	0.1504	0.0147	0.0978
CTSD	0.1029	0.0109	0.1063	0.13	0.0143	0.1098	0.1029	0.0109	0.1063	0.0894	0.0098	0.1101
CTSF	0.4773	0.0249	0.0521	0.6778	0.0289	0.0427	0.4893	0.0209	0.0426	0.4817	0.0213	0.0443
CTSH	0.1425	0.0087	0.061	0.154	0.0067	0.0433	0.2487	0.0114	0.0458	0.1689	0.0117	0.0693
CTSO	0.345	0.0102	0.0297	0.2267	0.0089	0.0391	0.5746	0.0144	0.025	0.3683	0.0075	0.0204
CTSZ	0.1503	0.0102	0.0679	0.1306	0.0102	0.0782	0.2007	0.0146	0.0729	0.4321	0.034	0.0787
CUL3	0.0199	0.0006	0.0281	0.0173	0.0006	0.0322	0.0428	0.0011	0.0262	0.0199	0.0006	0.0281
CYB561	0.8111	0.1369	0.1688	0.8007	0.1351	0.1687	0.8403	0.1341	0.1595	0.882	0.1404	0.1592
CYB5R2	0.2356	0.0127	0.0541	0.2057	0.0111	0.0541	0.2658	0.0159	0.06	0.2619	0.0127	0.0486
DAG1	0.2235	0.0086	0.0385	0.1738	0.0068	0.0392	0.1675	0.0068	0.0407	0.2323	0.012	0.0516
DBI												
DCD	0.4175	0.0291	0.0698	0.5269	0.0291	0.0553	0.5246	0.0294	0.0561	0.4362	0.0242	0.0554
DCXR	0.3255	0.0228	0.07	0.1469	0.0094	0.0642	0.163	0.0114	0.0698	0.1899	0.0144	0.0761
DDAH1	0.037	0.0018	0.048	0.0657	0.0036	0.0542	0.0739	0.0036	0.0483	0.0986	0.0053	0.0542
DDB1	0.0089	0.0004	0.0433	0.0086	0.0004	0.0455	0.0075	0.0004	0.0512	0.0565	0.0023	0.0408
DDR1	0.0302	0.0015	0.0485	0.0302	0.0015	0.0485	0.039	0.002	0.05	0.0459	0.002	0.0425
DDT	1.0482	0.0166	0.0159	1.0482	0.0166	0.0159				0.6964	0.0223	0.032
DEFB129	0.4104	0.0168	0.041	0.4104	0.0168	0.041	0.4702	0.0193	0.041	0.8896	0.0217	0.0244
DNAJB9	0.3251	0.0173	0.0532	0.3148	0.0192	0.0611	0.3153	0.0192	0.061	0.2966	0.0134	0.0452
DNAJC3	0.0452	0.0026	0.0565	0.034	0.0017	0.05	0.0302	0.0017	0.0571	0.0782	0.0036	0.0458
DNASE1	0.2668	0.0192	0.072	0.2315	0.0192	0.0829	0.1623	0.0144	0.0884	0.1926	0.0192	0.0997
DNASE2	0.3113	0.0123	0.0396	0.2054	0.0123	0.0601	0.2625	0.0136	0.0519	0.3356	0.0167	0.0498
DPEP3	0.4936	0.0193	0.0391	0.4613	0.016	0.0347	0.5677	0.0193	0.034	0.3745	0.0161	0.043

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
CAMP	0.8195	0.0687	0.0838	0.7868	0.0658	0.0837	0.9516	0.0715	0.0752	1.1661	0.0773	0.0663
CANT1	0.121	0.0167	0.1382	0.1459	0.019	0.1301	0.1035	0.0156	0.1507	0.1215	0.0146	0.1204
CAP1	0.1677	0.0102	0.0611	0.0761	0.0046	0.061	0.1191	0.0065	0.0546	0.0641	0.0037	0.0579
CAPG	0.0725	0.0051	0.0703	0.0484	0.0038	0.0789	0.0485	0.0038	0.0788	0.0726	0.0051	0.0702
CAPN1	0.0552	0.0068	0.1231	0.0486	0.0055	0.114	0.0564	0.0062	0.1094	0.0551	0.0062	0.1118
CAPNS1	0.0557	0.0056	0.0998	0.0735	0.007	0.0951	0.0689	0.0071	0.103	0.0162	0.0014	0.0854
CAPZA1	0.0677	0.0015	0.022	0.0539	0.0015	0.0277	0	0	0.0288	0.0447	0.0015	0.0333
CAPZA2	0	0	0.0329	0.1095	0.003	0.0274	0	0	0.0329	0	0	0.0386
CAPZB	0.8099	0.1018	0.1258	0.7621	0.1002	0.1315	0.8099	0.1018	0.1258	0.7421	0.1018	0.1372
CAT	0.1603	0.0141	0.088	0.1828	0.0149	0.0817	0.1855	0.0158	0.0854	0.2611	0.0158	0.0604
CCT2	0	0	0.0506	0	0	0.0561	0	0	0.0561	0	0	0.0673
CCT3	0.0629	0.0052	0.0833	0.0726	0.006	0.0833	0.2979	0.0461	0.1548	0.0642	0.0044	0.069
CCT4	0.0511	0.0025	0.0487	0.054	0.0025	0.046	0.092	0.0036	0.0389	0.0461	0.0025	0.054
CCT5	0	0	0.0758	0	0	0.0758	0	0	0.0847	0.0161	0.0016	0.0998
CCT7	0.0094	0.0008	0.0861	0.0105	0.0008	0.0776	0.0091	0.0008	0.0889	0.0457	0.0041	0.089
CCT8	0.0505	0.0024	0.0476	0.0674	0.0032	0.0476	0.0375	0.0024	0.0641	0.0569	0.0024	0.0422
CD109	0.3876	0.0275	0.0708	0.3965	0.0281	0.0708	0.3536	0.029	0.082	0.366	0.0287	0.0785
CD14	0.3706	0.0238	0.0641	0.3529	0.0263	0.0746	0.3524	0.0225	0.0639	0.3343	0.0238	0.0711
CD151	0.136	0.0177	0.1301	0.1507	0.0177	0.1174	0.1509	0.0177	0.1172	0.1053	0.0123	0.1172
CD38	0.6429	0.0346	0.0538	0.6083	0.0361	0.0593	0.6067	0.0361	0.0594	0.6411	0.0346	0.0539
CD44	0.4062	0.022	0.0542	0.3493	0.0226	0.0647	0.3542	0.0214	0.0604	0.3675	0.0214	0.0583
CD47	0.1276	0.0055	0.0432	0.1565	0.0072	0.0459	0.0953	0.0042	0.0439	0.0968	0.0055	0.0569
CD59	0.9971	0.0744	0.0746	1.38	0.086	0.0624	1.2098	0.0907	0.0749	0.8801	0.0862	0.098
CD63	0	0	0.055	0.0337	0.0019	0.055	0	0	0.049	0.0547	0.0037	0.0677
CD81	0.0523	0.0075	0.1433	0.055	0.0075	0.1362	0.061	0.0084	0.1384	0.0618	0.0083	0.1336
CD9	0.094	0.0067	0.0711	0.1008	0.0086	0.0854	0.0938	0.0074	0.0794	0.0976	0.0116	0.119
CDC42	0.0781	0.0019	0.0241	0.1045	0.0019	0.018				0.0781	0.0019	0.0241
CDH1	0.216	0.0199	0.0923	0.2336	0.0213	0.0913	0.2278	0.021	0.0924	0.1915	0.0219	0.1144
CFB	0.2949	0.0272	0.0923	0.2785	0.0272	0.0976	0.316	0.0308	0.0976	0.2082	0.0214	0.1027
CFL1	0.0227	0.0026	0.1153	0.0249	0.0026	0.105	0.0221	0.0027	0.1206	0.0225	0.0026	0.1168
CKB	0.0573	0.0035	0.0607	0.0538	0.0035	0.0646	0.0515	0.0031	0.061	0.0475	0.0032	0.0669
CLIC1	0.2271	0.0149	0.0657	0.2276	0.0149	0.0655	0.4093	0.0168	0.041	0.2571	0.0168	0.0654
CLN5	0.3113	0.0318	0.1021	0.3026	0.0273	0.0902	0.3106	0.0226	0.0727	0.3603	0.0296	0.082
CLSTN1	0.0464	0.0062	0.1342	0.049	0.0062	0.1273	0.0464	0.0062	0.1342	0.0623	0.0085	0.1359
CLTC	0.0114	0.0005	0.0451	0.0114	0.0005	0.0451	0.0124	0.0005	0.0415	0.0107	0.0005	0.0479
CLU	0.2321	0.0246	0.106	0.2371	0.0228	0.0963	0.2294	0.0228	0.0995	0.2747	0.0228	0.0831
CNDP2	0.1352	0.0139	0.1028	0.1042	0.0111	0.1065	0.1307	0.0139	0.1063	0.0893	0.0092	0.1033
CNP	0.1496	0.0106	0.0709	0.1661	0.0106	0.0638	0.1889	0.0127	0.0674	0.1564	0.0117	0.0746
CNTN3	0.099	0.0082	0.0825	0.0881	0.0069	0.078	0.0936	0.0077	0.0826	0.1307	0.0098	0.0747
CNTNAP2	0.0566	0.0062	0.1096	0.0546	0.0062	0.1135	0.1583	0.0217	0.137	0.0877	0.0088	0.1007
col12A1	0.0953	0.0058	0.0609	0.0993	0.0059	0.0592	0.0911	0.0054	0.0597	0.0941	0.0054	0.0578
COL18A1	0.2028	0.0291	0.1435	0.205	0.0289	0.1408	0.277	0.0413	0.1489	0.2622	0.0312	0.1189
COL6A1	0.0713	0.0105	0.147	0.0772	0.011	0.142	0.0518	0.0077	0.1477			
COL6A2	0.1993	0.0274	0.1374	0.1835	0.0269	0.1467	0.1953	0.0274	0.1402	0.1774	0.0261	0.147
COL9A1	0.1608	0.0102	0.0637	0.1572	0.0102	0.0652	0.2546	0.017	0.0668	0.1576	0.0102	0.0651
COLEC12	0.0458	0.0048	0.1054	0.0392	0.0042	0.1078	0.0418	0.0042	0.101	0.0735	0.0073	0.0987
COMP	0.1798	0.0196	0.1089	0.2385	0.0294	0.1232				0.1966	0.0208	0.1056
COPB2	0.0379	0.0019	0.0503	0.0257	0.0014	0.0556	0.0458	0.0024	0.0521	0.0393	0.0024	0.0607
CP	0.2207	0.0138	0.0624	0.2112	0.0142	0.0671	0.2733	0.0153	0.0558	0.2239	0.0154	0.0688
CPAMD8	0.2167	0.0205	0.0947	0.1667	0.0172	0.1032				0.19	0.0192	0.1012
CPD												
CPE	0.0398	0.0028	0.0692	0.0507	0.0037	0.0725	0.0664	0.0046	0.0692	0.0265	0.0018	0.0691
CPM	0.2525	0.0167	0.0663	0.2391	0.0167	0.07	0.1816	0.0147	0.0812	0.2368	0.0157	0.0665
CPO	0.4591	0.0738	0.1607	0.4822	0.0751	0.1557	0.4242	0.0732	0.1725	0.5023	0.0763	0.1518
CPVL	0.3559	0.0193	0.0543	0.3674	0.0212	0.0577	0.3025	0.0175	0.0577	0.2723	0.0203	0.0744
CPZ												
CREG1	0.2699	0.0146	0.0541	0.2779	0.0167	0.0601	0.3123	0.0188	0.0603	0.158	0.0146	0.0924
CRISP1	0.9822	0.0835	0.085	1.0623	0.0864	0.0814	1.0048	0.0854	0.085	0.8422	0.0835	0.0991
Crisp2	0.6859	0.0371	0.0541	0.7962	0.0339	0.0425	0.7332	0.0355	0.0484	0.5954	0.0398	0.0669
CRISP3	0.3626	0.0414	0.1141	0.3408	0.0414	0.1214	0.3887	0.0414	0.1065	0.5048	0.0396	0.0784
CRTAC1												
CRYZ	0.1466	0.0136	0.0926	0.1209	0.0095	0.0785	0.316	0.0207	0.0656	0.3495	0.0149	0.0428
CST1	0.3488	0.0984	0.282	0.3778	0.1037	0.2746				0.4247	0.1019	0.2399
CST3	0.0978	0.0125	0.1273							0.1167	0.0124	0.1066
CST6	0.4568	0.0213	0.0466	0.5231	0.0244	0.0466	0.4343	0.0244	0.0562	0.3242	0.0182	0.0562
CTBS	0.4501	0.0229	0.0508	0.3512	0.0252	0.0717	0.3972	0.0252	0.0634	0.3605	0.0229	0.0636
CTSB	0.1357	0.0129	0.0954	0.123	0.0129	0.1052	0.1224	0.0118	0.096	0.1033	0.0103	0.1001
CTSD	0.2456	0.0243	0.0989	0.2291	0.0277	0.1209	0.1945	0.0243	0.1249	0.2005	0.0243	0.1212
CTSF	0.1807	0.0177	0.0977	0.2363	0.0224	0.0947	0.1935	0.0177	0.0913	0.2014	0.0181	0.09
CTSH	0.1415	0.0134	0.0947	0.1637	0.0121	0.0737	0.1921	0.0161	0.084	0.1453	0.0176	0.1213
CTSO	0.3665	0.0221	0.0602	0.2951	0.0207	0.07	0.4239	0.0235	0.0554	0.4698	0.0193	0.0411
CTSZ	0.2407	0.0203	0.0846	0.2088	0.0203	0.0975	0.2657	0.0241	0.0908	0.2543	0.0316	0.1244
CUL3	0.0261	0.0011	0.0423	0.0238	0.0011	0.0465	0.0373	0.0017	0.0446	0.0238	0.0011	0.0465
CYB561	0.1503	0.0236	0.1569	0.1559	0.022	0.1411	0.1433	0.0189	0.1321	0.1555	0.0204	0.1311
CYB5R2	0.1644	0.0176	0.1068	0.168	0.0159	0.0949	0.2326	0.0208	0.0893	0.1969	0.0175	0.0891
DAG1	0.2043	0.0091	0.0448	0.1353	0.0071	0.0525	0.141	0.0076	0.054	0.2352	0.0126	0.0536
DBI	0.3378	0.0317	0.0938	0.2994	0.0281	0.0938	0.2596	0.0253	0.0974	0.3727	0.0352	0.0944
DCD	0.6212	0.0479	0.0771	0.7933	0.0521	0.0656	0.728	0.0483	0.0664	0.6196	0.0479	0.0773
DCXR	0.3282	0.0296	0.0901	0.2831	0.0238	0.084	0.2445	0.022	0.0898	0.3095	0.0303	0.0978
DDAH1	0	0	0.0608	0.0235	0.0015	0.066	0.0254	0.0016	0.0611	0.051	0.0031	0.0607
DDB1	0	0	0.0607	0	0	0.0633	0	0	0.0717	0.0303	0.002	0.065
DDR1	0.0436	0.0029	0.0671	0.0417	0.0029	0.0703	0.0521	0.0034	0.0655	0.0485	0.0034	0.0704
DDT	0.1369	0.0157	0.1148	0.1534	0.0157	0.1025				0.2256	0.0317	0.1407
DEFB129	0.3195	0.0241	0.0756	0.3195	0.0241	0.0756	0.3523	0.0266	0.0755	0.4989	0.0291	0.0582
DNAJB9	0.5167	0.0154	0.0297	0.4633	0.0173	0.0374	0.4641	0.0173	0.0373	0.3086	0.0115	0.0373
DNAJC3	0.038	0.0034	0.0897	0.0284	0.0026	0.0897	0.0286	0.0026	0.0906	0.0514	0.0045	0.0873
DNASE1	0.2764	0.0256	0.0925	0.234	0.0256	0.1093	0.1895	0.0207	0.1093	0.2111	0.0255	0.121
DNASE2	0.4268	0.0319	0.0747	0.3652	0.0319	0.0874	0.3802	0.0333	0.0876	0.43	0.0357	0.0831
DPEP3	0.3448	0.0316	0.0917	0.3347	0.0295	0.0881	0.3557	0.0307	0.0863	0.3243	0.0302	0.0932

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
CAMP	1.5006	0.0743	0.0495
CANT1	0.2658	0.0417	0.1571
CAP1	0.0461	0.0037	0.0805
CAPG	0.0458	0.0038	0.0834
CAPN1	0.0486	0.0058	0.1194
CAPNS1	0.0173	0.0017	0.0997
CAPZA1	0.054	0.0015	0.0277
CAPZA2	0	0	0.0273
CAPZB	0.6354	0.086	0.1353
CAT	0.1798	0.0175	0.0972
CCT2	0.0147	0.0008	0.0561
CCT3	0.1094	0.0085	0.0775
CCT4	0.061	0.0025	0.0408
CCT5	0	0	0.0909
CCT7	0.0076	0.0008	0.1063
CCT8	0.0796	0.004	0.0503
CD109	0.3581	0.0285	0.0794
CD14	0.3707	0.0276	0.0745
CD151	0.1435	0.0148	0.1035
CD38	1.0294	0.0391	0.038
CD44	0.3684	0.0265	0.0721
CD47	0.0727	0.0041	0.0568
CD59	1.3788	0.1019	0.0739
CD63	0.0273	0.0019	0.0678
CD81	0.0553	0.0083	0.1494
CD9	0.0782	0.0067	0.0854
CDC42			
CDH1	0.195	0.0188	0.0964
CFB	0.2133	0.0204	0.0955
CFL1	0.0192	0.0026	0.1364
CKB	0.0799	0.0058	0.0726
CLIC1	0.2561	0.0095	0.0371
CLN5	0.4133	0.0307	0.0742
CLSTN1	0.0413	0.005	0.1213
CLTC	0.0117	0.0005	0.0442
CLU	0.2559	0.0233	0.091
CNDP2	0.0953	0.0112	0.1171
CNP	0.1084	0.0085	0.0781
CNTN3	0.1087	0.0082	0.0751
CNTNAP2	0.0672	0.0077	0.1142
col12A1	0.1454	0.0097	0.0667
COL18A1			
COL6A1	0.2534	0.0521	0.2055
COL6A2	0.4732	0.0869	0.1835
COL9A1	0.1643	0.0134	0.0812
COLEC12	0.0449	0.0042	0.0942
COMP	0.15	0.0206	0.1373
COPB2	0.0177	0.001	0.0538
CP	0.1765	0.0121	0.0688
CPAMD8	0.1969	0.021	0.1066
CPD			
CPE	0.0696	0.0055	0.0792
CPM	0.216	0.015	0.0694
CPO	0.5006	0.0712	0.1422
CPVL	0.2616	0.0231	0.0882
CPZ			
CREG1	0.2277	0.0167	0.0733
CRISP1	1.0293	0.0874	0.0849
Crisp2	0.5498	0.0347	0.0631
CRISP3	0.5031	0.0395	0.0786
CRTAC1			
CRYZ	0.4607	0.0177	0.0384
CST1	0.3661	0.0877	0.2397
CST3	0.1167	0.0124	0.1066
CST6	0.3204	0.0213	0.0664
CTBS	0.2432	0.0207	0.0851
CTSB	0.1547	0.0174	0.1127
CTSD	0.1799	0.0249	0.1382
CTSF	0.2618	0.0239	0.0912
CTSH	0.1266	0.0107	0.0845
CTSO	0.4018	0.0214	0.0532
CTSZ	0.2658	0.026	0.0977
CUL3	0.0282	0.0017	0.0594
CYB561	0.5365	0.1436	0.2677
CYB5R2	0.1331	0.0143	0.1075
DAG1	0.0943	0.0066	0.0699
DBI			
DCD	0.9	0.0494	0.0548
DCXR	0.2897	0.0295	0.102
DDAH1	0.0179	0.0018	0.0994
DDB1	0.0053	0.0004	0.0746
DDR1	0.0455	0.0034	0.075
DDT	0.095	0.0111	0.1169
DEFB129	0.5483	0.0365	0.0667
DNAJB9	0.2519	0.0173	0.0687
DNAJC3	0.0284	0.0026	0.0898
DNASE1	0.1048	0.0128	0.1218
DNASE2	0.3737	0.0344	0.0921
DPEP3	0.4311	0.0372	0.0862

Gene	CH_*ω*	CH_*Ka*	CH_*Ks*	GH_*ω*	GH_*Ka*	GH_*Ks*	GC_*ω*	GC_*Ka*	GC_*Ks*
DPP4	0.142	0.0017	0.0119	0.3159	0.0056	0.0178	0.6286	0.0062	0.0098
DPP7	0.1951	0.0037	0.0188	0.3354	0.0078	0.0231	0.5403	0.0089	0.0164
DSC2	0.3668	0.0063	0.0173	0.4278	0.0054	0.0125	0.3964	0.0068	0.0173
DSC3	0.2295	0.0044	0.0192	0.142	0.0034	0.0241	0.1405	0.0029	0.0208
ECM1	0.5333	0.0039	0.0073	0.5617	0.0055	0.0097	0.3635	0.0062	0.0172
EDIL3	0.0582	0.0009	0.0155	0.0287	0.0009	0.0313	0	0	0.0282
EEF1A1	0	0	0.0061	0	0	0.0091	0	0	0.0091
EEF1G	0.1004	0.0009	0.0089	0.1246	0.0032	0.026	0.0725	0.0022	0.0298
EEF2	0.0171	0.0006	0.0353	0	0	0.0452	0.0122	0.0006	0.0495
EFEMP1	0	0	0.003	0.0585	0.0009	0.015	0.0733	0.0009	0.012
EFHD2	0	0.0018	0	0	0	0.0257	0	0	0.0257
EGF	0.3627	0.0061	0.0169	0.5385	0.0068	0.0125	0.3455	0.0056	0.0163
ELSPBP1	0.2401	0.0084	0.0349	0.1516	0.0057	0.0375	0.2416	0.0063	0.026
ENO1	0	0	0.0261	0	0	0.0261	0	0	0.0327
ENPP3	0.283	0.0029	0.0104	0.2811	0.0031	0.0112	0.1551	0.0031	0.0203
ENPP5	0.1678	0.0027	0.0162	0.2116	0.0027	0.0128	0.5625	0.0054	0.0097
EPHA5	0.1022	0.0013	0.0124	0.3632	0.0081	0.0223	0.4245	0.0077	0.0181
ESD	0.0566	0.0015	0.027						
EXTL2	0	0.0026	0	0.2867	0.0026	0.0091	0.2867	0.0026	0.0091
F11R	0	0.0027	0	0.3416	0.0028	0.0081	0	0	0.0081
FAM12A	0	0.0057	0						
FAM12B	0.4838	0.0057	0.0118						
fam3B	0.3055	0.0034	0.0111	0.2026	0.0034	0.0168	0.6117	0.0034	0.0056
FAM3C	0.2964	0.0019	0.0065	0	0	0.0064	0.1475	0.0019	0.013
FASN	0.163	0.0046	0.0279	0.2014	0.0064	0.0316	0.1847	0.0066	0.0359
FBLN2	0.192	0.0057	0.0297	0.1486	0.0058	0.0389	0.1601	0.0063	0.0395
FBP1	0.2391	0.0039	0.0164	0.1066	0.0014	0.0136	0.0635	0.0014	0.0228
FCGBP	0.2442	0.0098	0.0401	0.243	0.0091	0.0376	0.2208	0.0094	0.0428
FDPS	0	0	0.01	0.2787	0.0087	0.0312	0.2502	0.0087	0.0347
FH	0.1593	0.0026	0.0163	0.0907	0.0017	0.0191	0.1057	0.0026	0.0246
FKBP4	0.4141	0.0033	0.008	0.2618	0.0086	0.0328	0.3964	0.011	0.0278
FLNB	0.0665	0.0017	0.0252	0.0626	0.0017	0.0268	0.0504	0.0013	0.025
FMOD	0	0	0.0111	0	0	0.0149	0	0	0.0263
FN1	0.0822	0.0018	0.0217	0.0884	0.0023	0.0263	0.0703	0.002	0.028
FOLH1	0.2986	0.0055	0.0185	0.8497	0.0101	0.0119	0.4882	0.0107	0.022
FSTL1	0.0692	0.0014	0.0201	0	0	0.0164	0.0903	0.0015	0.0164
FTH1	0	0	0.0259						
FUCA1	0.3468	0.0076	0.0218	0.3812	0.0047	0.0123	0.3027	0.0085	0.0281
FUCA2	0	0	0.0126	0.0422	0.0009	0.0221	0.0994	0.0009	0.0094
FUT3	0.1961	0.0099	0.0505	0.1327	0.0062	0.0467	0.1687	0.0099	0.059
GAA	0.2145	0.0066	0.0308	0.3182	0.0081	0.0255	0.2531	0.0072	0.0283
GALC	0.0379	0.0007	0.0174						
GALNS	0.2381	0.0084	0.0352	0.2824	0.0085	0.0303	0.1535	0.006	0.0389
GALNT6	0.184	0.0022	0.0119	0.2039	0.0014	0.0069	0.77	0.0037	0.0048
GALNT7	0.1069	0.002	0.0184	0.0937	0.0007	0.0074	0.0932	0.0014	0.015
GANAB	0.1849	0.0018	0.0099	0.1623	0.0009	0.0056	0.2775	0.0028	0.0099
GAPDH	0	0	0.0169	0	0	0.0299	0	0	0.0212
GAPDHS	0.3344	0.0055	0.0164	0.1249	0.0033	0.0264	0.4026	0.0066	0.0164
GAS6	0.2063	0.0064	0.0311						
GBA	0.2585	0.0033	0.0128	1.3397	0.0961	0.0717	1.2203	0.0943	0.0773
GC	0.1215	0.0018	0.0146	0.1013	0.0009	0.0088	0.0504	0.0009	0.0177
GCHFR	0	0	0.0168	0.6316	0.0107	0.0169	0	0.0107	0
GDF15	0.4725	0.0152	0.0321	0.5693	0.0136	0.0239	0.5209	0.0167	0.0321
GDI2	0.0408	0.001	0.0235	0.0283	0.001	0.0339	0.0815	0.0019	0.0236
GFRA2	0.0619	0.0013	0.0214	0.0448	0.0009	0.0212	0.1037	0.0013	0.0128
GGH	0.0974	0.0014	0.014	0.2831	0.0029	0.0101	0.568	0.0029	0.005
GGT1	0.1465	0.0048	0.0325	0.4251	0.0131	0.0309	0.253	0.0105	0.0415
GLA	0	0.006	0	0	0.0012	0	0	0.0082	0
GLB1	0.4506	0.0043	0.0095	0.4134	0.0055	0.0134	0.2008	0.0031	0.0153
GLB1L	0.2823	0.0054	0.0192						
GLG1	0.048	0.0007	0.0153	0.0453	0.0011	0.0238	0.0898	0.0018	0.0205
GLO1	0.069	0.0023	0.0339	0.069	0.0023	0.0339	0	0	0.0167
GM2A	0.3282	0.0046	0.0141	0.4931	0.007	0.0141	0.1651	0.0023	0.014
GMPPA	0	0.0009	0	0.0564	0.0009	0.0168	0.1129	0.0019	0.0168
GNAI3	0	0	0.0173	0	0	0.0129	0	0	0.0305
GNB1	0.1029	0.0014	0.0139	0	0	0.0174	0.3133	0.0015	0.0049
GNB2	0	0	0.0162	0	0	0.0203	0	0	0.0287
GNB2L1	0	0	0.0218	0	0	0.0176	0	0	0.0087
GNG12	0	0	0	0	0	0	0	0	0
GNMT	0	0	0.0142	0	0	0.0337	0	0	0.0288
GNPDA1	0	0	0.0104	0.1437	0.0015	0.0104	0.1437	0.0015	0.0104
GNPTG	0.3246	0.0058	0.018	0.2808	0.0103	0.0366	0.276	0.0088	0.0319
GNS	0.1231	0.0015	0.0122	0.0512	0.0007	0.0146	0.0615	0.0007	0.0122
GOT1	0	0	0.0101	0	0	0.0306	0	0	0.0202
GP2	0.1977	0.0045	0.0227	0.2766	0.0078	0.0281	0.3831	0.0082	0.0214
GPC1	0.0726	0.0022	0.0297	0.1111	0.0036	0.032	0.0359	0.0012	0.0345
GPC4	0	0	0.0027	0.1906	0.0015	0.0081	0.2865	0.0015	0.0054
GPD1L				0.133	0.0058	0.0436			
GPI	0.4195	0.0059	0.0141	0.126	0.0018	0.0144	0.2087	0.0054	0.0261
GPR115	0.3448	0.0046	0.0135	0.2678	0.0047	0.0174	0.2682	0.0047	0.0174
GPR56	0.4858	0.0081	0.0166	0.3064	0.009	0.0295	0.3074	0.0094	0.0305
GPR64	0.4288	0.0018	0.0041	0.4839	0.0039	0.0081	0.9672	0.004	0.0041
GPRC5C	0.2121	0.0046	0.0218	0.2358	0.0065	0.0275	0.1683	0.0056	0.033
GPX3	0	0	0	0	0	0.0124	0	0	0.0124
GRHPR	0.2062	0.0041	0.02	0.1376	0.0028	0.0201	0.2591	0.0042	0.0161
GRN	0.4073	0.0029	0.0072	0.3714	0.0081	0.0219	0.2718	0.0066	0.0245
GSN	0.0824	0.0011	0.0138	0.1834	0.0051	0.028	0.2102	0.0051	0.0245
GSR	0.1471	0.0043	0.029	0.1186	0.0055	0.046	0.1634	0.0064	0.0394
GSS	0.1692	0.0019	0.0112	0.1347	0.0019	0.014	0.0961	0.0019	0.0197

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
DPP4	0.1206	0.0034	0.0279	0.1979	0.0039	0.0199	0.2523	0.0045	0.0178
DPP7	0.1905	0.011	0.0579	0.1731	0.011	0.0637	0.2363	0.0178	0.0754
DSC2	0.1911	0.0073	0.0383	0.2209	0.0088	0.0399	0.2303	0.0088	0.0382
DSC3	0.374	0.013	0.0348	0.397	0.0125	0.0315	0.2323	0.01	0.0432
ECM1	0.6384	0.0141	0.0221	0.4476	0.0133	0.0297	0.5492	0.0149	0.0271
EDIL3	0.0582	0.0009	0.0155	0	0	0.0186	0	0	0.0282
EEF1A1	0	0	0.0309	0	0	0.0309	0	0	0.0341
EEF1G	0.223	0.0054	0.0242	0.1648	0.0045	0.0273	0.2241	0.0076	0.034
EEF2	0	0	0.0914	0.0064	0.0006	0.0938	0	0	0.0896
EFEMP1	0.1255	0.0026	0.021	0.1096	0.0026	0.0241	0.1165	0.0035	0.0302
EFHD2	0.2151	0.0239	0.1112	0.2325	0.0259	0.1114	0.1984	0.026	0.1312
EGF	0.4934	0.0147	0.0298	0.4731	0.0129	0.0273	0.4977	0.0129	0.026
ELSPBP1	0.1233	0.0096	0.0778	0.1155	0.0082	0.0706	0.1064	0.0072	0.0675
ENO1	0	0	0.0601	0	0	0.0811	0	0	0.0811
ENPP3	0.1619	0.0069	0.0427	0.1767	0.0069	0.0391	0.1376	0.0063	0.0458
ENPP5	0.1012	0.0036	0.0356	0.161	0.0064	0.0394	0.0638	0.0027	0.0423
EPHA5	0.0725	0.0025	0.0349	0.0688	0.0021	0.0306	0.2656	0.009	0.0338
ESD	0.0306	0.0018	0.0582	0.1411	0.0036	0.0253			
EXTL2	0.1893	0.0052	0.0277	0.1419	0.0039	0.0277	0.1406	0.0052	0.0372
F11R	0.6806	0.0138	0.0203	0.5429	0.011	0.0203	0.3849	0.011	0.0287
FAM12A	0.3302	0.0115	0.0349	0.3302	0.0115	0.0349			
FAM12B	0.2389	0.0086	0.0358	0.3595	0.0086	0.0238			
fam3B	0.6109	0.0211	0.0346	0.9223	0.0211	0.0229	0.734	0.0211	0.0288
FAM3C	0.148	0.0019	0.013	0.1962	0.0038	0.0196	0.0983	0.0019	0.0195
FASN	0.2307	0.0165	0.0717	0.2297	0.0169	0.0738	0.2526	0.0159	0.0631
FBLN2	0.1661	0.0102	0.0612	0.1847	0.0107	0.0581	0.1359	0.0087	0.064
FBP1	0.0627	0.0026	0.0418	0.0313	0.0013	0.0418	0	0	0.0415
FCGBP	0.1929	0.0133	0.0689	0.1791	0.0131	0.0729	0.2083	0.0135	0.0649
FDPS	0.279	0.0085	0.0303	0.3146	0.0085	0.0269	0.2897	0.0153	0.0527
FH	0.067	0.0026	0.0388	0.0692	0.0035	0.0501	0.0549	0.0026	0.0473
FKBP4	0.1582	0.0057	0.0359	0.2305	0.0071	0.0308	0.2366	0.0134	0.0567
FLNB	0.0494	0.0026	0.0523	0.051	0.0026	0.0506	0.0554	0.0029	0.0529
FMOD	0.1098	0.0059	0.0535	0.0897	0.0059	0.0655	0.0845	0.0059	0.0698
FN1	0.0656	0.0029	0.0436	0.0567	0.0025	0.0441	0.0817	0.0035	0.0427
FOLH1	0.2781	0.0087	0.0314	0.2249	0.0093	0.0415	0.5973	0.0144	0.024
FSTL1	0.0459	0.0014	0.0303	0.0919	0.0028	0.0303	0.0538	0.0015	0.0275
FTH1	0.0673	0.0023	0.0347	0.0903	0.0023	0.0259			
FUCA1	0.1547	0.0078	0.0502	0.2056	0.0134	0.0654	0.174	0.01	0.0575
FUCA2	0.0887	0.0033	0.0369	0.108	0.0033	0.0303	0.0976	0.0033	0.0335
FUT3	0.2884	0.0166	0.0574	0.2627	0.0193	0.0733	0.2182	0.0175	0.0801
GAA	0.1643	0.0123	0.0751	0.1731	0.0114	0.0658	0.1451	0.011	0.0759
GALC	0.111	0.0045	0.0403	0.1317	0.0046	0.0351			
GALNS	0.1564	0.0127	0.0813	0.1273	0.01	0.0784	0.1124	0.0104	0.0927
GALNT6	0.0149	0.0007	0.0472	0.063	0.0029	0.0465	0.0527	0.0021	0.04
GALNT7	0.0817	0.0013	0.016	0.0653	0.002	0.0301	0.0349	0.0007	0.02
GANAB	0.1832	0.0055	0.0301	0.2132	0.0074	0.0345	0.214	0.0064	0.0301
GAPDH	0.0699	0.0039	0.0564	0.083	0.0039	0.0475	0.0759	0.0039	0.0519
GAPDHS	0.1161	0.0066	0.057	0.1541	0.0077	0.0501	0.1447	0.0077	0.0534
GAS6	0.1241	0.0086	0.069	0.1347	0.0086	0.0638			
GBA	0.1875	0.0083	0.0443	0.1415	0.0066	0.0469	0.918	0.0958	0.1043
GC	0.0902	0.0027	0.0295	0.082	0.0027	0.0325	0.0668	0.0018	0.0267
GCHFR	0	0.0107	0	0.6316	0.0107	0.0169	0	0	0.0169
GDF15	0.2376	0.0106	0.0445	0.2579	0.0136	0.0529	0.2721	0.0121	0.0445
GDI2	0.0147	0.001	0.0655	0.0403	0.0019	0.0478	0.0375	0.0019	0.0513
GFRA2	0.0435	0.0029	0.0655	0.075	0.0053	0.0708	0.0612	0.0038	0.0622
GGH	0.2233	0.0096	0.0429	0.1719	0.0082	0.0478	0.3184	0.0115	0.0361
GGT1	0.1398	0.0104	0.0741	0.1036	0.0072	0.069	0.2084	0.0149	0.0715
GLA	0.4276	0.006	0.0141	0.7845	0.0111	0.0141	0.507	0.0082	0.0161
GLB1	0.201	0.0086	0.0427	0.1638	0.008	0.0487	0.1658	0.0068	0.0409
GLB1L	0.3386	0.0102	0.0301	0.3516	0.0129	0.0367			
GLG1	0.0448	0.0024	0.0541	0.0419	0.0021	0.0495	0.0554	0.0028	0.0511
GLO1	0.2767	0.0118	0.0425	0.3734	0.0094	0.0252	0.3734	0.0094	0.0252
GM2A	0.1592	0.0069	0.0436	0.4063	0.0116	0.0286	0.3224	0.014	0.0433
GMPPA	0.0957	0.0038	0.0397	0.1198	0.0048	0.0397	0.0926	0.0048	0.0514
GNAI3	0	0	0.0173	0	0	0.0349	0	0	0.0216
GNB1	0	0	0.0598	0.0302	0.0014	0.0473	0	0	0.0536
GNB2	0.1048	0.0052	0.0499	0.0892	0.0052	0.0586	0.0831	0.0052	0.0629
GNB2L1	0	0	0.0308	0	0	0.0398	0	0	0.0356
GNG12	0	0	0	0	0	0	0	0	0
GNMT	0.0773	0.0087	0.1127	0.0819	0.0087	0.1064	0.0928	0.0087	0.0938
GNPDA1	0	0	0.0156	0	0	0.0156	0.0955	0.0015	0.0156
GNPTG	0.1525	0.0161	0.1058	0.1536	0.0147	0.0955	0.1749	0.0177	0.1011
GNS	0.1323	0.0053	0.0398	0.1413	0.0053	0.0372	0.1133	0.0045	0.0398
GOT1	0.0818	0.0054	0.0657	0.0818	0.0054	0.0657	0.0669	0.0054	0.0803
GP2	0.33	0.0103	0.0311	0.2771	0.009	0.0325	0.2793	0.0098	0.0352
GPC1	0.079	0.0068	0.0865	0.0708	0.0069	0.097	0.0711	0.0066	0.0927
GPC4	0.0354	0.0008	0.0219	0.0405	0.0008	0.0191	0.1216	0.0023	0.0191
GPD1L	0.0608	0.0025	0.0412				0.1631	0.0087	0.0534
GPI	0.1451	0.0059	0.0409	0.1753	0.0089	0.0508	0.1086	0.0055	0.0503
GPR115	0.3107	0.0125	0.0401	0.2486	0.01	0.0401	0.268	0.0125	0.0467
GPR56	0.3359	0.0175	0.0521	0.336	0.0178	0.0531	0.2807	0.0175	0.0624
GPR64	0.167	0.0048	0.0288	0.1947	0.0049	0.0251	0.1824	0.0052	0.0288
GPRC5C	0.1003	0.0069	0.0684	0.0862	0.0059	0.0682	0.0858	0.0059	0.0685
GPX3	0.0625	0.002	0.0314	0.0625	0.002	0.0314	0.0443	0.002	0.0444
GRHPR	0.1034	0.0055	0.0533	0.1689	0.0083	0.049	0.17	0.0069	0.0408
GRN	0.3385	0.0134	0.0395	0.32	0.0119	0.037	0.2122	0.0111	0.0523
GSN	0.1333	0.0069	0.0514	0.1334	0.0069	0.0514	0.1702	0.0097	0.0572
GSR	0.198	0.0142	0.0718	0.2024	0.0152	0.0749	0.1361	0.0078	0.0572
GSS	0.1682	0.0028	0.0169	0.1261	0.0028	0.0225	0.1115	0.0028	0.0255

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
DPP4	0.1692	0.0051	0.0299	0.2174	0.0056	0.0259	0.2601	0.0062	0.0238	0.2845	0.0039	0.0138
DPP7	0.1572	0.0145	0.0921	0.1417	0.0135	0.0953	0.2107	0.0212	0.1008	0.1561	0.0154	0.0989
DSC2	0.2776	0.0142	0.0512	0.3092	0.0152	0.0493	0.2886	0.0145	0.0502	0.2774	0.0137	0.0493
DSC3												
ECM1	0.5115	0.0165	0.0323	0.4313	0.0173	0.0401	0.413	0.0165	0.04	0.2538	0.0102	0.04
EDIL3	0.0963	0.0027	0.0281	0.0575	0.0018	0.0313	0.0439	0.0018	0.041	0.0967	0.0018	0.0186
EEF1A1	0	0	0.0404	0	0	0.0404	0	0	0.0436	0	0	0.0404
EEF1G	0.2463	0.0102	0.0414	0.2087	0.0093	0.0445	0.2255	0.0134	0.0596	0.1996	0.0102	0.0512
EEF2	0	0	0.0995	0.0057	0.0007	0.1198	0	0	0.1215	0	0	0.119
EFEMP1	0.146	0.0035	0.0241	0.1672	0.0035	0.0211	0.1619	0.0044	0.0272	0.0974	0.0026	0.0271
EFHD2	0.1312	0.0112	0.0852	0.1537	0.0131	0.0854	0.1026	0.0122	0.1188	0.2163	0.036	0.1663
EGF	0.4815	0.0171	0.0355	0.4212	0.0149	0.0354	0.5476	0.0166	0.0304	0.547	0.0129	0.0236
ELSPBP1												
ENO1	0.0191	0.001	0.0531	0.0169	0.001	0.0599	0.0152	0.001	0.0669	0.0131	0.001	0.0775
ENPP3	0.2048	0.0131	0.064	0.1889	0.0121	0.0641	0.1428	0.0098	0.0686	0.1943	0.0121	0.0624
ENPP5												
EPHA5	0.0789	0.0025	0.032	0.0758	0.0021	0.0278	0.2654	0.009	0.0338	0.0825	0.0025	0.0306
ESD	0.035	0.0015	0.0437	0.1904	0.0031	0.0161				0.141	0.0036	0.0253
EXTL2	0.286	0.0052	0.0183	0.2143	0.0039	0.0183	0.1888	0.0052	0.0277	0.0703	0.0026	0.0372
F11R	0.2046	0.011	0.0539	0.2043	0.011	0.0539	0.1757	0.0111	0.0629	0.1996	0.0082	0.0413
FAM12A	0.4955	0.0292	0.0588	0.4955	0.0292	0.0588				0.3021	0.0292	0.0965
FAM12B	0.2953	0.0143	0.0485	0.3951	0.0143	0.0362				0.9633	0.0114	0.0119
fam3B	0.6712	0.0242	0.0361	1.1524	0.0262	0.0227	0.891	0.0262	0.0294	0.7243	0.0262	0.0361
FAM3C	0.1968	0.0038	0.0195	0.22	0.0058	0.0262	0.1469	0.0038	0.0261	0.0585	0.0019	0.0328
FASN	0.1844	0.0162	0.0881	0.1827	0.0168	0.092	0.2062	0.0169	0.082	0.2325	0.02	0.0858
FBLN2	0.1461	0.0103	0.0704	0.1607	0.0108	0.0674	0.1242	0.0092	0.0744	0.0937	0.0073	0.0782
FBP1	0.1532	0.0078	0.051	0.102	0.0047	0.0458	0.0677	0.0035	0.0519	0.0829	0.0047	0.0564
FCGBP	0.1984	0.0142	0.0713	0.1898	0.0143	0.0754	0.203	0.0143	0.0703	0.186	0.0133	0.0718
FDPS	0.2597	0.0107	0.041	0.2392	0.0107	0.0446	0.222	0.0143	0.0643	0.1648	0.0085	0.0517
FH	0.1262	0.0035	0.0275	0.0672	0.0026	0.0387	0.0966	0.0035	0.0359	0.067	0.0026	0.0388
FKBP4	0.0785	0.0031	0.0389	0.0642	0.002	0.0317	0.088	0.0041	0.0466	0.1433	0.0071	0.0499
FLNB	0.0301	0.0018	0.0585	0.0324	0.0018	0.0544	0.0317	0.0018	0.0555	0.0458	0.0023	0.0513
FMOD	0.1414	0.0059	0.0416	0.1102	0.0059	0.0534	0.1025	0.0059	0.0575	0.0358	0.0023	0.0655
FN1	0.0782	0.0038	0.0491	0.0756	0.0037	0.0485	0.0949	0.0044	0.0462	0.0794	0.0035	0.0439
FOLH1	0.2519	0.0064	0.0254	0.1895	0.0073	0.0384	0.4586	0.0119	0.026	0.2251	0.0093	0.0414
FSTL1	0	0	0.0565	0.0303	0.0014	0.0459	0	0	0.0445	0.0303	0.0014	0.0459
FTH1	0.0536	0.0023	0.0437	0.0674	0.0023	0.0347				0.1075	0.0047	0.0436
FUCA1	0.1482	0.0085	0.0572	0.1741	0.0123	0.0708	0.1478	0.0094	0.0638	0.1858	0.01	0.0539
FUCA2	0.2048	0.0066	0.032	0.2574	0.0066	0.0255	0.2286	0.0066	0.0287	0.2275	0.0066	0.0288
FUT3	0.3159	0.0528	0.167	0.3199	0.0473	0.1479	0.2898	0.0517	0.1784	0.3256	0.0581	0.1784
GAA	0.1881	0.0122	0.0649	0.2115	0.0117	0.0555	0.1813	0.0113	0.0625	0.1692	0.0112	0.0663
GALC	0.1384	0.0077	0.0556	0.1499	0.0073	0.0487				0.1597	0.0064	0.0402
GALNS	0.2082	0.0219	0.1052	0.1609	0.0185	0.1151	0.1552	0.0185	0.1189	0.1527	0.02	0.1313
GALNT6	0.0646	0.0021	0.0326	0.1401	0.0044	0.0315	0.1376	0.0035	0.0256	0.075	0.0028	0.0375
GALNT7	0.16	0.0028	0.0174	0.1156	0.0035	0.0301	0.1046	0.0021	0.02	0.1871	0.0028	0.0149
GANAB	0.0844	0.003	0.0353	0.1212	0.0048	0.0398	0.1105	0.0039	0.0353	0.1454	0.0046	0.0316
GAPDH	0.0375	0.0026	0.0701	0.0431	0.0026	0.0609	0.0401	0.0026	0.0655	0.0422	0.0039	0.0934
GAPDHS	0.2361	0.011	0.0468	0.2468	0.0133	0.0537	0.2427	0.0122	0.0501	0.1751	0.01	0.0568
GAS6	0.2659	0.0212	0.0796	0.3083	0.0224	0.0726				0.2704	0.0247	0.0915
GBA	0.1311	0.0058	0.0443	0.0951	0.005	0.0523	0.9539	0.0953	0.0999	0.0625	0.005	0.0797
GC	0.132	0.0071	0.0539	0.125	0.0071	0.0569	0.1223	0.0063	0.0512	0.1069	0.0044	0.0415
GCHFR	0.2073	0.0107	0.0515	0.1537	0.0107	0.0695	0.1028	0.0053	0.0517	0.156	0.0053	0.0341
GDF15	0.5189	0.0167	0.0321	0.5661	0.0228	0.0404	0.6152	0.0198	0.0321	0.4088	0.0182	0.0446
GDI2	0	0	0.0692	0.0187	0.001	0.0513	0.0175	0.001	0.0549	0.0318	0.001	0.0303
GFRA2												
GGH	0.4575	0.0284	0.062	0.3974	0.0268	0.0674	0.5339	0.0299	0.056	0.9068	0.0268	0.0295
GGT1	0.2548	0.012	0.0469	0.1224	0.0088	0.0715	0.2781	0.0176	0.0632	0.1428	0.0128	0.0894
GLA	0.2191	0.007	0.0322	0.4075	0.0131	0.0322	0.1903	0.007	0.0368	0.2297	0.0091	0.0395
GLB1	0.2887	0.0123	0.0426	0.2451	0.0104	0.0426	0.2384	0.0093	0.0389	0.2115	0.0086	0.0406
GLB1L	0.5488	0.0146	0.0267	0.4615	0.0174	0.0377				0.5216	0.014	0.0267
GLG1	0.0273	0.0016	0.0601	0.0215	0.0013	0.0587	0.0341	0.002	0.0601	0.0069	0.0004	0.0615
GLO1	0.1559	0.0094	0.0603	0.1657	0.007	0.0425	0.1657	0.007	0.0425	0.166	0.007	0.0424
GM2A	0.2157	0.0093	0.0431	0.1084	0.0046	0.0429	0.1628	0.007	0.0429	0.2292	0.0116	0.0507
GMPPA	0.1054	0.0047	0.045	0.129	0.0058	0.045	0.1131	0.0058	0.0513	0.1532	0.0069	0.0448
GNAI3	0	0	0.0261	0	0	0.044	0	0	0.0395	0	0	0.044
GNB1	0	0	0.025	0.077	0.0014	0.0186	0	0	0.0263	0	0	0.0422
GNB2	0	0	0.0245	0	0	0.0396	0	0	0.0345	0.1278	0.0064	0.0499
GNB2L1	0	0	0.0628	0	0	0.0723	0	0	0.0682	0	0	0.0582
GNG12	0.1931	0.0123	0.0637	0.1931	0.0123	0.0637	0.1931	0.0123	0.0637	0.1931	0.0123	0.0637
GNMT	0.0674	0.0075	0.1113	0.0709	0.0075	0.1059	0.0789	0.0075	0.0952	0.0993	0.0087	0.0877
GNPDA1	0.0282	0.0017	0.06	0.0315	0.0017	0.0538	0.0565	0.0034	0.06	0.0315	0.0017	0.0538
GNPTG	0.1317	0.0162	0.123	0.1395	0.0162	0.1162	0.1262	0.018	0.1429	0.1213	0.0171	0.1408
GNS	0.0948	0.0038	0.0396	0.089	0.0038	0.0422	0.0671	0.003	0.0448	0.1423	0.006	0.0423
GOT1	0.0365	0.0021	0.0586	0.0365	0.0021	0.0586	0.0293	0.0021	0.0731	0.0492	0.0032	0.0655
GP2	0.3171	0.0165	0.0519	0.3183	0.0152	0.0477	0.3342	0.0169	0.0505	0.3983	0.0169	0.0424
GPC1	0.1453	0.0104	0.0713	0.0315	0.0026	0.0842	0.1528	0.0098	0.0642	0.1841	0.0121	0.0655
GPC4	0.2066	0.0051	0.0247	0.2367	0.0051	0.0216	0.276	0.0068	0.0247	0.1493	0.0051	0.0342
GPD1L	0.0693	0.0051	0.0732				0.0919	0.0087	0.0948	0.0793	0.0051	0.064
GPI	0.012	0.0008	0.0707	0.0499	0.0034	0.0678	0.0129	0.0011	0.0828	0.0574	0.0042	0.0738
GPR115	0.4104	0.0288	0.0701	0.4399	0.0288	0.0654	0.3917	0.0302	0.077	0.3795	0.0275	0.0724
GPR56												
GPR64	0.3203	0.0065	0.0204	0.4002	0.0066	0.0166	0.3422	0.007	0.0204	0.1916	0.0052	0.0274
GPRC5C	0.1813	0.0142	0.0785	0.1689	0.0132	0.0782	0.1553	0.0122	0.0784	0.1798	0.0119	0.066
GPX3	0.177	0.0079	0.0445	0.177	0.0079	0.0445	0.1364	0.0079	0.0578	0.0915	0.0059	0.0645
GRHPR	0.1033	0.0058	0.056	0.1688	0.0087	0.0515	0.1407	0.0073	0.0517	0.195	0.0058	0.0296
GRN	0.5468	0.0134	0.0244	0.5329	0.0137	0.0257	0.4223	0.013	0.0307	0.3188	0.0122	0.0383
GSN	0.0969	0.0057	0.0588	0.097	0.0057	0.0588	0.1169	0.008	0.0685	0.1603	0.0091	0.057
GSR	0.2183	0.0172	0.0788	0.2293	0.0181	0.0788	0.2471	0.015	0.0606	0.2789	0.0205	0.0734
GSS	0.097	0.0021	0.0221	0.0849	0.0021	0.0252	0.0675	0.0021	0.0317	0.1129	0.0032	0.0285

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
DPP4	0.1585	0.009	0.0569	0.1975	0.0096	0.0485	0.2192	0.0102	0.0464	0.1679	0.0068	0.0402
DPP7	0.1823	0.0203	0.1115	0.1772	0.0203	0.1147	0.224	0.0269	0.1201	0.1868	0.0203	0.1087
DSC2	0.2585	0.0175	0.0675	0.2739	0.0182	0.0665	0.2744	0.0187	0.0682	0.227	0.0165	0.0726
DSC3	0.2064	0.0186	0.09	0.2062	0.0186	0.0901	0.1568	0.0157	0.1003	0.2374	0.0217	0.0914
ECM1	0.4802	0.0252	0.0525	0.4292	0.026	0.0606	0.3874	0.0245	0.0631	0.4267	0.0236	0.0553
EDIL3	0.1039	0.0063	0.0608	0.0842	0.0054	0.0643	0.0761	0.0054	0.0711	0.1219	0.0054	0.0444
EEF1A1	0	0	0.0533	0	0	0.0533	0	0	0.05	0	0	0.0631
EEF1G	0.1464	0.0081	0.0552	0.123	0.0072	0.0584	0.1268	0.0098	0.0771	0.1181	0.0081	0.0686
EEF2	0.0029	0.0005	0.175	0.0077	0.0012	0.1574	0.0029	0.0005	0.177	0.003	0.0005	0.1729
EFEMP1	0.0724	0.0026	0.0364	0.0792	0.0026	0.0333	0.089	0.0035	0.0396	0.0192	0.0009	0.0457
EFHD2	0	0	0.0967	0.0188	0.0018	0.0969	0	0	0.1304	0.1479	0.0239	0.1618
EGF	0.4732	0.0294	0.062	0.4328	0.0268	0.0619	0.4253	0.0251	0.059	0.4148	0.0245	0.0592
ELSPBP1	0.078	0.0134	0.1712	0.07	0.0105	0.15	0.0794	0.0114	0.1441	0.0791	0.012	0.1521
ENO1	0.012	0.001	0.0847	0.011	0.001	0.0919	0.012	0.001	0.0846	0.0205	0.002	0.0992
ENPP3	0.1961	0.0136	0.0694	0.2101	0.0146	0.0695	0.1911	0.0117	0.0613	0.1991	0.0146	0.0735
ENPP5	0.3074	0.0179	0.0583	0.286	0.019	0.0663	0.3048	0.0189	0.0619	0.2318	0.016	0.069
EPHA5	0.0471	0.0025	0.0537	0.0454	0.0021	0.0464	0.1654	0.009	0.0542	0.0484	0.0025	0.0522
ESD	0.0851	0.0077	0.0902	0.1518	0.0092	0.0608				0.1535	0.0089	0.0583
EXTL2	0.2437	0.0079	0.0323	0.2029	0.0066	0.0323	0.1877	0.0079	0.0419	0.125	0.0052	0.0419
F11R	0.3334	0.0194	0.0582	0.333	0.0194	0.0583	0.3323	0.0194	0.0585	0.3329	0.0159	0.0477
FAM12A	0.7503	0.0533	0.0711	0.7503	0.0533	0.0711				0.4319	0.0472	0.1094
FAM12B	0.3142	0.0231	0.0734	0.3784	0.023	0.0609				0.5609	0.0201	0.0359
fam3B	0.572	0.0372	0.065	0.5712	0.0371	0.065	0.6301	0.0371	0.0589	0.525	0.0409	0.078
FAM3C	0.0734	0.0019	0.0261	0.1962	0.0038	0.0196	0.0584	0.0019	0.0328	0	0	0.0395
FASN	0.2454	0.0318	0.1297	0.226	0.0316	0.1396	0.2257	0.0308	0.1364	0.2441	0.0345	0.1413
FBLN2												
FBP1	0.0672	0.0105	0.1569	0.0551	0.0092	0.1672	0.0484	0.0087	0.1807	0.0537	0.0079	0.1471
FCGBP												
FDPS	0.1776	0.0117	0.0656	0.1684	0.0117	0.0692	0.2079	0.0164	0.0787	0.1535	0.0095	0.062
FH	0.0985	0.007	0.0706	0.1025	0.0078	0.0764	0.1029	0.007	0.0676	0.0736	0.0061	0.0826
FKBP4	0.1246	0.0084	0.0672	0.1586	0.0098	0.0619	0.1811	0.0161	0.0892	0.1569	0.0122	0.0778
FLNB	0.0437	0.0041	0.0945	0.0391	0.0034	0.0879	0.0438	0.004	0.0924	0.0495	0.0048	0.0962
FMOD	0.072	0.0047	0.0653	0.0607	0.0047	0.0775	0.0677	0.0047	0.0696	0.0329	0.0035	0.1069
FN1	0.0985	0.0066	0.0672	0.0918	0.0064	0.0693	0.1095	0.0073	0.0663	0.0858	0.0056	0.0657
FOLH1	0.2063	0.0111	0.0537	0.1781	0.012	0.0672	0.3164	0.0168	0.053	0.2223	0.0129	0.0578
FSTL1	0	0	0.0619	0.0272	0.0014	0.0513	0	0	0.0561	0.0272	0.0014	0.0512
FTH1	0.0259	0.0023	0.0902	0.0234	0.0023	0.0998				0.0428	0.0047	0.1094
FUCA1	0.1562	0.0156	0.0999	0.1728	0.0186	0.1074	0.155	0.0166	0.1068	0.2041	0.0213	0.1042
FUCA2	0.1625	0.0122	0.0753	0.1791	0.0122	0.0684	0.1708	0.0122	0.0717	0.1878	0.0122	0.0651
FUT3	0.2013	0.0307	0.1523	0.2314	0.0332	0.1435	0.1969	0.0321	0.1631	0.2421	0.0377	0.1556
GAA	0.2053	0.0215	0.1046	0.1848	0.0196	0.1058	0.1776	0.0188	0.1056	0.1907	0.0213	0.1114
GALC	0.1925	0.0142	0.0736	0.1946	0.014	0.0718				0.2229	0.0129	0.0578
GALNS	0.1171	0.0153	0.1304	0.1009	0.0136	0.1345	0.0961	0.0138	0.144	0.0751	0.0128	0.171
GALNT6	0.1033	0.0085	0.0819	0.1289	0.0103	0.08	0.1284	0.0099	0.077	0.1084	0.0092	0.0846
GALNT7	0.0923	0.0035	0.0378	0.0918	0.0042	0.0457	0.0853	0.0028	0.0328	0.0594	0.0021	0.0352
GANAB	0.1092	0.0069	0.0632	0.1289	0.0087	0.0678	0.1239	0.0078	0.0631	0.1911	0.0106	0.0555
GAPDH	0.0565	0.0039	0.0699	0.0565	0.0039	0.0699	0.053	0.0039	0.0744	0.0566	0.0053	0.0931
GAPDHS	0.198	0.02	0.1008	0.2089	0.0211	0.1009	0.2177	0.0211	0.0969	0.1709	0.0178	0.1039
GAS6	0.0999	0.0168	0.1678	0.1007	0.0151	0.1499				0.1136	0.0168	0.1476
GBA	0.4683	0.0313	0.0668	0.3937	0.0296	0.0751	0.9132	0.1031	0.1129	0.3125	0.0287	0.0919
GC	0.4226	0.0307	0.0727	0.4054	0.0307	0.0758	0.4701	0.03	0.0637	0.4495	0.0298	0.0663
GCHFR	0.3097	0.016	0.0518	0.47	0.016	0.0341	0.1548	0.0053	0.0343	0.102	0.0053	0.052
GDF15	0.4869	0.0376	0.0772	0.6423	0.0439	0.0683	0.5755	0.0431	0.0749	0.3981	0.036	0.0904
GDI2	0.0488	0.0053	0.1085	0.0644	0.0063	0.0972	0.062	0.0063	0.101	0.0764	0.0063	0.082
GFRA2	0.0227	0.0025	0.1083	0.0367	0.004	0.1085	0.0227	0.0025	0.1083	0.0486	0.0061	0.1266
GGH	0.173	0.0207	0.1197	0.1547	0.0193	0.125	0.2049	0.0232	0.1133	0.1875	0.0165	0.0881
GGT1	0.1464	0.0184	0.1259	0.1069	0.0152	0.1421	0.1957	0.0229	0.1171	0.1094	0.0161	0.1474
GLA	0.1928	0.0091	0.047	0.3218	0.0152	0.0471	0.1735	0.0094	0.0539	0.1877	0.0106	0.0564
GLB1	0.4219	0.0366	0.0867	0.3826	0.0344	0.0898	0.4092	0.0352	0.086	0.3441	0.0331	0.0962
GLB1L	0.2867	0.015	0.0522	0.2783	0.0177	0.0637				0.2597	0.0136	0.0523
GLG1	0.0253	0.0024	0.0964	0.0252	0.0025	0.0991	0.0283	0.0028	0.0994	0.0135	0.0013	0.0944
GLO1	0.1209	0.0118	0.0973	0.1197	0.0094	0.0785	0.1197	0.0094	0.0785	0.1199	0.0094	0.0784
GM2A	0.4402	0.0355	0.0807	0.4134	0.0332	0.0802	0.4437	0.0356	0.0802	0.5281	0.0428	0.081
GMPPA	0.0251	0.0019	0.0757	0.0377	0.0028	0.0757	0.0349	0.0029	0.0817	0.058	0.0043	0.0738
GNAI3	0	0	0.026	0	0	0.0439	0	0	0.0394	0	0	0.0439
GNB1	0	0	0.0687	0.025	0.0014	0.0572	0	0	0.0629	0	0	0.0869
GNB2	0.0183	0.0013	0.0714	0.0162	0.0013	0.0804	0.0172	0.0013	0.0758	0.0813	0.0065	0.0804
GNB2L1	0	0	0.0628	0	0	0.077	0	0	0.0682	0	0	0.0675
GNG12	0	0	0.042	0	0	0.042	0	0	0.042	0	0	0.042
GNMT	0.0513	0.006	0.1168	0.0597	0.006	0.1005	0.0596	0.006	0.1006	0.0696	0.007	0.1
GNPDA1	0.0231	0.0015	0.0646	0.0231	0.0015	0.0646	0.0462	0.003	0.0646	0.0253	0.0015	0.059
GNPTG	0.1892	0.0267	0.1411	0.2015	0.0252	0.125	0.1791	0.0283	0.1579	0.1439	0.0236	0.1642
GNS	0.0988	0.0068	0.0685	0.0988	0.0068	0.0685	0.0913	0.006	0.0658	0.114	0.0075	0.0659
GOT1	0.1174	0.0108	0.0918	0.1336	0.0108	0.0806	0.1127	0.0108	0.0955	0.1064	0.0097	0.0912
GP2	0.3834	0.0363	0.0946	0.325	0.0333	0.1024	0.3941	0.0367	0.0931	0.424	0.0358	0.0845
GPC1	0.1161	0.0146	0.1256	0.0295	0.0043	0.1461	0.0979	0.0134	0.1373	0.0948	0.0114	0.1204
GPC4	0.0876	0.0047	0.0531	0.0927	0.0047	0.0502	0.111	0.0062	0.0559	0.0838	0.0054	0.0648
GPD1L	0.0363	0.0038	0.1033				0.0681	0.0087	0.1279	0.04	0.0038	0.0939
GPI	0.0892	0.0081	0.0913	0.1152	0.0111	0.0966	0.0768	0.0082	0.1065	0.1181	0.0112	0.0945
GPR115	0.2631	0.0249	0.0946	0.2896	0.0255	0.088	0.2639	0.025	0.0946	0.3785	0.0259	0.0683
GPR56	0.2165	0.0215	0.0992	0.2177	0.0218	0.1002	0.2125	0.0215	0.1011	0.2226	0.0221	0.0994
GPR64	0.2877	0.0131	0.0457	0.3162	0.0134	0.0422	0.3175	0.0136	0.0428	0.2441	0.0118	0.0485
GPRC5C	0.152	0.0177	0.1166	0.1302	0.0168	0.129	0.1362	0.0168	0.1231	0.1349	0.0158	0.1168
GPX3	0.2039	0.0209	0.1024	0.2039	0.0209	0.1024	0.1789	0.0209	0.1167	0.1722	0.0189	0.1095
GRHPR	0.2138	0.023	0.1078	0.2463	0.0238	0.0965	0.1853	0.0196	0.106	0.2734	0.0252	0.0921
GRN	0.4163	0.0343	0.0824	0.3836	0.0327	0.0854	0.3526	0.032	0.0907	0.3402	0.0281	0.0827
GSN	0.049	0.0046	0.0931	0.049	0.0046	0.093	0.0719	0.0074	0.1034	0.0858	0.008	0.0931
GSR	0.1787	0.026	0.1454	0.2144	0.0285	0.1329	0.1393	0.0206	0.148	0.1928	0.0293	0.1522
GSS	0.2527	0.0124	0.0489	0.2258	0.0124	0.0548	0.2134	0.0124	0.0579	0.2078	0.0114	0.0549

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
DPP4	0.158	0.0073	0.0464
DPP7	0.1888	0.0242	0.1284
DSC2	0.3503	0.0244	0.0696
DSC3			
ECM1	0.415	0.0253	0.0609
EDIL3	0.1187	0.0072	0.0609
EEF1A1	0	0	0.073
EEF1G	0.139	0.0111	0.0799
EEF2	0.0036	0.0007	0.1838
EFEMP1	0.0725	0.0026	0.0364
EFHD2	0.0746	0.0112	0.15
EGF	0.4298	0.0271	0.0632
ELSPBP1			
ENO1	0.0191	0.002	0.1064
ENPP3	0.2477	0.0199	0.0802
ENPP5			
EPHA5	0.0544	0.0025	0.0464
ESD	0.1115	0.0061	0.055
EXTL2	0.1251	0.0052	0.0419
F11R	0.1927	0.0138	0.0716
FAM12A	0.6617	0.0721	0.1089
FAM12B	0.5348	0.0259	0.0485
fam3B	0.4487	0.0271	0.0604
FAM3C	0.0414	0.0019	0.0463
FASN	0.2078	0.0314	0.151
FBLN2			
FBP1	0.0862	0.0141	0.1641
FCGBP			
FDPS	0.1449	0.0096	0.0662
FH	0.1074	0.007	0.0647
FKBP4	0.104	0.008	0.0769
FLNB	0.0315	0.0031	0.0974
FMOD	0.0411	0.0035	0.0857
FN1	0.0994	0.0069	0.0694
FOLH1	0.1824	0.0117	0.064
FSTL1	0	0	0.0672
FTH1	0.047	0.0047	0.0996
FUCA1	0.2147	0.0185	0.086
FUCA2	0.258	0.0151	0.0584
FUT3	0.3761	0.074	0.1966
GAA	0.2102	0.0213	0.1015
GALC	0.2614	0.0168	0.0643
GALNS	0.1192	0.0204	0.171
GALNT6	0.1236	0.0092	0.0743
GALNT7	0.1388	0.0049	0.0353
GANAB	0.1406	0.0078	0.0556
GAPDH	0.0337	0.0039	0.1171
GAPDHS	0.2324	0.0234	0.1005
GAS6	0.1382	0.0234	0.1694
GBA	0.3126	0.0287	0.0919
GC	0.4124	0.0326	0.079
GCHFR	0.1209	0.0107	0.0882
GDF15	0.7455	0.0494	0.0663
GDI2	0.0618	0.0053	0.0857
GFRA2			
GGH	0.421	0.0331	0.0787
GGT1	0.1527	0.0192	0.1259
GLA	0.1728	0.0101	0.0583
GLB1	0.3948	0.0337	0.0855
GLB1L	0.4515	0.016	0.0355
GLG1	0.0051	0.0004	0.0851
GLO1	0.0802	0.007	0.0877
GM2A	0.4332	0.0381	0.0878
GMPPA	0.0702	0.0047	0.0676
GNAI3	0	0	0.0439
GNB1	0	0	0.0778
GNB2	0.032	0.0016	0.0497
GNB2L1	0	0	0.0818
GNG12	0.1125	0.0123	0.1094
GNMT	0.0789	0.0075	0.0952
GNPDA1	0.0368	0.0034	0.092
GNPTG	0.1066	0.0236	0.221
GNS	0.0951	0.0075	0.0791
GOT1	0.1124	0.0086	0.0766
GP2	0.3905	0.0371	0.095
GPC1	0.1121	0.0156	0.139
GPC4	0.1201	0.0068	0.0567
GPD1L	0.0575	0.0063	0.1104
GPI	0.0396	0.0042	0.1069
GPR115	0.3983	0.0407	0.1021
GPR56			
GPR64	0.2837	0.0109	0.0386
GPRC5C	0.0911	0.0122	0.1336
GPX3	0.2371	0.0219	0.0922
GRHPR	0.3363	0.0279	0.0829
GRN	0.4355	0.0331	0.076
GSN	0.0677	0.0068	0.1011
GSR	0.1789	0.0222	0.1243
GSS	0.1824	0.0118	0.065

Gene	CH_ω	CH_*Ka*	CH_*Ks*	GH_ω	GH_*Ka*	GH_*Ks*	GC_ω	GC_*Ka*	GC_*Ks*
GSTM3	0.1362	0.0019	0.0139	0.2727	0.0038	0.0139	0.0674	0.0019	0.0282
GSTO1	0.2894	0.0036	0.0124	0.1916	0.0036	0.0188	0.5819	0.0036	0.0062
GSTP1	0.3446	0.0021	0.0062	0.519	0.0065	0.0125	0.6949	0.0043	0.0062
GSTT1	0	0	0.0056	0.3331	0.0019	0.0056	0.166	0.0019	0.0112
GSTZ1	1.327	0.0083	0.0063	1.9961	0.0125	0.0063	1.0022	0.0125	0.0125
GUSB	0.2359	0.002	0.0086	0.4016	0.0179	0.0446	0.3696	0.0165	0.0446
HDHD2	0.6538	0.0034	0.0053	0.8144	0.0086	0.0106	0.9818	0.0052	0.0053
HEBP2	0.5764	0.0042	0.0073	0.095	0.0021	0.0222	0.0707	0.0021	0.0298
HEXA	0.1255	0.0016	0.013	0.2363	0.0024	0.0104	0.063	0.0008	0.0129
HEXB	0.701	0.0071	0.0102	0.3145	0.0058	0.0184	0.4743	0.0058	0.0122
HINT1	0	0	0.0113	0	0	0	0	0	0.0113
HIST2H2BE	0	0	0.0217	0	0	0.0108	0	0	0.0328
HPRT1	0	0	0.0137	0.6249	0.0151	0.0241	0.394	0.0151	0.0382
HPX	0.105	0.001	0.0091	0.9065	0.0618	0.0682	0.8488	0.0608	0.0716
HRSP12	0.3349	0.0033	0.0098	0.3349	0.0033	0.0098	0	0	0
HSPA1L	0.2084	0.0027	0.0132	0.1127	0.0027	0.0243	0.0889	0.0014	0.0154
HSPA4	0.283	0.001	0.0036	0.0936	0.0011	0.0113	0.07	0.0011	0.0151
HSPA5	0	0	0.0129	0	0	0.0133	0	0	0.0133
HSPA8	0	0	0.029	0	0	0.0313	0	0	0.0291
HSPB1	0.3502	0.0044	0.0127	0	0	0.0126	0.1737	0.0044	0.0255
HSPG2	0.1996	0.0056	0.0278	0.1419	0.0042	0.0296	0.1869	0.0051	0.0271
Hyou1	0.3611	0.0035	0.0098	0.1568	0.0026	0.0169	0.1931	0.0035	0.0183
IDE	0.057	0.0004	0.0074	0.0851	0.0013	0.0149	0.1627	0.0017	0.0104
IDH1	0.0694	0.0021	0.0299	0.139	0.0042	0.0299	0.0919	0.0042	0.0452
IDI1	0.2877	0.0061	0.0212	0.178	0.0036	0.02	0.0875	0.0036	0.0407
IDS	0.9508	0.0048	0.0051	0.1538	0.0017	0.011	0.3835	0.0042	0.0111
IDUA	0.9879	0.0145	0.0147	0.5419	0.0093	0.0172	1.1273	0.0195	0.0173
IGF2R	0.1427	0.0029	0.02	0.1078	0.0034	0.0313	0.1581	0.004	0.0252
IGFBP2	0	0	0.0122						
IGFBP5	0.4672	0.0049	0.0104						
IGHG1	0.1125	0.006	0.0531						
IGHG2	0.4938	0.0351	0.071						
IGHG4	0.3959	0.0339	0.0855						
IGJ	0.6208	0.005	0.0081	0.4613	0.0076	0.0165	0.9246	0.0076	0.0082
IGKC	0	0.0052	0	0	0.0423	0	0	0.0361	0
IL1R1	0.5714	0.0016	0.0027	0.1064	0.0023	0.0213	0.1211	0.0023	0.0193
IL1RAP	0	0	0.0173	0.0483	0.0013	0.0261	0.0413	0.0013	0.0305
IL1RL1	0.3302	0.0062	0.0189	0.5815	0.0078	0.0134	0.4136	0.0078	0.0189
IL6ST	0.245	0.0024	0.0096						
IMPA1	0.3086	0.0052	0.017						
INHBB	0.4449	0.0061	0.0138	0.228	0.0022	0.0097	0.3318	0.0061	0.0185
IQGAP1	0.0244	0.0003	0.0107	0.0529	0.0011	0.0203	0.0486	0.0008	0.0165
IQGAP2	0.1448	0.0016	0.0113	0.1691	0.0019	0.0113	0.145	0.0014	0.0094
ITIH5	0.2291	0.006	0.0263	0.4008	0.0136	0.034	0.3751	0.0121	0.0323
KAL1	0.0458	0.0007	0.0142	0.029	0.0006	0.0224	0.08	0.0013	0.0163
KIF5B	0.0925	0.0004	0.0048	0.0922	0.0009	0.0096	0.0554	0.0004	0.008
KLK11	0.7639	0.0111	0.0145	1.6183	0.0095	0.0059	0.2125	0.0038	0.0178
KLK2	1.2942	0.0068	0.0053						
KLK3	0.3932	0.0219	0.0556	0.2413	0.0064	0.0264	0.1594	0.0064	0.04
KPNB1	0	0	0.0147	0	0	0.0196	0	0	0.0213
KRT1	0.0935	0.0043	0.0459	0.0292	0.0007	0.0237	0.0781	0.0036	0.0461
KRT10	0.3332	0.0062	0.0186	0.1322	0.0045	0.0343	0.1155	0.0036	0.0314
KRT5	0.0704	0.003	0.0427	0.088	0.0038	0.0427	0.0594	0.0023	0.0379
KRT8	0.4399	0.0086	0.0196	0.2071	0.0035	0.017	0.4874	0.0097	0.0199
KRT9	0.1063	0.0014	0.0133	0.2744	0.0127	0.0461	0.3643	0.0136	0.0373
LAMA5	0.1846	0.0059	0.0318						
LAMB2	0.3009	0.0056	0.0186	0.2231	0.0047	0.0211	0.2264	0.0064	0.0281
LAMC1	0.1534	0.003	0.0193	0.1956	0.0038	0.0193	0.1263	0.0035	0.0277
LAMP1	0.2908	0.0086	0.0295	0.1987	0.0086	0.0432	0.2491	0.0107	0.0431
LAMP2	0.6386	0.0051	0.008	0.5381	0.0071	0.0133	0.4926	0.0054	0.0109
LAP3	0	0	0.0329	0	0	0.0329	0	0	0.0273
LCN1	0.4871	0.0076	0.0156	0.2412	0.0077	0.0318	0.2123	0.0102	0.0482
LCN2	0.3074	0.0044	0.0145	0.0759	0.0022	0.0292	0.2293	0.0067	0.0291
LCP1	0.0365	0.0007	0.0189	0.0587	0.0007	0.0118	0	0	0.0118
LDHA	0.2021	0.0024	0.012	0.1008	0.0012	0.012	0.1518	0.0012	0.008
LDHB	0	0	0.0087	0	0	0.0136	0	0	0.0136
LDHC	0	0	0.0085	0.6211	0.0026	0.0043	0.6221	0.0026	0.0043
LDLR	0.0983	0.0048	0.0487	0.1671	0.006	0.0357	0.1506	0.0054	0.0356
LEFTY2	0	0	0.0322	0.1153	0.0037	0.0322	0.0733	0.0037	0.0507
LGALS3	0.8616	0.0091	0.0105	0.2555	0.0054	0.0212	0.5135	0.0109	0.0212
LGALS3BP	0.3261	0.0053	0.0163	0.2163	0.0061	0.0283	0.1351	0.0038	0.0283
LGMN	0.1083	0.003	0.0277	0.4777	0.0296	0.0619	0.609	0.0263	0.0433
LIFR	0.2927	0.002	0.0067	0.2626	0.0035	0.0135	0.2334	0.0032	0.0135
LIPA	0.4662	0.0087	0.0186	1.3192	0.0099	0.0075	0.5106	0.0077	0.015
LIPG	0.0418	0.0009	0.0207	0.4251	0.022	0.0518	0.4342	0.0211	0.0487
LIPI	0.2394	0.0054	0.0224						
LMAN2	0.1043	0.0012	0.0118	0.0782	0.0012	0.0158	0.1247	0.0025	0.0198
LNPEP	0.1682	0.0017	0.0102	0.0827	0.0019	0.0234	0.1334	0.003	0.0223
LPL	0.037	0.0009	0.0248	0.0489	0.0018	0.0375	0.0244	0.0009	0.0375
LRG1	0.2694	0.0039	0.0146	0.1985	0.0066	0.0332	0.2042	0.0053	0.0258
LSAMP	0	0	0.0074	0	0	0.0111	0	0	0.0111
LTA4H	0	0	0.007	0.0766	0.0007	0.0093	0.0436	0.0007	0.0164
LTF	0.5939	0.0094	0.0158	0.5403	0.015	0.0278	0.5205	0.0144	0.0277
LYZ	0	0	0.0197	0.1968	0.0059	0.0301	0.2965	0.0074	0.025
LZTFL1	0.569	0.0029	0.0051	0.1884	0.0029	0.0153	0.2836	0.0029	0.0102
MAMDC2	0.0985	0.0006	0.0064	0.0585	0.0013	0.0216	0.0325	0.0006	0.0194
MAN2A1	0.0645	0.0008	0.0117	0.1616	0.0019	0.0117	0.1453	0.0019	0.013
MAN2B1	0.2585	0.0031	0.0119	0.3316	0.0044	0.0133	0.2292	0.004	0.0173
MAN2B2	0.1843	0.0074	0.0403	0.3818	0.0071	0.0186	0.2582	0.0096	0.0371

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
GSTM3	0.1351	0.0038	0.0282	0.073	0.0028	0.039	0.135	0.0038	0.0282
GSTO1	0.2294	0.0072	0.0314	0.3871	0.0072	0.0186	0.2883	0.0072	0.025
GSTP1	0.2517	0.013	0.0516	0.2893	0.013	0.0449	0.2535	0.013	0.0513
GSTT1	0.3248	0.015	0.0462	0.2876	0.015	0.0522	0.4204	0.0169	0.0402
GSTZ1	0.5507	0.0104	0.0189	0.5004	0.0062	0.0125	0.4147	0.0104	0.0251
GUSB	0.1978	0.015	0.076	0.1793	0.0136	0.0761	0.3313	0.0263	0.0795
HDHD2	0.2577	0.0069	0.0267	0.3244	0.0069	0.0212	0.3225	0.0086	0.0267
HEBP2	0.0564	0.0021	0.0374	0.0466	0.0021	0.0452	0	0	0.0609
HEXA	0.2431	0.0057	0.0235	0.1561	0.0041	0.0262	0.1391	0.0033	0.0235
HEXB	0.2838	0.0103	0.0363	0.3068	0.0095	0.031	0.2143	0.0087	0.0405
HINT1	0.0602	0.0035	0.0583	0.0758	0.0035	0.0462	0.0602	0.0035	0.0583
HIST2H2BE	0	0	0.0217	0	0	0.0441	0	0	0.0328
HPRT1	0	0	0.0137	0	0	0.0276	0.394	0.0151	0.0382
HPX	0.3592	0.0077	0.0213	0.3526	0.0086	0.0244	0.8022	0.068	0.0848
HRSP12	0.082	0.0033	0.04	0	0	0.0298	0	0	0.0298
HSPA1L	0.0853	0.0048	0.0564	0.0728	0.0034	0.0471	0.038	0.0021	0.0542
HSPA4	0.0841	0.0015	0.0182	0.0699	0.0015	0.0219	0.0595	0.0016	0.0266
HSPA5	0	0	0.0327	0	0	0.0327	0	0	0.0313
HSPA8	0	0	0.0429	0	0	0.0452	0	0	0.057
HSPB1	0.2683	0.0157	0.0587	0.2795	0.0203	0.0725	0.2177	0.0157	0.0723
HSPG2	0.1003	0.0068	0.0676	0.1082	0.0072	0.0666	0.0871	0.0057	0.066
Hyou1	0.1165	0.004	0.0341	0.1367	0.0049	0.0355	0.1215	0.004	0.0327
IDE	0.0732	0.0025	0.0346	0.0894	0.003	0.0331	0.0854	0.003	0.0346
IDH1	0.1046	0.0031	0.0298	0.0637	0.0031	0.049	0.0637	0.0031	0.049
IDI1	0.2242	0.0185	0.0825	0.2065	0.0177	0.0857	0.2339	0.0162	0.0691
IDS	0.1653	0.0065	0.0391	0.2475	0.0097	0.0393	0.1074	0.0043	0.0397
IDUA	0.3857	0.0179	0.0465	0.6096	0.0285	0.0468	0.5168	0.0231	0.0447
IGF2R	0.128	0.0083	0.065	0.1563	0.0096	0.0614	0.1465	0.0091	0.062
IGFBP2	0.0386	0.0014	0.0374	0.0435	0.0014	0.0331			
IGFBP5	0.1026	0.0032	0.0316	0.1537	0.0049	0.0317			
IGHG1	0.2594	0.0191	0.0737	0.2148	0.0178	0.0829			
IGHG2	0.5564	0.0417	0.0749	0.2602	0.0195	0.0749			
IGHG4	0.3867	0.0363	0.0938	0.174	0.014	0.0802			
IGJ	0.5129	0.0127	0.0247	0.7711	0.0126	0.0164	0.611	0.0153	0.025
IGKC	1.1748	0.0818	0.0696	1.2707	0.0884	0.0696	1.2449	0.088	0.0707
IL1R1	0.1652	0.0053	0.0322	0.1978	0.0055	0.0277	0.1612	0.0061	0.0377
IL1RAP	0.0431	0.0019	0.0439	0.0391	0.0019	0.0484	0.0651	0.0032	0.0485
IL1RL1	0.4596	0.0208	0.0453	0.4323	0.0208	0.0482	0.5255	0.0208	0.0396
IL6ST	0.2246	0.0047	0.021	0.2021	0.0042	0.021			
IMPA1	0.2331	0.0085	0.0366	0.2337	0.0085	0.0365			
INHBB									
IQGAP1	0.0499	0.0021	0.0418	0.048	0.0018	0.0381	0.0719	0.0027	0.0373
IQGAP2	0.0804	0.0019	0.0238	0.0804	0.0019	0.0238	0.0689	0.0016	0.0238
ITIH5	0.1358	0.0095	0.07	0.1526	0.0109	0.0715	0.2438	0.0174	0.0713
KAL1	0.1329	0.0052	0.0392	0.1784	0.0059	0.0329	0.1579	0.0059	0.0371
KIF5B	0.0652	0.0027	0.0409	0.0566	0.0022	0.0392	0.0473	0.0018	0.0375
KLK11	0.3394	0.0223	0.0658	0.3358	0.0239	0.0712	0.3779	0.0209	0.0553
KLK2	0.4628	0.0277	0.0598	0.369	0.0242	0.0655			
KLK3	0.296	0.0247	0.0836	0.3781	0.0354	0.0936	0.1515	0.0171	0.1127
KPNB1	0.0757	0.0025	0.033	0.072	0.0025	0.0347	0.0628	0.0025	0.0398
KRT1	0.1887	0.006	0.0318	0.1621	0.0096	0.0595	0.1763	0.0052	0.0293
KRT10	0.257	0.0118	0.046	0.2354	0.0104	0.044	0.0825	0.0045	0.055
KRT5	0.0834	0.0049	0.0587	0.0953	0.0049	0.0513	0.0921	0.0056	0.0613
KRT8	0.1115	0.006	0.0541	0.2472	0.0112	0.0454	0.1021	0.0044	0.0431
KRT9	0.4305	0.0267	0.0621	0.472	0.0282	0.0597	0.7333	0.034	0.0463
LAMA5	0.1937	0.0151	0.0781	0.2045	0.0156	0.0763			
LAMB2	0.2603	0.0115	0.0442	0.2556	0.0132	0.0517	0.2502	0.0123	0.049
LAMC1	0.0904	0.0046	0.0507	0.0709	0.0039	0.0551	0.0904	0.0046	0.0507
LAMP1	0.155	0.0103	0.0668	0.1316	0.0085	0.0647	0.1166	0.0085	0.0729
LAMP2	0.3769	0.0064	0.0171	0.1892	0.0038	0.0201	0.6432	0.0057	0.0088
LAP3	0.0564	0.0017	0.0301	0.0564	0.0017	0.0301	0.0475	0.0017	0.0357
LCN1	0.5225	0.0379	0.0725	0.5386	0.045	0.0835	0.572	0.0418	0.073
LCN2	0.2645	0.0157	0.0593	0.3423	0.0203	0.0592	0.2271	0.0134	0.0592
LCP1	0.0159	0.0007	0.0433	0	0	0.0433	0	0	0.0409
LDHA	0.0296	0.0012	0.0408	0.0331	0.0012	0.0366	0	0	0.0366
LDHB	0	0	0.0175	0	0	0.0264	0	0	0.0322
LDHC	0.153	0.004	0.0259	0.1533	0.004	0.0259	0.1845	0.004	0.0215
LDLR	0.1242	0.0106	0.0857	0.1435	0.0117	0.0817	0.1656	0.0121	0.073
LEFTY2	0.1534	0.0112	0.0731	0.1212	0.0112	0.0926	0.1689	0.015	0.0888
LGALS3	0.4568	0.0072	0.0158	0.8033	0.0127	0.0158	0.3402	0.0091	0.0266
LGALS3BP	0.273	0.0243	0.089	0.2806	0.0235	0.0838	0.331	0.0245	0.0739
LGMN	0.078	0.007	0.09	0.0534	0.004	0.075	0.3204	0.0308	0.0963
LIFR	0.1999	0.0071	0.0356	0.2048	0.0067	0.0328	0.2112	0.0075	0.0356
LIPA	0.3808	0.0219	0.0574	0.3269	0.0175	0.0535	0.3261	0.0176	0.054
LIPG	0.1115	0.0043	0.039	0.0602	0.0035	0.0576	0.2421	0.0211	0.0873
LIPI	0.4802	0.0194	0.0405	0.4168	0.019	0.0456			
LMAN2	0.0559	0.0025	0.0443	0.0924	0.0037	0.0402	0.0235	0.0012	0.0526
LNPEP	0.2922	0.0098	0.0335	0.305	0.0105	0.0343	0.2304	0.0087	0.0376
LPL	0.1525	0.0101	0.0661	0.13	0.0091	0.0697	0.1613	0.0101	0.0625
LRG1	0.356	0.0173	0.0485	0.3883	0.0159	0.041	0.4173	0.0186	0.0446
LSAMP	0.0556	0.0012	0.0223	0.0556	0.0012	0.0223	0.0475	0.0012	0.0261
LTA4H	0.1165	0.0036	0.0308	0.108	0.0036	0.0332	0.0708	0.0029	0.0405
LTF	0.3832	0.0236	0.0617	0.3737	0.0233	0.0625	0.3632	0.0227	0.0625
LYZ	0.2971	0.0089	0.03	0.4487	0.0089	0.0198	1.0935	0.0164	0.015
LZTFL1	0.0933	0.0029	0.0309	0.1124	0.0029	0.0256	0.1124	0.0029	0.0256
MAMDC2	0.1042	0.0032	0.0304	0.0898	0.0025	0.0282	0.1217	0.0032	0.026
MAN2A1	0.1439	0.0042	0.0289	0.1509	0.0042	0.0276	0.151	0.0042	0.0275
MAN2B1	0.1813	0.0084	0.0464	0.1492	0.008	0.0534	0.1707	0.0084	0.0492
MAN2B2	0.3465	0.0207	0.0599	0.2865	0.0238	0.0829	0.3614	0.0216	0.0599

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
GSTM3	0.2152	0.0076	0.0354	0.1436	0.0067	0.0464	0.2151	0.0076	0.0354	0.0759	0.0038	0.0501
GSTO1	0.2149	0.0054	0.0251	0.4351	0.0054	0.0124	0.288	0.0054	0.0187	0.2874	0.009	0.0314
GSTP1	0.3338	0.024	0.0718	0.3694	0.024	0.0649	0.3362	0.024	0.0714	0.1767	0.0152	0.0858
GSTT1	0.2467	0.0056	0.0227	0.1966	0.0056	0.0285	0.4414	0.0075	0.0169	0.2247	0.0131	0.0583
GSTZ1	0.1727	0.0125	0.0722	0.1279	0.0083	0.0649	0.1589	0.0125	0.0786	0.1212	0.0062	0.0514
GUSB	0.25	0.0276	0.1102	0.2368	0.0261	0.1104	0.3339	0.0349	0.1044	0.2283	0.0234	0.1024
HDHD2	0.1056	0.0052	0.0488	0.0398	0.0017	0.0431	0.0703	0.0034	0.0488	0.1193	0.0052	0.0432
HEBP2	0.1046	0.0063	0.0607	0.0921	0.0063	0.0688	0.0497	0.0042	0.085	0.0613	0.0042	0.0688
HEXA	0.3134	0.0138	0.044	0.2581	0.0121	0.0468	0.2401	0.0112	0.0467	0.2485	0.0095	0.0382
HEXB	0.3169	0.0196	0.0617	0.3049	0.0171	0.0562	0.3251	0.02	0.0614	0.329	0.0204	0.0619
HINT1	0.1794	0.0105	0.0588	0.1483	0.0105	0.0711	0.1794	0.0105	0.0588	0.0986	0.007	0.0711
HIST2H2BE	0	0	0.0671	0	0	0.0909	0	0	0.0789	0	0	0.0671
HPRT1	0.9339	0.0215	0.023	0.5782	0.0215	0.0371	0.6194	0.0164	0.0265	0.5782	0.0215	0.0371
HPX	0.2729	0.0144	0.0529	0.2395	0.0134	0.0562	0.6331	0.0733	0.1157	0.2887	0.0125	0.0432
HRSP12	0.1097	0.0033	0.0299	0	0	0.0198	0	0	0.0198	0	0	0.0504
HSPA1L	0.0468	0.0463	0.9885	0.0471	0.0462	0.9826	0.0444	0.0448	1.0086	0.0461	0.0441	0.957
HSPA4	0.0795	0.002	0.0258	0.0694	0.002	0.0295	0.055	0.0021	0.0386	0.0769	0.0026	0.0333
HSPA5	0.1055	0.0056	0.0526	0.1055	0.0056	0.0526	0.1107	0.0057	0.0517	0.1012	0.0056	0.0549
HSPA8	0	0	0.0568	0	0	0.0592	0	0	0.0616	0	0	0.0546
HSPB1												
HSPG2	1.0025	0.2885	0.2877	1.0429	0.3005	0.2881	0.9904	0.2658	0.2684	1.005	0.2869	0.2855
Hyou1	0.0641	0.0028	0.0431	0.0827	0.0037	0.0446	0.0598	0.0028	0.0462	0.0676	0.0032	0.0477
IDE	0.0144	0.0005	0.032	0.0172	0.0005	0.0269	0.0305	0.0009	0.0303	0.0577	0.0018	0.032
IDH1	0.4945	0.0319	0.0645	0.3955	0.0319	0.0807	0.4222	0.0341	0.0807	0.514	0.033	0.0643
IDI1	0.3989	0.0271	0.068	0.3451	0.0255	0.074	0.3539	0.0207	0.0585	0.555	0.0162	0.0291
IDS	0.2432	0.0058	0.0238	0.3814	0.0091	0.0239	0.0876	0.0017	0.0195	0.1537	0.0067	0.0433
IDUA	0.2722	0.0172	0.0632	0.4298	0.0282	0.0656	0.3886	0.0229	0.059	0.2779	0.0165	0.0593
IGF2R												
IGFBP2	0	0	0.0678	0	0	0.0634				0.0434	0.0014	0.0332
IGFBP5	0.1027	0.0032	0.0315	0.1539	0.0049	0.0317				0.1028	0.0032	0.0315
IGHG1												
IGHG2												
IGHG4												
IGJ	0.826	0.0204	0.0247	1.2417	0.0203	0.0164	1.3921	0.023	0.0165	0.69	0.0229	0.0332
IGKC	1.2156	0.0707	0.0582	1.1179	0.0651	0.0582	1.2014	0.0621	0.0517	1.319	0.0684	0.0519
IL1R1	0.1575	0.0068	0.0433	0.1566	0.007	0.0449	0.155	0.0076	0.049	0.1982	0.0091	0.046
IL1RAP	0.0228	0.0013	0.0552	0.0211	0.0013	0.0599	0.0456	0.0025	0.0553	0.0527	0.0032	0.0598
IL1RL1	0.6705	0.1486	0.2217	0.6584	0.1472	0.2236	0.7141	0.1506	0.2108	0.7323	0.1434	0.1958
IL6ST	0.2079	0.0059	0.0284	0.155	0.0054	0.0351				0.1647	0.005	0.0301
IMPA1	0.6946	0.0118	0.017	0.8527	0.0145	0.017				0.544	0.0151	0.0278
INHBB	0	0	0.0235	0.0625	0.0017	0.0273	0	0	0.0189			
IQGAP1	0.0234	0.001	0.0446	0.0192	0.0008	0.0409	0.0401	0.0016	0.0402	0.0499	0.0021	0.0418
IQGAP2	0.1189	0.0041	0.0346	0.0982	0.003	0.0307	0.1008	0.0033	0.0326	0.1109	0.0038	0.0346
ITIH5	0.2022	0.0166	0.0823	0.2082	0.0171	0.0822	0.2668	0.0233	0.0872	0.1879	0.0159	0.0848
KAL1	0.1938	0.0064	0.0331	0.2633	0.0071	0.0269	0.2276	0.0071	0.0311	0.2618	0.0092	0.035
KIF5B	0.1097	0.0027	0.0243	0.098	0.0022	0.0226	0.1	0.0018	0.0177	0.018	0.0009	0.0494
KLK11	0.2599	0.0143	0.055	0.2882	0.0159	0.0551	0.3125	0.0152	0.0486	0.2887	0.0207	0.0716
KLK2												
KLK3	0.3407	0.0258	0.0756	0.3407	0.0258	0.0756	0.2314	0.0192	0.083	0.3227	0.0367	0.1136
KPNB1	0	0	0.0364	0	0	0.0381	0	0	0.0398	0.0757	0.0025	0.033
KRT1	0.0977	0.0043	0.0437	0.0895	0.007	0.0783	0.062	0.0034	0.055	0.1317	0.0075	0.0572
KRT10	0.1905	0.0105	0.0551	0.1955	0.0095	0.0488	0.1311	0.0087	0.0665	0.1655	0.0086	0.0518
KRT5	0.0789	0.0075	0.0956	0.094	0.0075	0.0802	0.0794	0.0068	0.0854	0.0667	0.006	0.0904
KRT8	0.5341	0.0562	0.1053	0.625	0.0606	0.097	0.5529	0.0582	0.1053	0.4959	0.0572	0.1155
KRT9	0.1414	0.0064	0.0453	0.1823	0.0078	0.043	0.2137	0.0163	0.0764	0.3427	0.0245	0.0716
LAMA5	0.1988	0.0176	0.0884	0.1881	0.0165	0.0875				0.1811	0.0171	0.0946
LAMB2	0.2356	0.0102	0.0432	0.2245	0.011	0.0491	0.2141	0.0102	0.0476	0.2583	0.0127	0.0491
LAMC1	0.0835	0.0043	0.0516	0.0649	0.0036	0.0561	0.0777	0.0043	0.0555	0.0609	0.0035	0.0575
LAMP1	0.1941	0.0134	0.0693	0.1513	0.0107	0.071	0.1906	0.0129	0.0676	0.1548	0.0091	0.0589
LAMP2	0.4497	0.0108	0.024	0.3161	0.0089	0.0283	1.1334	0.01	0.0088	0.4727	0.0065	0.0136
LAP3	0.6095	0.0867	0.1422	0.6238	0.0867	0.139	0.6384	0.0867	0.1358	0.7032	0.0886	0.126
LCN1	0.4908	0.0462	0.0942	0.4374	0.0462	0.1056	0.4249	0.05	0.1177	0.6694	0.0786	0.1174
LCN2	0.2736	0.0188	0.0688	0.3442	0.0236	0.0687	0.3114	0.0165	0.0529	0.3134	0.0165	0.0526
LCP1	0.0124	0.0007	0.0558	0	0	0.0558	0	0	0.0533	0	0	0.061
LDHA	0.0539	0.0024	0.0449	0.0595	0.0024	0.0407	0.0297	0.0012	0.0407	0.033	0.0012	0.0366
LDHB	0	0	0.0632	0	0	0.0632	0	0	0.0561	0	0	0.0726
LDHC	0.1746	0.0053	0.0303	0.1749	0.0053	0.0303	0.2047	0.0053	0.0259	0.1013	0.004	0.0392
LDLR												
LEFTY2	0.1263	0.0163	0.1288	0.1263	0.0163	0.1288	0.1461	0.0201	0.1373	0.1178	0.0176	0.1491
LGALS3	0.6898	0.022	0.0318	0.8665	0.0276	0.0318	1.1293	0.0238	0.0211	0.4897	0.0183	0.0373
LGALS3BP	0.2372	0.0184	0.0777	0.2473	0.0192	0.0777	0.2753	0.0193	0.0702	0.3003	0.0318	0.1059
LGMN	0.1164	0.0098	0.0844	0.1053	0.0076	0.0725	0.1218	0.0098	0.0806	0.111	0.0098	0.0886
LIFR	0.1753	0.0075	0.0428	0.1661	0.0071	0.0428	0.1848	0.0079	0.0428	0.2025	0.0075	0.0371
LIPA	0.4513	0.0241	0.0534	0.4656	0.023	0.0495	0.5205	0.0198	0.0381	0.4285	0.0263	0.0614
LIPG	0.2385	0.0078	0.0328	0.1354	0.007	0.0514	0.2616	0.0211	0.0808	0.1155	0.0052	0.0451
LIPI	0.4001	0.0126	0.0315	0.3744	0.0111	0.0297				0.6181	0.0195	0.0315
LMAN2	0.0512	0.0013	0.0257	0.0437	0.0013	0.0301	0.0382	0.0013	0.0344	0.0231	0.0013	0.0568
LNPEP	0.3645	0.0108	0.0297	0.4129	0.0119	0.0289	0.3192	0.0105	0.0328	0.3743	0.0128	0.0343
LPL	0.0526	0.0046	0.0871	0.0421	0.0037	0.0871	0.0526	0.0046	0.0871	0.1677	0.0111	0.0661
LRG1	0.1659	0.0159	0.0961	0.1653	0.0146	0.0882	0.1881	0.0173	0.0919	0.1829	0.0146	0.0798
LSAMP	0.0368	0.0012	0.0337	0.0475	0.0012	0.0261	0.033	0.0012	0.0375	0	0	0.0185
LTA4H	0.1108	0.003	0.0274	0.1014	0.003	0.03	0.0808	0.003	0.0376	0.1525	0.0046	0.0299
LTF	0.3655	0.0352	0.0964	0.3601	0.0349	0.097	0.3691	0.0346	0.0938	0.3709	0.0314	0.0847
LYZ	0.2441	0.0149	0.0611	0.2441	0.0149	0.0611	0.4098	0.0209	0.051	0.2339	0.0119	0.0508
LZTFL1	0.1687	0.0043	0.0256	0.2115	0.0043	0.0204	0.2116	0.0043	0.0204	0.2847	0.0014	0.0051
MAMDC2	0.0623	0.0032	0.0507	0.0521	0.0025	0.0485	0.0622	0.0032	0.0508	0.0916	0.0051	0.0553
MAN2A1	0.1818	0.008	0.0438	0.2005	0.008	0.0397	0.1764	0.008	0.0451	0.209	0.0081	0.039
MAN2B1	0.1317	0.0073	0.0554	0.1001	0.0063	0.0632	0.1082	0.0058	0.0539	0.179	0.0102	0.0572
MAN2B2	0.4049	0.0464	0.1145	0.3731	0.0554	0.1485	0.3878	0.0458	0.1181	0.4057	0.0527	0.1299

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
GSTM3	0.1304	0.0115	0.0879	0.1143	0.0105	0.0919	0.1303	0.0115	0.088	0.0735	0.0076	0.1037
GSTO1	0.1972	0.0127	0.0642	0.2496	0.0127	0.0508	0.2489	0.0127	0.0509	0.1794	0.0127	0.0707
GSTP1	0.1137	0.013	0.1141	0.107	0.013	0.1213	0.1015	0.013	0.1281	0.0298	0.0043	0.144
GSTT1	0.1934	0.0112	0.0581	0.1751	0.0112	0.0642	0.2523	0.0131	0.052	0.2723	0.0226	0.083
GSTZ1	0.2659	0.0209	0.0787	0.2344	0.0167	0.0714	0.2464	0.021	0.0851	0.2533	0.0146	0.0578
GUSB	0.2059	0.0282	0.1372	0.1953	0.0268	0.1374	0.292	0.0384	0.1316	0.2301	0.0297	0.129
HDHD2	0.1987	0.0087	0.0439	0.1057	0.0052	0.0494	0.1261	0.007	0.0552	0.1579	0.0087	0.0552
HEBP2	0.1377	0.0128	0.0926	0.126	0.0127	0.1012	0.0899	0.0106	0.118	0.1049	0.0106	0.1012
HEXA	0.1456	0.0098	0.0675	0.14	0.0098	0.0702	0.1339	0.009	0.0673	0.1248	0.0074	0.059
HEXB	0.3483	0.02	0.0574	0.3848	0.02	0.052	0.3583	0.0225	0.0627	0.3472	0.02	0.0576
HINT1	0.0758	0.0035	0.0462	0.1019	0.0035	0.0344	0.0758	0.0035	0.0462	0	0	0.0344
HIST2H2BE	0	0	0.0671	0	0	0.0909	0	0	0.0789	0	0	0.0671
HPRT1	0	0	0.0347	0	0	0.049	0.2514	0.0151	0.0599	0	0	0.049
HPX	0.513	0.0271	0.0529	0.4651	0.0261	0.0562	0.6685	0.0775	0.1159	0.5944	0.0273	0.0459
HRSP12	0.2478	0.0232	0.0938	0.2407	0.0199	0.0826	0.2407	0.0199	0.0826	0.2122	0.0199	0.0937
HSPA1L	0.0517	0.0062	0.1197	0.0438	0.0048	0.1097	0.0313	0.0034	0.1098	0.0251	0.0027	0.1096
HSPA4	0.0353	0.002	0.0579	0.033	0.002	0.0618	0.0219	0.0016	0.0725	0.0367	0.0026	0.0697
HSPA5	0	0	0.0599	0	0	0.0599	0	0	0.0592	0	0	0.0576
HSPA8	0	0	0.1082	0	0	0.1057	0	0	0.1134	0	0	0.1008
HSPB1	0	0	0.1148	0.0341	0.0044	0.1299	0	0	0.1295	0.1566	0.0157	0.1005
HSPG2	0.095	0.0105	0.1104	0.0918	0.0101	0.1104	0.0808	0.009	0.1114	0.0885	0.0102	0.1155
Hyou1	0.0838	0.0069	0.0822	0.0855	0.0069	0.0806	0.0854	0.0069	0.0806	0.099	0.0073	0.0742
IDE	0.0403	0.0025	0.0628	0.0483	0.003	0.0612	0.0637	0.0038	0.0596	0.075	0.0051	0.0676
IDH1	0.0918	0.0042	0.0452	0.0784	0.0042	0.053	0.1041	0.0057	0.0549	0.0917	0.0052	0.0567
IDI1	0.1867	0.025	0.1341	0.1556	0.0219	0.1405	0.1523	0.0162	0.1062	0.1515	0.0156	0.1027
IDS	0.2265	0.0137	0.0605	0.2924	0.017	0.0581	0.1574	0.0085	0.054	0.1908	0.0154	0.0809
IDUA	0.2927	0.0342	0.1168	0.3867	0.0455	0.1176	0.3577	0.0414	0.1158	0.3198	0.0338	0.1056
IGF2R	0.2114	0.0235	0.1112	0.2179	0.0242	0.1113	0.2045	0.0233	0.1139	0.1823	0.0206	0.1128
IGFBP2	0.0531	0.0043	0.0814	0.0563	0.0043	0.0769				0.1054	0.0058	0.0547
IGFBP5	0.0763	0.0032	0.0424	0.1143	0.0049	0.0427				0.0676	0.0032	0.0479
IGHG1												
IGHG2	0.5745	0.0697	0.1214	0.4747	0.0694	0.1462				0.651	0.0626	0.0961
IGHG4	0.4464	0.0526	0.1178	0.3194	0.0413	0.1294				0.4749	0.0422	0.0889
IGJ	0.6812	0.0282	0.0414	0.8535	0.0282	0.033	0.7706	0.0257	0.0333	0.5225	0.0307	0.0588
IGKC	1.739	0.1014	0.0583	1.6359	0.0954	0.0583	2.4127	0.125	0.0518	2.4873	0.1632	0.0656
IL1R1	0.3281	0.0211	0.0643	0.3261	0.0217	0.0666	0.2999	0.0219	0.0729	0.358	0.025	0.0698
IL1RAP	0.0378	0.0032	0.0834	0.0357	0.0032	0.0882	0.0529	0.0044	0.0835	0.0683	0.0051	0.0739
IL1RL1	0.285	0.0317	0.1113	0.27	0.0313	0.116	0.2939	0.0313	0.1066	0.2928	0.0313	0.1069
IL6ST	0.1642	0.0104	0.0634	0.1611	0.0099	0.0617				0.1624	0.0095	0.0583
IMPA1	0.2783	0.0151	0.0544	0.279	0.0152	0.0543				0.2405	0.0158	0.0658
INHBB	0.0298	0.0024	0.0814	0.0351	0.0034	0.0973	0.0156	0.0012	0.0777			
IQGAP1	0.0302	0.0019	0.0621	0.0276	0.0016	0.0581	0.0428	0.0025	0.058	0.0515	0.0029	0.0572
IQGAP2	0.1365	0.0066	0.0481	0.1426	0.0066	0.0461	0.1429	0.0063	0.044	0.1366	0.0069	0.0502
ITIH5	0.1467	0.0158	0.108	0.1424	0.0163	0.1146	0.1924	0.0227	0.1178	0.1485	0.0163	0.1098
KAL1	0.1092	0.0101	0.0928	0.1192	0.0108	0.0906	0.1253	0.0108	0.0862	0.129	0.0124	0.0965
KIF5B	0.2222	0.0162	0.073	0.2212	0.0158	0.0713	0.2202	0.0153	0.0696	0.1558	0.0144	0.0926
KLK11	0.3219	0.025	0.0777	0.3417	0.0289	0.0845	0.4243	0.0288	0.0678	0.3423	0.0269	0.0785
KLK2	0.3536	0.0295	0.0835	0.3093	0.0277	0.0897				0.245	0.0278	0.1133
KLK3	0.4473	0.0545	0.1217	0.4639	0.0614	0.1325	0.374	0.0491	0.1313	0.5037	0.0686	0.1361
KPNB1	0	0	0.0622	0	0	0.0675	0	0	0.0693	0.0402	0.0025	0.0622
KRT1	0.085	0.0063	0.0746	0.0872	0.0094	0.1076	0.073	0.0057	0.0775	0.1065	0.0105	0.0982
KRT10	0.133	0.0159	0.1199	0.1355	0.0153	0.1127	0.0951	0.0101	0.1067	0.1543	0.0168	0.1086
KRT5	0.0322	0.0038	0.1167	0.0451	0.0053	0.1169	0.054	0.006	0.1116	0.0338	0.0038	0.1114
KRT8	0.0918	0.0078	0.0844	0.1742	0.0121	0.0694	0.0885	0.0071	0.0797	0.1088	0.0095	0.0873
KRT9	0.1719	0.0129	0.0753	0.2065	0.0145	0.0701	0.242	0.0202	0.0833	0.3418	0.0285	0.0834
LAMA5	0.174	0.0245	0.1409	0.1794	0.025	0.1394				0.189	0.0264	0.1397
LAMB2	0.1981	0.0159	0.0801	0.2052	0.0178	0.0869	0.1991	0.0166	0.0835	0.2137	0.0186	0.087
LAMC1	0.0557	0.0053	0.0943	0.0464	0.0043	0.0928	0.0541	0.005	0.0923	0.0468	0.0046	0.098
LAMP1	0.1345	0.014	0.1042	0.1396	0.014	0.1004	0.155	0.0162	0.1044	0.1318	0.0134	0.102
LAMP2	0.3105	0.013	0.0417	0.2811	0.0115	0.0409	0.3886	0.0158	0.0406	0.2764	0.0086	0.0311
LAP3	0.0812	0.0059	0.0732	0.0812	0.0059	0.0732	0.0751	0.0059	0.0792	0.119	0.0077	0.0643
LCN1	0.4517	0.0414	0.0916	0.4019	0.044	0.1096	0.4321	0.0456	0.1056	0.5988	0.0681	0.1137
LCN2	0.4855	0.0481	0.099	0.5353	0.0529	0.0988	0.683	0.0458	0.067	0.5143	0.0506	0.0983
LCP1	0.0194	0.0014	0.071	0.0194	0.0014	0.0711	0.0201	0.0014	0.0686	0.0209	0.0014	0.0661
LDHA	0.073	0.0048	0.0664	0.0782	0.0048	0.062	0.0585	0.0036	0.0621	0.0628	0.0036	0.0578
LDHB	0	0	0.0538	0	0	0.0631	0	0	0.0659	0	0	0.0584
LDHC	0.1788	0.012	0.0669	0.1791	0.012	0.0668	0.1925	0.012	0.0622	0.1745	0.0133	0.0762
LDLR	0.2039	0.0278	0.1364	0.2216	0.0286	0.1291	0.2889	0.0334	0.1154	0.1723	0.0244	0.1417
LEFTY2	0.2331	0.0258	0.1107	0.1906	0.0258	0.1353	0.233	0.0296	0.1272	0.1533	0.0246	0.1601
LGALS3	0.3563	0.0277	0.0778	0.381	0.0296	0.0777	0.3802	0.0296	0.0778	0.3321	0.0258	0.0778
LGALS3BP	0.2389	0.0231	0.0967	0.231	0.0223	0.0966	0.2397	0.0232	0.0969	0.2542	0.033	0.1298
LGMN	0.0513	0.006	0.1173	0.0365	0.004	0.1097	0.2474	0.0308	0.1247	0.053	0.006	0.1134
LIFR	0.2023	0.0129	0.0637	0.1923	0.0117	0.0608	0.2187	0.0133	0.0608	0.2125	0.0129	0.0607
LIPA	0.296	0.0247	0.0833	0.3099	0.0259	0.0834	0.3303	0.0238	0.072	0.3626	0.0347	0.0958
LIPG	0.126	0.0113	0.09	0.1082	0.0105	0.0966	0.1979	0.0247	0.1249	0.0902	0.0087	0.0966
LIPI	0.626	0.0493	0.0787	0.6056	0.0488	0.0805				0.7315	0.055	0.0752
LMAN2	0.051	0.0025	0.0485	0.0703	0.0037	0.0528	0.0217	0.0012	0.057	0.0316	0.0025	0.0783
LNPEP	0.2104	0.0128	0.0607	0.2152	0.013	0.0605	0.1788	0.0107	0.06	0.2345	0.0145	0.0618
LPL	0.0263	0.0027	0.1044	0.0175	0.0018	0.1044	0.0304	0.0027	0.0905	0.0946	0.0091	0.0958
LRG1	0.2851	0.0329	0.1153	0.3189	0.0342	0.1072	0.3213	0.037	0.1152	0.3462	0.037	0.1069
LSAMP	0.0321	0.0014	0.0446	0.0321	0.0014	0.0446	0.0321	0.0014	0.0446	0.0463	0.0014	0.0309
LTA4H	0.1937	0.0067	0.0346	0.1805	0.0067	0.0372	0.133	0.006	0.0448	0.1809	0.0067	0.0371
LTF	0.5604	0.0736	0.1313	0.5845	0.0751	0.1284	0.5349	0.0737	0.1377	0.5788	0.0721	0.1245
LYZ	1.5916	0.0565	0.0355	1.5916	0.0565	0.0355	1.2151	0.0563	0.0464	1.1524	0.0532	0.0462
LZTFL1	0.0826	0.0043	0.0523	0.0922	0.0043	0.0469	0.0922	0.0043	0.0469	0.1041	0.0043	0.0415
MAMDC2	0.0582	0.0044	0.0761	0.0515	0.0038	0.0737	0.062	0.0044	0.0714	0.0711	0.0051	0.0713
MAN2A1	0.186	0.0102	0.0551	0.2152	0.0102	0.0476	0.1666	0.0094	0.0565	0.2003	0.0098	0.0491
MAN2B1	0.1428	0.0131	0.0917	0.1277	0.0127	0.0991	0.1381	0.0131	0.0948	0.1564	0.0153	0.098
MAN2B2	0.268	0.0256	0.0954	0.213	0.0246	0.1153	0.2878	0.0268	0.0931	0.282	0.0291	0.1033

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
GSTM3	0.1024	0.0115	0.1118
GSTO1	0.2258	0.0145	0.0642
GSTP1	0.1008	0.0108	0.107
GSTT1	0.1863	0.0131	0.0704
GSTZ1	0.2329	0.0167	0.0717
GUSB	0.289	0.0375	0.1297
HDHD2	0.052	0.0035	0.0668
HEBP2	0.1605	0.0149	0.0928
HEXA	0.2116	0.0155	0.0733
HEXB	0.3717	0.031	0.0835
HINT1	0.0838	0.007	0.0836
HIST2H2BE	0	0	0.0671
HPRT1	0.3649	0.0215	0.0589
HPX	0.4455	0.0286	0.0643
HRSP12	0.2397	0.0199	0.0829
HSPA1L	0.0457	0.0452	0.9893
HSPA4	0.0465	0.0031	0.0661
HSPA5	0.0836	0.0056	0.0664
HSPA8	0	0	0.0956
HSPB1			
HSPG2	0.9207	0.289	0.3139
Hyou1	0.0686	0.0062	0.0909
IDE	0.0385	0.0023	0.06
IDH1	0.4703	0.0341	0.0725
IDI1	0.2402	0.0211	0.0877
IDS	0.2251	0.0141	0.0627
IDUA	0.2408	0.0314	0.1303
IGF2R			
IGFBP2	0.0848	0.0058	0.068
IGFBP5	0.0677	0.0032	0.0478
IGHG1			
IGHG2			
IGHG4			
IGJ	0.9314	0.0308	0.033
IGKC	3.3139	0.0952	0.0287
IL1R1	0.4258	0.025	0.0587
IL1RAP	0.0414	0.0032	0.0762
IL1RL1	0.5326	0.1521	0.2856
IL6ST	0.1447	0.0099	0.0687
IMPA1	0.3913	0.0178	0.0455
INHBB	0.0217	0.0015	0.0679
IQGAP1	0.0339	0.0019	0.0553
IQGAP2	0.1303	0.0076	0.0581
ITIH5	0.1716	0.0202	0.1176
KAL1	0.155	0.0125	0.0804
KIF5B	0.1805	0.0135	0.0749
KLK11	0.3508	0.023	0.0656
KLK2			
KLK3	0.4211	0.0558	0.1324
KPNB1	0	0	0.0657
KRT1	0.0871	0.007	0.0806
KRT10	0.0561	0.0048	0.0855
KRT5	0.05	0.0068	0.1357
KRT8	0.4263	0.0523	0.1226
KRT9	0.1031	0.0091	0.0885
LAMA5	0.1819	0.0271	0.1488
LAMB2	0.1842	0.0159	0.0863
LAMC1	0.0423	0.0043	0.1021
LAMP1	0.2048	0.0184	0.0897
LAMP2	0.3399	0.013	0.0381
LAP3	0.5645	0.0914	0.162
LCN1	0.299	0.0461	0.154
LCN2	0.5081	0.0431	0.0848
LCP1	0.0175	0.0014	0.079
LDHA	0.0781	0.0048	0.062
LDHB	0	0	0.087
LDHC	0.1478	0.012	0.0809
LDLR			
LEFTY2	0.1457	0.0271	0.1862
LGALS3	0.4411	0.0315	0.0715
LGALS3BP	0.2358	0.0278	0.118
LGMN	0.0827	0.0082	0.0989
LIFR	0.1898	0.0113	0.0595
LIPA	0.2569	0.023	0.0895
LIPG	0.1131	0.0087	0.077
LIPI	0.725	0.0526	0.0726
LMAN2	0.0502	0.0026	0.0523
LNPEP	0.2216	0.0128	0.0576
LPL	0.0363	0.0037	0.101
LRG1	0.2789	0.0356	0.1278
LSAMP	0.0404	0.0014	0.0355
LTA4H	0.2743	0.0071	0.026
LTF	0.4181	0.0675	0.1614
LYZ	0.6785	0.0533	0.0785
LZTFL1	0.1594	0.0058	0.0362
MAMDC2	0.0718	0.0063	0.0882
MAN2A1	0.2469	0.014	0.0565
MAN2B1	0.1316	0.0132	0.1003
MAN2B2	0.4084	0.0567	0.1387

Gene	CH_*ω*	CH_*Ka*	CH_*Ks*	GH_*ω*	GH_*Ka*	GH_*Ks*	GC_*ω*	GC_*Ka*	GC_*Ks*
MANBA	0.1553	0.0029	0.0189	0.1593	0.0025	0.0154	0.1424	0.0034	0.0241
MARCKS	0.3525	0.0041	0.0116						
MATN2	0.1446	0.0032	0.0219	0.1114	0.0023	0.0204	0.0772	0.0018	0.0236
MDH1	0.1562	0.0012	0.008	0.2077	0.0025	0.0121	0.1038	0.0013	0.0121
MDH2	0.087	0.0013	0.0154	0.1391	0.0027	0.0193	0.2087	0.004	0.0193
MFAP4				0	0	0.0151			
MGAM	0.1544	0.0048	0.0312	0.1416	0.0053	0.0372	0.1525	0.0048	0.0316
MINPP1	0.2703	0.0054	0.0201	0.1576	0.0027	0.0172	0.225	0.0045	0.0202
MLPH	0.4226	0.0111	0.0263	0.6815	0.0162	0.0238	0.4244	0.0116	0.0273
MME	0.0796	0.0011	0.0143	0.0151	0.0006	0.0385	0	0	0.0319
MMP14	0	0.0015	0	0.0856	0.0017	0.0198	0.0428	0.0008	0.0198
MMP2	0.0292	0.0007	0.0228	0.0209	0.0007	0.0314	0	0	0.0228
MMP7	0.2073	0.0066	0.032	0.0786	0.0021	0.0264	0.1906	0.0063	0.0329
MPI	0.1597	0.001	0.0065	0	0	0.0065	0.1596	0.001	0.0065
MPST	0.1936	0.0057	0.0294	0.1216	0.0057	0.047	0.0845	0.0029	0.0338
MSLN	0.7036	0.0125	0.0177	1.1213	0.0191	0.017	0.7793	0.0183	0.0235
MSMB	0.5441	0.0075	0.0139	0	0.0113	0	0.2705	0.0038	0.0139
MUC5B	0.4838	0.0251	0.0519						
MUC6	0.4692	0.0222	0.0474	0.4761	0.024	0.0505	0.5151	0.0235	0.0456
MYH9	0.036	0.0012	0.033	0	0	0.0331	0.0318	0.0012	0.0376
MYO1C	0.3035	0.0105	0.0346	0.181	0.0043	0.0238	0.2602	0.0099	0.0381
NAGA	0.3005	0.0021	0.0071	0.1648	0.0053	0.0322	0.128	0.0032	0.0249
NAGLU	0.0578	0.0006	0.0105	0.1565	0.003	0.0194	0.1975	0.0024	0.0123
NAPA	0	0	0.0209	0	0	0.0359	0	0	0.0237
NBL1				0.123	0.0041	0.0334			
NCSTN	0.0922	0.0012	0.0135	0	0	0.0175	0.162	0.0012	0.0077
NELL1	0.3253	0.0041	0.0127	0.2835	0.0079	0.0279	0.264	0.0085	0.0323
NEO1	0.0994	0.0012	0.0122	0.0455	0.001	0.021	0.0398	0.001	0.024
NEU1	0	0	0.0161	0	0	0.0096	0	0	0.0259
NIF3L1	0.1648	0.0024	0.0144	0.1977	0.0036	0.018	0.3309	0.0036	0.0107
NME3	0	0	0.0166	0.1712	0.0054	0.0314	0.3472	0.0058	0.0167
NP	0.1547	0.003	0.0197						
NPC2	0	0	0.0097	0	0	0.0295	0	0	0.0195
NPEPPS	0	0	0.0015						
NRCAM	0.0277	0.0003	0.0121	0.1076	0.002	0.019	0.0953	0.0017	0.0178
NRP1	0.0838	0.0019	0.0224	0.0802	0.0014	0.0176	0.0586	0.0014	0.024
NUCB1	0.1566	0.001	0.0066	0.1326	0.0029	0.0216	0.1769	0.0041	0.0234
NUCB2	0.122	0.001	0.0081	0.122	0.001	0.0081	0	0	0.0081
NUTF2	0	0	0.0132	0	0	0.0267	0	0	0.0132
ODZ2	0.0211	0.0003	0.016	0.0299	0.0006	0.0216	0.0229	0.0005	0.0226
OLFM1	0.0328	0.001	0.0297	0	0	0.0391	0	0	0.0189
OLFM4	0.0434	0.0009	0.0198	0.11	0.0034	0.0312	0.1516	0.0043	0.0283
ORM1	0.1947	0.0087	0.0447	0.3344	0.0175	0.0524	0.3358	0.0175	0.0522
ORM2	0.3987	0.04	0.1004						
OS9	0.2073	0.0013	0.0063						
P4HB	0.0643	0.0017	0.0265	0.0261	0.0009	0.0326	0.0533	0.0026	0.0479
PACSIN2	0.2184	0.0035	0.0161	0.1166	0.0026	0.0226	0.2272	0.0044	0.0193
PAEP	0.4005	0.0098	0.0245						
PAICS	0.375	0.0051	0.0135	0.3568	0.0065	0.0182	0.5989	0.0043	0.0072
PAM	0.1516	0.0013	0.0089	0.2595	0.0027	0.0103	0.506	0.0022	0.0044
Park7	0.1123	0.0024	0.0212						
PCMT1	0	0.0016	0	0.6511	0.0035	0.0054	0.3247	0.0018	0.0054
PDCD6	0.4132	0.008	0.0194						
PDCD6IP	0.0308	0.0005	0.0163	0.0402	0.0011	0.0285	0.0303	0.0006	0.0189
PDGFA	0.5085	0.0153	0.03	0.2725	0.0163	0.0599	0.251	0.0093	0.0369
PDIA3	0	0	0.0089	0.5328	0.0113	0.0213	0.6237	0.0113	0.0182
PEBP4	0.1922	0.0077	0.0399	0.1943	0.0038	0.0198	0.3919	0.0077	0.0197
PFAS	0.1728	0.0044	0.0254	0.1808	0.0041	0.0224	0.1663	0.0051	0.0304
PFKP	0.0331	0.0018	0.0535	0.0107	0.0006	0.0563	0.0293	0.0015	0.0513
PFN1	1.3715	0.0139	0.0101	0	0	0.0096	0	0.0139	0
PFN2	0	0	0.008	0	0	0	0	0	0.008
PGAM2	0	0	0.0056	0.1035	0.0017	0.0168	0.1558	0.0017	0.0112
PGC	1.2432	0.0045	0.0036	0.1534	0.0023	0.0148	0.4116	0.0046	0.0111
PGCP	0.5268	0.0047	0.0089						
PGD	0.091	0.0027	0.0299	0.0378	0.0012	0.0314	0.0433	0.0012	0.0274
PGK1	0	0	0.0034	0	0	0.0068	0	0	0.0034
PGK2	0.1021	0.0021	0.0206						
PGLS	0.0742	0.0018	0.0241	0.1909	0.0049	0.0257	0.0759	0.0025	0.0323
PGM1	0.1755	0.003	0.0172	0.1918	0.0038	0.0197	0.2196	0.0038	0.0172
PGM2	0.085	0.0022	0.026	0.6922	0.1015	0.1467	0.7466	0.1073	0.1437
PHGDH	0.0693	0.0008	0.0122	0.1534	0.0034	0.0221	0.2158	0.0042	0.0196
PI15	0	0	0.0167	0	0	0.0055	0	0	0.0111
PIGR	0.7749	0.009	0.0117	0.2877	0.0102	0.0355	0.1884	0.0058	0.0309
PIP	0.7754	0.0152	0.0196	1.8864	0.0183	0.0097	2.1858	0.0214	0.0098
PITPNA	0	0	0	0.5495	0.0032	0.0058	0.5495	0.0032	0.0058
PKM2	0.3257	0.0022	0.0068	0.3896	0.0044	0.0113	0.1614	0.0022	0.0136
PLA1A	0.0524	0.001	0.0184	0.3543	0.0087	0.0247	0.3147	0.0078	0.0247
pla2g2A	0.2822	0.0121	0.0429	1.7614	0.0184	0.0105	0.1124	0.0061	0.0541
PLA2G7	0.8617	0.0029	0.0034	0.2214	0.0034	0.0155	0.367	0.0044	0.012
PLOD2	0.1424	0.0011	0.0081	0.0347	0.0006	0.0186	0.0229	0.0007	0.0285
PLOD3	0.1402	0.0018	0.0129	0.0889	0.0018	0.0203	0.3282	0.0036	0.011
PLXNB2	0.1442	0.0035	0.024	0.0668	0.0024	0.0354	0.1139	0.0042	0.0369
PODXL2	0.082	0.0009	0.0106	0.2426	0.0023	0.0094	0.219	0.0017	0.0079
PPAP2A	0.3177	0.0015	0.0049	0	0	0.0197	0.1052	0.0015	0.0147
PPIA	0	0	0.0276	0.2875	0.0053	0.0183	0.1905	0.0053	0.0276
PPIB	0	0.002	0	0	0	0.0131	0.1559	0.002	0.0131
PPIC	0.6534	0.0084	0.0129	1.9743	0.0127	0.0064	0.2171	0.0042	0.0194
PPP1CC	0	0	0.0093	0	0	0.0192	0	0	0.0096
PPP1R7	0.0716	0.0012	0.0167	0	0	0.0167	0.0717	0.0012	0.0167

Gene	OH_*ω*	OH_*Ka*	OH_*Ks*	OC_*ω*	OC_*Ka*	OC_*Ks*	OG_*ω*	OG_*Ka*	OG_*Ks*
MANBA	0.269	0.0084	0.0311	0.1918	0.0084	0.0436	0.1976	0.0079	0.0399
MARCKS	0.0752	0.0055	0.073	0.0938	0.0069	0.0732			
MATN2	0.1908	0.0082	0.0428	0.1532	0.0068	0.0444	0.1877	0.0068	0.0364
MDH1	0.3123	0.005	0.016	0.4705	0.0038	0.008	0.249	0.005	0.0202
MDH2	0.0685	0.0027	0.0391	0.1027	0.004	0.0391	0.1245	0.0054	0.0431
MFAP4	0.028	0.0016	0.0566				0.0255	0.0016	0.0623
MGAM	0.2035	0.0108	0.053	0.1724	0.0097	0.0561	0.1797	0.01	0.0558
MINPP1	0.2233	0.0091	0.0408	0.3381	0.0128	0.0378	0.2166	0.0082	0.0378
MLPH	0.4172	0.0291	0.0698	0.3205	0.0218	0.0679	0.4019	0.0263	0.0654
MME	0.061	0.0023	0.0374	0.0367	0.0011	0.0311	0.0287	0.0012	0.0406
MMP14	0.2075	0.0045	0.0219	0.2075	0.0045	0.0219	0.1491	0.0051	0.0342
MMP2	0.0438	0.0023	0.0533	0.0389	0.0016	0.0407	0.0325	0.0016	0.0479
MMP7	0.2125	0.0116	0.0546	0.2286	0.015	0.0655	0.2219	0.0104	0.047
MPI	0.1574	0.0042	0.0266	0.1973	0.0052	0.0265	0.1573	0.0042	0.0266
MPST	0.2893	0.0194	0.067	0.3091	0.0165	0.0533	0.3365	0.0158	0.047
MSLN	0.4504	0.0339	0.0752	0.3837	0.0348	0.0907	0.5351	0.0383	0.0716
MSMB	2.7579	0.0385	0.014	1.0871	0.0306	0.0282	2.4679	0.0345	0.014
MUC5B	0.5382	0.0547	0.1017	0.512	0.0603	0.1177			
MUC6	0.3339	0.0338	0.1012	0.3481	0.0366	0.105	0.3362	0.0306	0.0909
MYH9	0.0193	0.0013	0.0688	0.02	0.0014	0.071	0.0201	0.0013	0.0661
MYO1C	0.0641	0.0042	0.0652	0.1217	0.0092	0.0756	0.0607	0.0039	0.0637
NAGA	0.2364	0.0085	0.036	0.2232	0.0064	0.0286	0.2427	0.0096	0.0395
NAGLU	0.0841	0.0049	0.0578	0.0786	0.0043	0.0541	0.0875	0.0042	0.0486
NAPA	0	0	0.0511	0	0	0.0452	0	0	0.0654
NBL1	0.0377	0.002	0.054				0.0613	0.002	0.0334
NCSTN	0.1595	0.0057	0.0355	0.2719	0.0069	0.0254	0.1922	0.0057	0.0294
NELL1	0.1851	0.0059	0.032	0.1946	0.007	0.036	0.2977	0.0119	0.04
NEO1	0.1662	0.0042	0.0256	0.1495	0.0042	0.0284	0.0932	0.0032	0.0343
NEU1	0.1381	0.0054	0.0392	0.0964	0.0054	0.0561	0.1096	0.0054	0.0493
NIF3L1	0.2737	0.0059	0.0217	0.2735	0.0059	0.0217	0.2812	0.0071	0.0253
NME3	0	0	0.0803	0	0	0.0595	0.0666	0.0054	0.0807
NP	0.1885	0.0099	0.0528	0.1883	0.0099	0.0528			
NPC2	0.1748	0.0087	0.0498	0.22	0.0087	0.0396	0.4458	0.0087	0.0195
NPEPPS	0.092	0.0014	0.0155	0.0835	0.0014	0.0171			
NRCAM	0.0685	0.0028	0.0407	0.0618	0.0024	0.0395	0.0912	0.0035	0.0389
NRP1	0.1313	0.0042	0.0322	0.1314	0.0042	0.0322	0.111	0.0038	0.0339
NUCB1	0.061	0.0029	0.0469	0.1023	0.0041	0.0405	0.101	0.0057	0.0568
NUCB2	0.0687	0.002	0.0289	0.0344	0.001	0.0288	0.0344	0.001	0.0288
NUTF2	0	0	0.0404	0	0	0.0267	0	0	0.0404
ODZ2	0.0242	0.0009	0.0392	0.0126	0.0005	0.0403	0.0208	0.0008	0.0389
OLFM1	0.0393	0.003	0.0772	0.0765	0.0043	0.0556	0.0423	0.0035	0.0824
OLFM4	0.1224	0.0086	0.0703	0.1346	0.0095	0.0703	0.1722	0.0121	0.0701
ORM1	0.2444	0.0287	0.1174	0.1807	0.0242	0.1341	0.1699	0.0242	0.1426
ORM2	0.538	0.0585	0.1088	0.1807	0.0242	0.1341			
OS9	0.0676	0.0036	0.0528	0.0995	0.005	0.0503			
P4HB	0.0598	0.0034	0.0571	0.0849	0.0051	0.0603	0.035	0.0026	0.0731
PACSIN2	0.0167	0.0009	0.0527	0.0534	0.0026	0.0493	0.0356	0.0018	0.0493
PAEP	0.4329	0.0183	0.0424	0.5247	0.0198	0.0376			
PAICS	0.2974	0.0071	0.0238	0.3587	0.0061	0.0169	0.5209	0.0076	0.0145
PAM	0.2212	0.0063	0.0284	0.2297	0.0058	0.0254	0.2332	0.0063	0.0269
Park7	0.1104	0.0048	0.0432	0.0663	0.0024	0.0358			
PCMT1	0.3258	0.0031	0.0095	0.1626	0.0016	0.0096	0.2154	0.0035	0.0165
PDCD6	0.1363	0.01	0.0735	0.2106	0.014	0.0667			
PDCD6IP	0.0644	0.002	0.0312	0.071	0.0015	0.0212	0.1103	0.0023	0.0208
PDGFA									
PDIA3	0	0	0.0362	0	0	0.0331	0.4139	0.0114	0.0274
PEBP4	0.2047	0.0096	0.0469	0.2228	0.0135	0.0606	0.2414	0.0097	0.04
PFAS	0.1999	0.0085	0.0424	0.2111	0.0098	0.0466	0.1785	0.0081	0.0455
PFKP	0.0292	0.0023	0.0774	0.0268	0.0024	0.088	0.0161	0.0012	0.0748
PFN1	0.2201	0.0064	0.0292	1.0289	0.0209	0.0204	0.3323	0.0064	0.0194
PFN2	0	0.0023	0	0.2858	0.0023	0.008	0	0.0023	0
PGAM2	0	0	0.0399	0	0	0.0458	0.0303	0.0017	0.0575
PGC	0.1495	0.0091	0.0607	0.2007	0.0114	0.0566	0.1319	0.0091	0.0693
PGCP	0.4739	0.0113	0.0238	0.698	0.0103	0.0148			
PGD	0.1442	0.0123	0.0854	0.1906	0.0151	0.0792	0.1836	0.0161	0.088
PGK1	0.0775	0.0011	0.0136	0.1036	0.0011	0.0102	0.1553	0.0011	0.0068
PGK2	0.1014	0.0032	0.0311	0.1836	0.0047	0.0258			
PGLS	0.0834	0.0054	0.0644	0.0478	0.0036	0.0748	0.1405	0.0074	0.0525
PGM1	0.0605	0.0023	0.0374	0.0189	0.0008	0.04	0.071	0.003	0.0426
PGM2	0.0384	0.0021	0.0551	0.0622	0.003	0.0475	0.61	0.1017	0.1667
PHGDH	0.02	0.0008	0.0423	0.0425	0.0017	0.0398	0.1066	0.0042	0.0398
PI15	0.228	0.0051	0.0224	0.1817	0.0051	0.0281	0.1817	0.0051	0.0281
PIGR	0.4952	0.0283	0.0572	0.4125	0.0232	0.0563	0.3738	0.0235	0.063
PIP	1.2573	0.0245	0.0195	1.7242	0.0339	0.0197	3.1647	0.0308	0.0097
PITPNA	0.0591	0.0032	0.0542	0.0591	0.0032	0.0542	0	0	0.0605
PKM2	0.1837	0.0059	0.032	0.1066	0.0037	0.0344	0.1277	0.0044	0.0345
PLA1A	0.2228	0.0097	0.0437	0.2451	0.0107	0.0437	0.2335	0.0117	0.0501
pla2g2A	1.097	0.0291	0.0265	0.2766	0.0197	0.0714	0.3561	0.0153	0.043
PLA2G7	0.3563	0.0049	0.0137	0.5717	0.0059	0.0103	0.2832	0.0064	0.0225
PLOD2	0.1622	0.0051	0.0313	0.1327	0.0052	0.0388	0.1495	0.0051	0.0344
PLOD3	0.0404	0.003	0.0746	0.0597	0.0036	0.0606	0.0705	0.0048	0.0685
PLXNB2	0.093	0.0068	0.0728	0.1121	0.0085	0.0762	0.0712	0.005	0.0701
PODXL2	0.2174	0.0093	0.0429	0.1374	0.0059	0.0429	0.2718	0.0102	0.0376
PPAP2A									
PPIA	0	0	0.0564	0	0	0.0564	0.0934	0.0053	0.0563
PPIB	0	0	0.0331	0.0617	0.002	0.0331	0	0	0.0468
PPIC	0.2126	0.0127	0.0598	0.0574	0.0042	0.0735	0.08	0.0042	0.0527
PPP1CC	0	0	0.0188	0	0	0.0093	0	0	0.0192
PPP1R7	0.0475	0.0012	0.0252	0.0708	0.0024	0.0339	0.0355	0.0012	0.0338

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
MANBA	0.2316	0.0089	0.0382	0.1664	0.0079	0.0473	0.1924	0.0084	0.0435	0.2243	0.0094	0.0417
MARCKS	0.2473	0.0115	0.0465	0.2762	0.0129	0.0466				0.1944	0.0115	0.059
MATN2	0.1522	0.0073	0.0477	0.138	0.0068	0.0493	0.138	0.0059	0.0429	0.2069	0.0082	0.0395
MDH1	0.1026	0.0038	0.0366	0.0883	0.0025	0.0283	0.092	0.0038	0.041	0.133	0.0038	0.0282
MDH2	0	0	0.07	0	0	0.07	0.0377	0.0028	0.0743	0.04	0.0028	0.0701
MFAP4	0	0	0.0786				0	0	0.087	0.0648	0.0023	0.0348
MGAM	0.1445	0.0094	0.0652	0.1326	0.0088	0.0666	0.1297	0.0091	0.0699	0.166	0.0094	0.0569
MINPP1	0.1808	0.0118	0.0655	0.2072	0.0155	0.0749	0.1667	0.0109	0.0655	0.2268	0.0155	0.0685
MLPH	0.5403	0.0826	0.1529	0.2672	0.0233	0.0872	0.5492	0.0824	0.15	0.5544	0.0802	0.1447
MME	0.0798	0.004	0.0502	0.0653	0.0029	0.0437	0.0618	0.0029	0.0472	0.0873	0.004	0.0459
MMP14	0.0659	0.0023	0.0344	0.0659	0.0023	0.0344	0.059	0.0025	0.0431	0.0661	0.0023	0.0343
MMP2	0.1288	0.0094	0.0732	0.1365	0.0082	0.0601	0.1281	0.0088	0.0684	0.161	0.0112	0.0694
MMP7	0.3942	0.0158	0.0402	0.3119	0.0159	0.0509	0.435	0.0158	0.0363	0.945	0.02	0.0212
MPI	0.0284	0.001	0.0367	0.057	0.0021	0.0367	0.0284	0.001	0.0367	0.1423	0.0052	0.0368
MPST	0.1751	0.0129	0.0735	0.1672	0.01	0.0598	0.1669	0.01	0.0601	0.3346	0.0216	0.0645
MSLN	0.4987	0.0507	0.1016	0.4607	0.0499	0.1083	0.5091	0.0489	0.096	0.481	0.0488	0.1015
MSMB	0.3688	0.0267	0.0725	0.2162	0.019	0.0878	0.3143	0.0228	0.0726	0.5975	0.0345	0.0577
MUC5B												
MUC6	0.3718	0.0333	0.0896	0.3161	0.0327	0.1033	0.3441	0.0331	0.0963	0.3014	0.0294	0.0975
MYH9	0.0079	0.0007	0.0857	0.0209	0.0019	0.0908	0.008	0.0007	0.0848	0.0131	0.0009	0.0688
MYO1C	0.0674	0.0056	0.0838	0.1308	0.0119	0.0911	0.0618	0.0049	0.0796	0.0468	0.0043	0.0927
NAGA	0.1453	0.0096	0.066	0.128	0.0075	0.0582	0.1724	0.0107	0.0619	0.1462	0.0085	0.0583
NAGLU	0.0699	0.0058	0.0837	0.0621	0.0052	0.0837	0.0753	0.0058	0.0776	0.0707	0.0052	0.0735
NAPA												
NBL1	0.067	0.0041	0.061				0.1543	0.0041	0.0266	0.0433	0.002	0.0471
NCSTN	0.2712	0.0159	0.0585	0.3564	0.0172	0.0481	0.3036	0.0159	0.0523	0.3151	0.0192	0.0608
NELL1	0.1553	0.0064	0.0414	0.1422	0.0065	0.0456	0.207	0.0104	0.0501	0.1304	0.0054	0.0414
NEO1	0.106	0.0039	0.0372	0.1059	0.0042	0.0401	0.1104	0.0045	0.0405	0.1431	0.0055	0.0382
NEU1	0.082	0.0043	0.0527	0.0618	0.0043	0.07	0.0685	0.0043	0.0631	0.1437	0.0076	0.0528
NIF3L1	0.3743	0.0179	0.0478	0.374	0.0179	0.0479	0.3703	0.0191	0.0516	0.3484	0.0167	0.0479
NME3	0	0	0.0637	0	0	0.0508	0.0966	0.0054	0.0556	0	0	0.0634
NP	0.2309	0.0092	0.0398	0.2307	0.0092	0.0398				0.189	0.01	0.0526
NPC2	0	0	0.0498	0	0	0.0395	0	0	0.0395	0.22	0.0087	0.0396
NPEPPS	0.0935	0.0027	0.0289	0.0879	0.0027	0.0307				0.1053	0.0032	0.0308
NRCAM	0.0512	0.0023	0.0459	0.0462	0.002	0.0436	0.0676	0.0031	0.0454	0.0784	0.0038	0.049
NRP1	0.1375	0.0038	0.0273	0.1229	0.0038	0.0306	0.1019	0.0033	0.0323	0.1248	0.0042	0.0339
NUCB1	0.0563	0.0035	0.063	0.0752	0.0047	0.0631	0.1056	0.0071	0.0673	0.0808	0.0071	0.088
NUCB2	0.08	0.003	0.0372	0.0534	0.002	0.0372	0.0534	0.002	0.0372	0.0902	0.003	0.033
NUTF2	0	0	0.0543	0	0	0.0404	0	0	0.0267	0	0	0.0404
ODZ2	0.0288	0.0014	0.0495	0.0191	0.001	0.053	0.0262	0.0013	0.0494	0.0192	0.0011	0.0576
OLFM1	0.0152	0.001	0.065	0.0235	0.0011	0.0463	0.0184	0.001	0.0538	0.073	0.0049	0.0667
OLFM4	0.233	0.0122	0.0523	0.2649	0.0131	0.0493	0.2134	0.0131	0.0612	0.3118	0.0192	0.0616
ORM1	0.3783	0.0198	0.0523	0.2098	0.0109	0.0521	0.3376	0.0176	0.052	0.245	0.0265	0.1081
ORM2	0.4993	0.0378	0.0757	0.2098	0.0109	0.0521				0.245	0.0265	0.1081
OS9	0.0754	0.0039	0.0524	0.1052	0.0053	0.0501				0.0948	0.0064	0.0679
P4HB	0.1214	0.0077	0.0634	0.1053	0.0077	0.073	0.0859	0.0068	0.0795	0.1096	0.0094	0.0859
PACSIN2	0.0314	0.0026	0.084	0.0546	0.0044	0.0806	0.0437	0.0035	0.0805	0.0228	0.0018	0.0769
PAEP	1.3918	0.0284	0.0204	0.761	0.0315	0.0414				0.7697	0.0376	0.0489
PAICS	0.2238	0.0132	0.059	0.2353	0.0122	0.0518	0.2529	0.0141	0.0559	0.2475	0.0106	0.043
PAM	0.2517	0.0075	0.0299	0.2983	0.0071	0.0237	0.2977	0.0075	0.0253	0.282	0.0084	0.0299
Park7	0	0	0.0356	0.0839	0.0024	0.0284				0.6785	0.0048	0.007
PCMT1	0.1293	0.0031	0.0241	0.0645	0.0016	0.0241	0.1068	0.0035	0.0332	0	0	0.0241
PDCD6	0.1686	0.0161	0.0957	0.156	0.0161	0.1033				0.1777	0.0151	0.085
PDCD6IP	0.0337	0.0015	0.0447	0.0305	0.001	0.0329	0.0501	0.0017	0.0343	0.0145	0.0005	0.0345
PDGFA	0.3921	0.0284	0.0724	0.283	0.0224	0.0792	0.1151	0.0116	0.1007			
PDIA3	0.0402	0.0017	0.0425	0.0434	0.0017	0.0393	0.3278	0.0131	0.04	0.0472	0.0017	0.0362
PEBP4	0.3808	0.0243	0.0638	0.4456	0.0283	0.0635	0.4302	0.0244	0.0568	0.3722	0.0263	0.0707
PFAS	0.2684	0.0119	0.0443	0.226	0.0123	0.0543	0.2241	0.011	0.0493	0.3666	0.0135	0.0369
PFKP	0.1205	0.0168	0.1392	0.1284	0.017	0.132	0.1394	0.0176	0.1264	0.179	0.0179	0.1003
PFN1	0.663	0.0064	0.0097	0	0.0209	0	0	0.0064	0	0.663	0.0129	0.0195
PFN2	0	0.0023	0	0.2859	0.0023	0.008	0	0.0023	0	0	0.0023	0
PGAM2	0	0	0.0517	0	0	0.0577	0.025	0.0017	0.0696	0	0	0.0576
PGC	0.28	0.0137	0.0488	0.3562	0.016	0.0449	0.2004	0.0115	0.0572	0.1884	0.0137	0.0725
PGCP	0.2339	0.0084	0.0361	0.2268	0.0075	0.033				0.2903	0.0122	0.0421
PGD	0.1035	0.0073	0.0704	0.1489	0.01	0.0675	0.0853	0.0048	0.0558	0.1875	0.016	0.0853
PGK1	0.4581	0.0133	0.029	0.5203	0.0133	0.0255	0.6	0.0134	0.0223	0.6491	0.0144	0.0221
PGK2	0.1507	0.0063	0.0419	0.2431	0.0084	0.0347				0.2364	0.0074	0.0312
PGLS	0.0932	0.0063	0.0672	0.0539	0.0045	0.083	0.061	0.0049	0.0804	0.0952	0.0072	0.0752
PGM1	0.0791	0.0038	0.0478	0.045	0.0023	0.0504	0.0571	0.003	0.0529	0.0377	0.0015	0.0401
PGM2	0.1006	0.0042	0.0422	0.1525	0.0052	0.0339	0.6615	0.1036	0.1566	0.0791	0.0035	0.0447
PHGDH	0.04	0.0017	0.0423	0.0638	0.0025	0.0398	0.1278	0.0051	0.0398	0.0565	0.0025	0.0449
PI15	0.0751	0.0034	0.0453	0.0861	0.0034	0.0395	0.0861	0.0034	0.0395	0.1491	0.0085	0.0572
PIGR	0.4068	0.0244	0.0601	0.3929	0.0217	0.0553	0.4464	0.0209	0.0467	0.3239	0.0235	0.0727
PIP	0.8341	0.05	0.0599	1.0965	0.0662	0.0604	1.134	0.0564	0.0498	1.2659	0.05	0.0395
PITPNA	0.0712	0.0049	0.0689	0.0712	0.0049	0.0689	0.0216	0.0016	0.0756	0.067	0.0016	0.0244
PKM2	0.221	0.0132	0.0599	0.1937	0.0132	0.0684	0.1937	0.0132	0.0684	0.206	0.0141	0.0684
PLA1A	0.2541	0.0136	0.0536	0.2357	0.0126	0.0536	0.236	0.0127	0.0536	0.2435	0.0146	0.0601
pla2g2A	0.7221	0.0353	0.0488	0.3088	0.0259	0.0837	0.3251	0.0215	0.066	0.3674	0.0243	0.0662
PLA2G7	0.1615	0.0039	0.0242	0.2362	0.0049	0.0207	0.1821	0.0054	0.0295	0.2016	0.0049	0.0242
PLOD2	0.1153	0.004	0.0345	0.0927	0.004	0.0434	0.0861	0.0039	0.0449	0.1657	0.0083	0.0499
PLOD3	0.1996	0.0173	0.0865	0.2508	0.0187	0.0747	0.2226	0.0187	0.0842	0.2455	0.0165	0.0674
PLXNB2	0.2288	0.0205	0.0895	0.2404	0.0226	0.0939	0.2058	0.0187	0.0911	0.1822	0.0192	0.1054
PODXL2	0.2584	0.0112	0.0434	0.2015	0.0088	0.0436	0.239	0.0093	0.0387	0.1167	0.0077	0.066
PPAP2A	0.0778	0.0031	0.0399	0.134	0.0047	0.0348	0.0779	0.0031	0.0399			
PPIA	0	0	0.0276	0	0	0.0276	0.1905	0.0053	0.0276	0	0	0.0467
PPIB	0.0633	0.0024	0.038	0.1268	0.0048	0.038	0.0525	0.0024	0.0458	0.0309	0.0024	0.0778
PPIC	0.2548	0.017	0.0667	0.105	0.0085	0.0805	0.142	0.0085	0.0595	0.0969	0.0085	0.0873
PPP1CC	0	0	0.0389	0	0	0.029	0	0	0.0399	0	0	0.029
PPP1R7	0.0256	0.0012	0.0468	0.0511	0.0024	0.0469	0.0256	0.0012	0.0468	0.0814	0.0024	0.0295

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
MANBA	0.1967	0.015	0.0763	0.169	0.015	0.0887	0.1762	0.0145	0.0822	0.1844	0.0155	0.0843
MARCKS	0.0534	0.0041	0.0773	0.071	0.0055	0.0775				0.0545	0.0048	0.0883
MATN2	0.149	0.0106	0.071	0.1498	0.0101	0.0674	0.1431	0.0092	0.0642	0.1497	0.0101	0.0674
MDH1	0.0937	0.005	0.0535	0.0702	0.0038	0.0535	0.0867	0.005	0.0581	0.087	0.005	0.0576
MDH2	0.0827	0.0081	0.0975	0.0688	0.0067	0.0976	0.1058	0.0108	0.1018	0.1102	0.0108	0.0976
MFAP4	0.0535	0.0057	0.1064				0.0505	0.0057	0.1131	0.0822	0.0073	0.0892
MGAM	0.1838	0.0168	0.0911	0.1913	0.0175	0.0913	0.1805	0.0159	0.0882	0.2099	0.0181	0.0861
MINPP1	0.1803	0.0146	0.081	0.1918	0.0174	0.0906	0.1688	0.0137	0.081	0.24	0.0202	0.084
MLPH	0.3805	0.0397	0.1043	0.3697	0.0352	0.0953	0.3319	0.034	0.1024	0.5187	0.0466	0.0899
MME	0.0563	0.0046	0.0813	0.0434	0.0034	0.079	0.0443	0.0035	0.079	0.0596	0.0046	0.0768
MMP14	0.0792	0.0045	0.0573	0.0792	0.0045	0.0573	0.0761	0.0051	0.0671	0.076	0.0045	0.0597
MMP2	0.0111	0.0013	0.119	0.0064	0.0007	0.1035	0.0059	0.0007	0.1113	0.0243	0.0023	0.0962
MMP7	0.1395	0.0116	0.0832	0.1411	0.015	0.1063	0.1673	0.0126	0.075	0.1921	0.0183	0.0953
MPI	0.1535	0.0105	0.0683	0.1694	0.0116	0.0682	0.1535	0.0105	0.0684	0.2153	0.0147	0.0684
MPST	0.2859	0.0362	0.1266	0.2744	0.0333	0.1212	0.2624	0.0326	0.1243	0.2865	0.0377	0.1315
MSLN	0.507	0.0639	0.1259	0.4638	0.0611	0.1317	0.5141	0.064	0.1244	0.5289	0.0591	0.1118
MSMB	1.0005	0.1009	0.1008	0.9006	0.1052	0.1168	1.0825	0.1095	0.1011	1.2256	0.105	0.0857
MUC5B	0.451	0.0669	0.1484	0.4316	0.0726	0.1682				0.4218	0.0647	0.1534
MUC6												
MYH9	0.0086	0.0009	0.1047	0.0176	0.0019	0.1101	0.0086	0.0009	0.1048	0.0258	0.0023	0.0874
MYO1C	0.05	0.0076	0.1513	0.0744	0.0112	0.1502	0.0396	0.0059	0.148	0.0397	0.0057	0.1426
NAGA	0.1223	0.0112	0.0915	0.125	0.0107	0.0853	0.156	0.0139	0.0891	0.1884	0.0139	0.0737
NAGLU	0.126	0.012	0.0948	0.1322	0.012	0.0904	0.1589	0.0134	0.0841	0.1192	0.0105	0.0884
NAPA	0	0	0.1113	0	0	0.0994	0	0	0.1203	0	0	0.0935
NBL1	0.1142	0.0102	0.0898				0.1507	0.0103	0.0683	0.1085	0.0082	0.0754
NCSTN	0.0854	0.0056	0.066	0.1154	0.0069	0.0598	0.0944	0.0056	0.0598	0.129	0.0088	0.0683
NELL1	0.155	0.0077	0.0498	0.1439	0.0078	0.0542	0.2261	0.0128	0.0568	0.1344	0.0077	0.0575
NEO1	0.1138	0.0055	0.048	0.1116	0.0055	0.049	0.0908	0.0051	0.0563	0.1239	0.0061	0.049
NEU1	0.1315	0.012	0.091	0.1097	0.012	0.1091	0.1174	0.012	0.1019	0.1031	0.0103	0.1
NIF3L1	0.2862	0.0203	0.071	0.3212	0.0203	0.0633	0.3631	0.0215	0.0593	0.2418	0.0191	0.079
NME3	0.0272	0.0029	0.1061	0.037	0.0031	0.0847	0.0895	0.0087	0.0971	0.0251	0.0029	0.1151
NP	0.3531	0.0224	0.0633	0.3528	0.0224	0.0634				0.3271	0.0216	0.066
NPC2	0	0	0.1374	0	0	0.1259	0	0	0.1259	0.069	0.0087	0.1261
NPEPPS	0.0165	0.0005	0.0316	0.0156	0.0005	0.0333				0.0296	0.001	0.0352
NRCAM	0.0816	0.0047	0.0576	0.0773	0.0044	0.0564	0.0974	0.0055	0.0561	0.086	0.0056	0.065
NRP1	0.0884	0.0064	0.0719	0.093	0.0064	0.0684	0.08	0.0059	0.0736	0.0819	0.0059	0.0719
NUCB1	0.1138	0.0149	0.1309	0.0887	0.0104	0.1173	0.1396	0.0178	0.1275	0.1257	0.0178	0.1417
NUCB2	0.8121	0.0586	0.0722	0.7982	0.0576	0.0721	0.7982	0.0576	0.0721	0.8642	0.0586	0.0678
NUTF2	0.2483	0.0498	0.2003	0.2711	0.0498	0.1835	0.2711	0.0498	0.1835	0.2287	0.0498	0.2176
ODZ2	0.0127	0.0009	0.0749	0.0086	0.0007	0.0786	0.0113	0.0008	0.0713	0.012	0.0009	0.0788
OLFM1	0.0384	0.0038	0.0987	0.046	0.0038	0.0823	0.036	0.0039	0.1096	0	0	0.1243
OLFM4	0.3051	0.0279	0.0915	0.3258	0.0288	0.0884	0.3051	0.0288	0.0945	0.3745	0.0332	0.0888
ORM1	0.4628	0.0411	0.0888	0.5165	0.0457	0.0885	0.4036	0.0457	0.1133	0.3945	0.0453	0.1149
ORM2	0.5658	0.0643	0.1136	0.5165	0.0457	0.0885				0.3945	0.0453	0.1149
OS9	0.0927	0.0059	0.0639	0.1094	0.0072	0.0662				0.1027	0.0086	0.0836
P4HB	0.0899	0.0077	0.0856	0.102	0.0094	0.0923	0.0627	0.0068	0.109	0.0815	0.0094	0.1155
PACSIN2	0.3333	0.061	0.183	0.3358	0.0629	0.1873	0.3174	0.062	0.1952	0.3143	0.0601	0.1911
PAEP	1.0817	0.0782	0.0723	1.1289	0.0768	0.068				1.0817	0.073	0.0675
PAICS	0.1563	0.0081	0.0521	0.1368	0.0071	0.052	0.1798	0.0087	0.0485	0.1717	0.0071	0.0414
PAM	0.1665	0.0082	0.0492	0.1928	0.0082	0.0426	0.1962	0.0087	0.0442	0.2293	0.0101	0.0442
Park7	0	0	0.0809	0.0325	0.0024	0.0732				0.094	0.0048	0.0507
PCMT1	0.1051	0.0062	0.0593	0.0786	0.0047	0.0594	0.1041	0.0071	0.0682	0.0524	0.0031	0.0593
PDCD6	0.12	0.0141	0.1176	0.1611	0.0202	0.1255				0.1277	0.0141	0.1104
PDCD6IP	0.0292	0.0015	0.0523	0.0243	0.001	0.0419	0.0408	0.0018	0.0429	0.0127	0.0005	0.0402
PDGFA	0.3281	0.0436	0.133	0.2826	0.0396	0.1403	0.1701	0.0268	0.1579			
PDIA3	0.0406	0.0034	0.0842	0.0423	0.0034	0.0808	0.1972	0.0149	0.0755	0.0442	0.0034	0.0774
PEBP4	0.4138	0.0383	0.0925	0.4603	0.0424	0.092	0.4268	0.0364	0.0854	0.3646	0.0363	0.0995
PFAS	0.1375	0.0129	0.0941	0.1394	0.0136	0.0977	0.1404	0.0129	0.0921	0.1687	0.0141	0.0838
PFKP	0.0249	0.003	0.1214	0.0284	0.0038	0.1338	0.0194	0.0026	0.1337	0.0263	0.003	0.1149
PFN1	0	0	0.0494	0.3359	0.0139	0.0414	0	0	0.0393	0.1079	0.0064	0.0596
PFN2	0	0	0.008	0	0	0.0162	0	0	0.008	0.2858	0.0023	0.008
PGAM2	0.0638	0.0052	0.082	0.0593	0.0052	0.0882	0.0695	0.007	0.1005	0.0593	0.0052	0.0881
PGC	0.1461	0.0148	0.1013	0.1766	0.0171	0.097	0.1138	0.0126	0.1108	0.1702	0.0194	0.1141
PGCP	0.2453	0.0103	0.0421	0.285	0.0094	0.0329				0.3413	0.0122	0.0359
PGD	0.0194	0.0018	0.0933	0.0485	0.0045	0.0937	0.0132	0.0012	0.0896	0.0981	0.0119	0.1208
PGK1	0.0354	0.0021	0.0595	0.0377	0.0021	0.0559	0.0431	0.0021	0.0493	0.0201	0.0011	0.0524
PGK2	0.1279	0.0106	0.0826	0.1694	0.0127	0.0749				0.1821	0.0116	0.0638
PGLS	0.1434	0.0124	0.0864	0.1045	0.0103	0.0987	0.1686	0.013	0.0773	0.1944	0.0145	0.0744
PGM1	0.049	0.0038	0.077	0.0474	0.0038	0.0797	0.0516	0.0045	0.0879	0.0354	0.003	0.0852
PGM2	0.0913	0.0092	0.1009	0.1121	0.0104	0.0926	0.5576	0.1088	0.1951	0.0844	0.0085	0.1008
PHGDH	0.0587	0.0051	0.0868	0.0706	0.0059	0.0842	0.1012	0.0085	0.0841	0.0664	0.0059	0.0895
PI15	0.0298	0.0017	0.0571	0.0332	0.0017	0.0512	0.0332	0.0017	0.0512	0.0985	0.0068	0.0692
PIGR	0.6382	0.057	0.0893	0.6455	0.0537	0.0831	0.6187	0.0533	0.0862	0.5396	0.0534	0.0989
PIP	1.7781	0.1431	0.0805	1.898	0.1538	0.081	2.1428	0.1503	0.0701	3.0481	0.1504	0.0493
PITPNA	0.051	0.0064	0.1259	0.051	0.0064	0.1259	0.0241	0.0032	0.1329	0.0346	0.0032	0.0925
PKM2	0.1461	0.0063	0.0433	0.0891	0.0041	0.0458	0.0806	0.0041	0.0506	0.1102	0.0056	0.0506
PLA1A	0.3641	0.0382	0.105	0.3808	0.0371	0.0975	0.3633	0.0388	0.1068	0.4006	0.0404	0.101
pla2g2A	0.4656	0.0527	0.1132	0.3914	0.0494	0.1263	0.4203	0.0451	0.1074	0.361	0.0479	0.1326
PLA2G7	0.3747	0.0274	0.0731	0.3696	0.0284	0.0768	0.3359	0.0284	0.0845	0.3117	0.0264	0.0846
PLOD2	0.0999	0.0051	0.0512	0.0854	0.0052	0.0607	0.0866	0.0052	0.0597	0.129	0.0083	0.0641
PLOD3	0.0707	0.0085	0.1199	0.0942	0.0103	0.1094	0.0943	0.0103	0.1093	0.0709	0.0085	0.1196
PLXNB2	0.0943	0.0128	0.1361	0.1046	0.0134	0.1279	0.0856	0.0117	0.1371	0.0876	0.0121	0.138
PODXL2	0.2467	0.0119	0.0484	0.262	0.0129	0.0491	0.2984	0.0128	0.043	0.1957	0.0128	0.0654
PPAP2A	0.2672	0.0093	0.0349	0.3653	0.0109	0.0298	0.2065	0.0093	0.0452			
PPIA	0	0	0.0564	0	0	0.0564	0.0934	0.0053	0.0563	0	0	0.0564
PPIB	0	0	0.0608	0.0336	0.002	0.0608	0	0	0.075	0	0	0.0821
PPIC	0.145	0.0148	0.1023	0.0907	0.0106	0.1167	0.1117	0.0106	0.0948	0.1283	0.0117	0.0909
PPP1CC	0	0	0.0429	0	0	0.0331	0	0	0.044	0	0	0.0331
PPP1R7	0.0185	0.0012	0.0648	0.037	0.0024	0.0649	0.0185	0.0012	0.0647	0.037	0.0024	0.0648

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
MANBA	0.1898	0.0145	0.0763
MARCKS	0.1501	0.0101	0.0675
MATN2	0.1493	0.0106	0.0709
MDH1	0.0607	0.0038	0.0619
MDH2	0.0667	0.007	0.1054
MFAP4	0.0875	0.0082	0.0939
MGAM	0.1588	0.0146	0.0919
MINPP1	0.204	0.0192	0.0941
MLPH	0.4542	0.0438	0.0964
MME	0.0778	0.0063	0.081
MMP14	0.0363	0.0023	0.0624
MMP2	0.0763	0.0094	0.1234
MMP7	0.305	0.0243	0.0797
MPI	0.1313	0.0094	0.0719
MPST	0.2989	0.037	0.1237
MSLN	0.4415	0.0666	0.1509
MSMB	1.6997	0.1108	0.0652
MUC5B			
MUC6			
MYH9	0.0092	0.0009	0.0993
MYO1C	0.0203	0.003	0.1453
NAGA	0.1373	0.0139	0.1011
NAGLU	0.099	0.0098	0.0994
NAPA			
NBL1	0.1241	0.0102	0.0825
NCSTN	0.1785	0.0155	0.0871
NELL1	0.0866	0.0059	0.0683
NEO1	0.1095	0.0067	0.0611
NEU1	0.1842	0.0142	0.0769
NIF3L1	0.3017	0.0215	0.0713
NME3	0.0684	0.0029	0.0423
NP	0.3324	0.0193	0.0579
NPC2	0	0	0.1034
NPEPPS	0.0851	0.0032	0.0381
NRCAM	0.1014	0.0057	0.0563
NRP1	0.0694	0.0052	0.0746
NUCB1	0.0705	0.0071	0.1008
NUCB2	0.8295	0.0597	0.072
NUTF2	0.2711	0.0498	0.1835
ODZ2	0.0168	0.0014	0.0845
OLFM1	0.0551	0.0051	0.0919
OLFM4	0.4693	0.0345	0.0734
ORM1	0.4038	0.0389	0.0963
ORM2	0.4038	0.0389	0.0963
OS9	0.0852	0.0072	0.085
P4HB	0.1255	0.012	0.0956
PACSIN2	0.2736	0.0591	0.216
PAEP	0.9465	0.0813	0.0859
PAICS	0.1771	0.0128	0.072
PAM	0.2591	0.0115	0.0446
Park7	0	0	0.043
PCMT1	0.0416	0.0031	0.0748
PDCD6	0.2268	0.0202	0.089
PDCD6IP	0	0	0.0419
PDGFA	0.2521	0.0353	0.1399
PDIA3	0.0723	0.0051	0.071
PEBP4	0.5005	0.0475	0.095
PFAS	0.1798	0.0137	0.0764
PFKP	0.1247	0.0198	0.1589
PFN1	0.1625	0.0064	0.0395
PFN2	0.2859	0.0023	0.008
PGAM2	0.0593	0.0052	0.0881
PGC	0.1912	0.0218	0.1138
PGCP	0.172	0.0094	0.0546
PGD	0.0589	0.0073	0.1236
PGK1	0.2252	0.0154	0.0685
PGK2	0.1926	0.0116	0.0603
PGLS	0.138	0.0103	0.0746
PGM1	0.0485	0.0045	0.0935
PGM2	0.113	0.0092	0.0816
PHGDH	0.0759	0.0068	0.0896
PI15	0.063	0.0051	0.0811
PIGR	0.5996	0.0485	0.0809
PIP	1.3838	0.1636	0.1183
PITPNA	0.0514	0.0049	0.0956
PKM2	0.1748	0.015	0.0856
PLA1A	0.4151	0.0398	0.096
pla2g2A	0.4098	0.0446	0.1087
PLA2G7	0.2871	0.0248	0.0865
PLOD2	0.0916	0.0057	0.062
PLOD3	0.1804	0.0228	0.1265
PLXNB2	0.1792	0.0238	0.1327
PODXL2	0.2147	0.0129	0.0602
PPAP2A	0.3141	0.0078	0.0247
PPIA	0	0	0.0467
PPIB	0.0254	0.0024	0.0946
PPIC	0.1463	0.0149	0.1017
PPP1CC	0	0	0.0439
PPP1R7	0.0347	0.0024	0.0692

Gene	CH_ω	CH_Ka	CH_Ks	GH_ω	GH_Ka	GH_Ks	GC_ω	GC_Ka	GC_Ks
PPP2CA	0.9079	0.0042	0.0047	0	0	0.0094	0.3008	0.0042	0.0141
PPP2R4	0.2494	0.0059	0.0235	0.1193	0.0027	0.0227	0.2994	0.0041	0.0136
PPP5C	0.0262	0.0009	0.0331	0.0523	0.0017	0.0331	0.0362	0.0009	0.0239
PPT1	0.2017	0.0029	0.0142	0.1202	0.0029	0.0238	0	0	0.0286
PRCP	0.9196	0.0025	0.0028	0.1523	0.0017	0.0111	0.102	0.0008	0.0083
PRDX1	0	0	0.0149	0.3036	0.003	0.0098	0.1508	0.003	0.0197
PRDX2	0	0	0.0069	0	0	0.0139	0	0	0.0069
PRDX4	0.6153	0.0075	0.0122	0.1705	0.0017	0.0097	0.4155	0.0092	0.0221
PRDX5	0.7327	0.0043	0.0059	0.2874	0.0086	0.0299	0.1802	0.0043	0.0238
PRDX6	0	0	0.0124	0	0	0.0124	0	0	0.0249
PRKACA	1.3297	0.0153	0.0115	0	0	0.0305	0.6212	0.0153	0.0246
PRKAR1A	0	0	0.0225	0.0615	0.0012	0.0187	0.3108	0.0012	0.0037
PRKAR2A	0.3066	0.0022	0.0071	0.1518	0.0011	0.0074	0.2268	0.0034	0.015
PRKCSH	0.0719	0.0027	0.0376	0.1332	0.0041	0.0305	0.1051	0.0036	0.0344
PROM2	0.2666	0.0054	0.0203	0.4393	0.0104	0.0236	0.2888	0.0082	0.0283
PROS1	0.3928	0.0026	0.0065	0.7785	0.006	0.0077	0.4364	0.0068	0.0155
PRSS22	0.4728	0.0057	0.0121	1.0663	0.013	0.0122	1.2488	0.0101	0.0081
PRSS8	0.1712	0.0026	0.0153	0.2832	0.0066	0.0232	0.3978	0.0092	0.0232
PSAP	0.0995	0.0008	0.0083	0.0593	0.0009	0.0154	0	0	0.0123
PSAT1	0.3069	0.0036	0.0116	0	0	0.0189	0.1781	0.0042	0.0237
PSCA	0.1712	0.0037	0.0215	0.3409	0.0074	0.0217	0	0.0111	0
PSMA1	0	0	0.016	0	0	0.0214	0	0	0.0053
PSMA2	0	0	0	2.9281	0.0172	0.0059	2.9281	0.0172	0.0059
PSMA3	0	0	0.0118	0.5918	0.0496	0.0838	0.6984	0.0496	0.071
PSMA4	0	0	0.0057	0	0	0.0174	0	0	0.0116
PSMA5	0	0	0.006	0	0	0.0061	0	0	0
PSMA6	0	0	0.0178	0	0	0.0059	0	0	0.0238
PSMA7	0.1049	0.0018	0.017	0.1579	0.0018	0.0113	0	0	0.017
PSMB1	0	0	0.0173						
PSMB2	0	0	0.0122	0.2279	0.0042	0.0183	0.1356	0.0042	0.0307
PSMB4	0.3333	0.0017	0.0051	0	0	0.0153	0.0825	0.0017	0.0205
PSMB5				0.0864	0.0017	0.0199			
PSMB6	0.0865	0.0019	0.0219	0.1381	0.0038	0.0275	0.1156	0.0019	0.0164
PSMB7	0.1094	0.0016	0.0147	0.3288	0.0048	0.0147	0.1084	0.0032	0.0297
PSMB8	0.1611	0.0048	0.0301	0.2417	0.0048	0.02	0.3234	0.0065	0.02
PSMD14	0	0	0	0	0	0	0	0	0
PSMD2	0	0	0.0136	0.0876	0.0015	0.0167	0.1614	0.0015	0.0091
PSME4	0.1712	0.0019	0.011	0.063	0.001	0.0157	0.126	0.002	0.0157
PTGDS	0.0904	0.0047	0.0519	0.0788	0.0047	0.0596	0.1062	0.0047	0.0442
PTN	0	0	0.0181	0	0	0.0366	0	0	0.0181
PTPRD	0.0281	0.0005	0.0163	0.1635	0.0039	0.0239	0.1594	0.0034	0.0216
PTPRF	0.0342	0.0009	0.0272	0.0542	0.0014	0.0258	0.0288	0.0009	0.0324
PTPRJ	0.2612	0.003	0.0114	0.17	0.0041	0.0238	0.1552	0.0047	0.0305
PTPRS	0.1126	0.0026	0.0233	0.0454	0.0015	0.0334	0.0599	0.0017	0.0276
PURA	0	0	0.0042	0	0	0.0045	0	0	0
PYGB	0	0	0.0274	0.1154	0.0055	0.0473	0.1064	0.0055	0.0513
QPCT	0.1856	0.0037	0.0197	0	0	0.0324	0.177	0.0041	0.0231
QSCN6	0.7992	0.0052	0.0065						
RAB10	0	0	0.0077	0	0	0	0	0	0.0077
RAB11B	0	0	0.0129	0	0	0.0261	0	0	0.0395
RAB13	0	0	0.0146	0	0	0.022	0	0	0.022
RAB14	0	0	0.0069	0	0	0.0209	0	0	0.0139
Rab18	0	0	0	0	0	0.0064	0	0	0.0064
RAB1A	0	0	0	0	0	0	0	0	0
RAB1B	0.3149	0.0022	0.007	1.5941	0.0167	0.0104	1.0805	0.0189	0.0175
RAB27A	0.8677	0.0059	0.0068	0.1418	0.0039	0.0276	0.0951	0.002	0.0206
RAB27B	0	0.002	0	0	0	0.0206	0.0962	0.002	0.0207
RAB2A	0	0	0						
RAB3B	0.1484	0.002	0.0134	0.0586	0.002	0.034	0	0	0.0201
RAB3D	0.059	0.002	0.0337	0.2234	0.006	0.0268	0.1487	0.004	0.0268
RAB5B	0	0	0.0068	0	0	0.0089	0	0	0
RAB5C	0.3197	0.0018	0.0056	0.1592	0.0018	0.0112	0	0	0.0168
RAC1	0	0	0.0193	0	0	0.0193	0	0	0.0259
RAD23B	0.1948	0.0033	0.0168	0	0	0.0201	0.1385	0.0033	0.0237
RALA	0	0	0.0151	0.3487	0.0541	0.155	0.3118	0.0541	0.1734
RALB	0	0	0	0.1395	0.0019	0.0136	0.1374	0.0025	0.0181
RAP1B	0	0	0.0079	0	0	0.0079	0	0	0.016
RBP4	0	0	0.0295	0	0	0.0159	0	0	0.024
RDX	0	0	0.0131	0.3717	0.0225	0.0606	0.4314	0.0225	0.0522
RELN	0.1508	0.003	0.0201	0.0453	0.0009	0.02	0.1311	0.0033	0.0249
RHOA	0	0	0	0	0	0	0	0	0
RNASE1	0.3054	0.0085	0.0278	0.4057	0.0113	0.0279	0.4612	0.0085	0.0184
RNASE4	0	0.003	0	0.6016	0.006	0.0099	0.2989	0.003	0.01
RNASET2	0.5832	0.0034	0.0058	0.0721	0.0017	0.0235	0.0573	0.0017	0.0295
RPLP0	0	0	0.0085	0.2203	0.0028	0.0128	0.1314	0.0028	0.0214
RRBP1	0.1635	0.004	0.0248	0.1075	0.0032	0.0294	0.1234	0.0027	0.0219
RTN4RL1	0.3377	0.0051	0.0151	0.0308	0.0014	0.0449	0.1903	0.007	0.0365
RUVBL1	0	0	0.0031	0	0	0.0093	0	0	0.0062
RUVBL2	0	0	0.0115	0	0	0.0321	0	0	0.0203
s100A11	0	0	0.0428	0	0	0.0288	0	0	0.0143
SCGB2A1	0	0.0135	0	1.0622	0.0182	0.0171	1.8691	0.0321	0.0172
SCPEP1	0.3675	0.0058	0.0158	0.0871	0.0019	0.0222	0.3622	0.0063	0.0174
SDC1	0.1358	0.0039	0.0287	0.177	0.0059	0.0334	0	0	0.0466
SDCBP	0	0	0.0047	0.061	0.0015	0.024	0.0765	0.0015	0.0192
SDCBP2	0.4464	0.0124	0.0277	0.3803	0.0124	0.0325	0.284	0.0092	0.0325
SDK2	0.0696	0.0017	0.0251	0.076	0.0025	0.0326	0.0634	0.0022	0.0342
SELENBP1	0.2707	0.0043	0.016	0.2445	0.0026	0.0106	0.1621	0.0035	0.0214
SEMA3C	0.0419	0.0006	0.0134	0.1255	0.0017	0.0137	0.1463	0.0023	0.0157
SEMA3F	0.388	0.004	0.0104	0.1875	0.0046	0.0244	0.2116	0.0052	0.0246

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
PPP2CA	0	0	0.0285	0.1791	0.0042	0.0237	0	0	0.0382
PPP2R4	0.1112	0.0035	0.0316	0.148	0.0047	0.0317	0.0596	0.0014	0.0227
PPP5C	0.0385	0.0026	0.0676	0.027	0.0017	0.0644	0.0405	0.0026	0.0644
PPT1	0.0851	0.0029	0.0336	0.059	0.0029	0.0484	0.0489	0.0029	0.0585
PRCP	0.1918	0.0059	0.0309	0.1817	0.0051	0.028	0.1373	0.0042	0.0308
PRDX1	0.0722	0.0022	0.0302	0.0476	0.0022	0.0458	0.1182	0.0059	0.0502
PRDX2	0.0528	0.0022	0.0425	0.0637	0.0022	0.0353	0.08	0.0022	0.0281
PRDX4	0.0845	0.0017	0.0196	0.2851	0.0092	0.0322	0.1692	0.0033	0.0196
PRDX5	0.2711	0.0064	0.0237	0.1209	0.0021	0.0177	0.3613	0.0064	0.0178
PRDX6	0	0	0.0249	0	0	0.0377	0	0	0.0377
PRKACA	0.261	0.0214	0.0819	0.2969	0.0214	0.0721	0.2464	0.0214	0.0868
PRKAR1A	0	0	0.0655	0	0	0.0495	0.0252	0.0012	0.0457
PRKAR2A	0.5112	0.0054	0.0106	0.428	0.0076	0.0178	0.3631	0.0068	0.0188
PRKCSH	0.0715	0.0049	0.0682	0.111	0.0063	0.0571	0.1126	0.0073	0.0651
PROM2	0.2175	0.0125	0.0576	0.1936	0.0114	0.0591	0.2096	0.0131	0.0627
PROS1	0.3256	0.0071	0.0217	0.2679	0.0078	0.029	0.3476	0.0101	0.0291
PRSS22	0.293	0.0159	0.0542	0.2607	0.013	0.0498	0.3478	0.0174	0.0501
PRSS8	0.3367	0.0166	0.0492	0.3631	0.0186	0.0512	0.4172	0.0206	0.0493
PSAP	0.0418	0.0017	0.0397	0.0226	0.0008	0.0368	0.0225	0.0009	0.0406
PSAT1	0.1008	0.0036	0.0353	0.2074	0.0077	0.0373	0.1102	0.0042	0.0383
PSCA	0.1637	0.0148	0.0906	0.2369	0.0186	0.0785	0.1877	0.0148	0.079
PSMA1	0	0	0.0546	0	0	0.0378	0	0	0.0433
PSMA2	0	0	0.0118	0	0	0.0118	0.9683	0.0172	0.0178
PSMA3	0	0	0.0481	0	0	0.0358	0.5933	0.0496	0.0836
PSMA4	0	0	0.0232	0	0	0.0173	0	0	0.0116
PSMA5	0.075	0.0018	0.0242	0.1004	0.0018	0.0181	0	0	0.0061
PSMA6	0	0	0.0118	0	0	0.0299	0	0	0.0177
PSMA7	0.0885	0.0036	0.0403	0.0385	0.0018	0.0462	0.0442	0.0018	0.0403
PSMB1	0.1271	0.0037	0.029	0.1055	0.0037	0.0349			
PSMB2	0.2258	0.0084	0.037	0.168	0.0084	0.0497	0.2733	0.0084	0.0306
PSMB4	0.1652	0.0051	0.0309	0.188	0.0068	0.0362	0.1989	0.0051	0.0256
PSMB5	0	0	0.0149				0.1157	0.0017	0.0149
PSMB6	0.1512	0.0076	0.0503	0.1465	0.0057	0.0388	0.085	0.0038	0.0446
PSMB7	0.0712	0.0032	0.0452	0.0264	0.0016	0.0609	0.0959	0.0048	0.0504
PSMB8	0.5384	0.0162	0.0302	0.4427	0.0179	0.0404	0.5903	0.0179	0.0303
PSMD14	0	0	0.0048	0	0	0.0048	0	0	0.0048
PSMD2	0.021	0.001	0.0464	0.0253	0.001	0.0385	0.069	0.0024	0.0353
PSME4	0.0721	0.0021	0.0295	0.0987	0.0031	0.0311	0.0666	0.0022	0.0334
PTGDS	0.157	0.0118	0.0751	0.1755	0.0118	0.0672	0.1423	0.0118	0.0829
PTN	0	0	0.0556	0	0	0.0366	0	0	0.0556
PTPRD	0.0223	0.0007	0.0316	0.0078	0.0002	0.03	0.0925	0.0033	0.0355
PTPRF	0.0575	0.0028	0.0487	0.0451	0.0023	0.0517	0.0612	0.0028	0.0457
PTPRJ	0.323	0.014	0.0433	0.2872	0.0143	0.0498	0.2881	0.0139	0.0484
PTPRS	0.0263	0.0017	0.0629	0.0535	0.003	0.0567	0.0202	0.0012	0.0587
PURA	0	0	0.0169	0	0	0.0126	0	0	0.0091
PYGB	0.1303	0.0086	0.066	0.138	0.0086	0.0623	0.0974	0.0072	0.0738
QPCT	0.2746	0.0098	0.0357	0.3382	0.0135	0.0399	0.2474	0.0068	0.0276
QSCN6	0.3685	0.0169	0.0458	0.3707	0.0161	0.0435			
RAB10	0	0	0.0077	0	0	0.0155	0	0	0.0077
RAB11B	0	0	0.046	0	0	0.0597	0	0	0.0601
RAB13	0	0	0.0447	0	0	0.0603	0	0	0.0682
RAB14	0	0	0.0069	0	0	0	0	0	0.0139
Rab18	0.0958	0.0037	0.0386	0.0958	0.0037	0.0386	0.082	0.0037	0.0455
RAB1A	0	0	0.0292	0	0	0.0292	0	0	0.0292
RAB1B	0	0	0.0729	0.0273	0.0022	0.0806	0.198	0.0167	0.0841
RAB27A	0.284	0.0059	0.0207	0.2858	0.0039	0.0137	0.056	0.002	0.0348
RAB27B	1.1738	0.008	0.0068	1.4652	0.01	0.0068	0.5856	0.008	0.0136
RAB2A	0	0	0.0139	0	0	0.0139			
RAB3B	0.0571	0.004	0.0697	0.0286	0.002	0.0695	0.0259	0.002	0.0768
RAB3D	0.0955	0.0068	0.0708	0.0969	0.0045	0.0464	0.0971	0.0045	0.0464
RAB5B	0	0	0.0415	0	0	0.0345	0	0	0.0363
RAB5C	0	0	0.0341	0.0446	0.0018	0.0398	0.0389	0.0018	0.0457
RAC1	0	0	0.0128	0	0	0.0193	0	0	0.0193
RAD23B	0.0266	0.0011	0.0408	0.1166	0.0044	0.0375	0.054	0.0011	0.0201
RALA	0	0	0.0384	0	0	0.0543	0.4867	0.0541	0.1111
RALB	0.0391	0.0019	0.0482	0	0	0.0546	0.0775	0.0038	0.049
RAP1B	0	0	0.0241	0	0	0.016	0	0	0.0323
RBP4	0	0	0.068	0	0	0.0837	0	0	0.0745
RDX	0	0	0.0345	0	0	0.0211	0.3897	0.0225	0.0578
RELN	0.0629	0.0028	0.0438	0.1107	0.0052	0.0465	0.0654	0.0027	0.0417
RHOA	0	0	0.0153	0	0	0.0153	0	0	0.0153
RNASE1	0.3632	0.0171	0.047	0.3824	0.0142	0.0372	0.3036	0.0113	0.0374
RNASE4	0.1086	0.009	0.0827	0.0719	0.006	0.083	0.0955	0.009	0.094
RNASET2	0.1286	0.0085	0.0661	0.1172	0.0085	0.0725	0.1267	0.0068	0.0537
RPLP0	0	0	0.0085	0	0	0.0085	0.2203	0.0028	0.0128
RRBP1	0.081	0.005	0.0611	0.0755	0.0045	0.0596	0.044	0.0027	0.0615
RTN4RL1	0.0928	0.0061	0.0658	0.2008	0.0112	0.056	0.1177	0.0083	0.0708
RUVBL1	0	0	0.0444	0	0	0.0412	0	0	0.0476
RUVBL2	0.0161	0.001	0.0622	0.0204	0.001	0.0493	0.014	0.001	0.072
s100A11	0	0	0.043	0	0	0.0284	0	0	0.0143
SCGB2A1	1.5851	0.0274	0.0173	2.1185	0.0367	0.0173	0.7923	0.0274	0.0346
SCPEP1	0.1094	0.0039	0.0354	0.3345	0.0102	0.0305	0.1344	0.0039	0.0288
SDC1	0.814	0.0238	0.0292	0.5434	0.0157	0.0288	0.3216	0.0178	0.0555
SDCBP	0.1297	0.0043	0.0334	0.1517	0.0043	0.0285	0.1201	0.0059	0.049
SDCBP2	0.6033	0.0139	0.0231	0.2344	0.0116	0.0494	0.1306	0.0061	0.047
SDK2	0.0699	0.0038	0.0549	0.0661	0.0035	0.0532	0.0628	0.0036	0.0579
SELENBP1	0.0725	0.0052	0.0716	0.0681	0.0061	0.0891	0.0688	0.0043	0.0632
SEMA3C	0.0878	0.0017	0.0192	0.1063	0.0023	0.0212	0.1301	0.0023	0.0176
SEMA3F	0.1228	0.0053	0.0434	0.1649	0.0066	0.04	0.1425	0.006	0.0419

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
PPP2CA	0	0	0.0236	0.1489	0.0042	0.0285	0	0	0.0333	0	0	0.0531
PPP2R4	0.5288	0.0576	0.109	0.5524	0.055	0.0995	0.5344	0.0635	0.1188	0.4677	0.0536	0.1146
PPP5C	0.0736	0.0052	0.0709	0.0643	0.0043	0.0676	0.0772	0.0052	0.0676	0.0843	0.0043	0.0516
PPT1	0.1344	0.0064	0.0475	0.0602	0.0032	0.0529	0.0458	0.0032	0.0695	0.1202	0.0064	0.0531
PRCP	0.4977	0.0368	0.0739	0.5083	0.0359	0.0707	0.4753	0.035	0.0737	0.5696	0.038	0.0667
PRDX1	0.292	0.0044	0.015	0.1445	0.0044	0.0302	0.3001	0.0089	0.0297	0.1456	0.0022	0.015
PRDX2	0.2572	0.0227	0.0883	0.2572	0.0227	0.0883	0.2362	0.0227	0.0962	0.2594	0.025	0.0964
PRDX4	0.096	0.0033	0.0346	0.2292	0.0109	0.0474	0.1442	0.005	0.0346	0.3401	0.005	0.0147
PRDX5	0.0574	0.0029	0.0502	0.0693	0.0029	0.0416	0.0574	0.0029	0.0503	0.0693	0.0029	0.0416
PRDX6	0.1049	0.004	0.0378	0.078	0.004	0.0508	0.0781	0.004	0.0508	0.0619	0.004	0.064
PRKACA												
PRKAR1A	0	0	0.0535	0	0	0.0378	0.0338	0.0012	0.034	0	0	0.0417
PRKAR2A	0.3648	0.0065	0.0178	0.3462	0.0087	0.0251	0.2568	0.0068	0.0265	0.2644	0.0076	0.0288
PRKCSH	0.1837	0.0121	0.066	0.1766	0.0126	0.0714	0.2472	0.0148	0.0597	0.1136	0.0104	0.0914
PROM2	0.4426	0.0354	0.0799	0.4036	0.0336	0.0833	0.4347	0.0355	0.0818	0.4143	0.0333	0.0804
PROS1	0.2039	0.0045	0.022	0.2012	0.0058	0.0287	0.3407	0.0098	0.0287	0.3363	0.0106	0.0316
PRSS22	0.3011	0.0365	0.1211	0.2855	0.0328	0.115	0.3172	0.0376	0.1184	0.2675	0.0301	0.1124
PRSS8	0.2962	0.0219	0.074	0.2796	0.0213	0.076	0.3498	0.026	0.0742	0.332	0.0246	0.0742
PSAP	0.1932	0.0085	0.044	0.1867	0.0077	0.041	0.1934	0.0075	0.0388	0.1515	0.0085	0.0562
PSAT1	0.0369	0.0024	0.0641	0.0927	0.0065	0.0704	0.0191	0.0014	0.0736	0.0638	0.0036	0.0557
PSCA	0.3385	0.0186	0.055	0.5141	0.0224	0.0436	0.4244	0.0186	0.0438	0.0552	0.0037	0.0668
PSMA1	0.124	0.0082	0.066	0.1674	0.0082	0.0489	0.1501	0.0082	0.0546	0.2538	0.0082	0.0323
PSMA2	0	0	0.0422	0	0	0.0422	0.3558	0.0172	0.0484	0	0	0.0422
PSMA3	0	0	0.0605	0	0	0.048	0.5148	0.0497	0.0964	0	0	0.0357
PSMA4	0.081	0.0033	0.0409	0.0949	0.0033	0.0349	0.1141	0.0033	0.0292	0.1921	0.0033	0.0173
PSMA5	0.0598	0.0018	0.0304	0.075	0.0018	0.0242	0	0	0.0122	0	0	0.0181
PSMA6	0.5932	0.015	0.0253	0.3238	0.015	0.0463	0.5932	0.015	0.0253	0.3833	0.015	0.0391
PSMA7	0.123	0.0071	0.0581	0.1027	0.0054	0.0521	0.0921	0.0054	0.0581	0.0934	0.0071	0.0766
PSMB1	0.1181	0.0055	0.0469	0.1046	0.0055	0.0529				0.0348	0.0018	0.0529
PSMB2	0	0	0.0342	0	0	0.0519	0	0	0.0254	0	0	0.0254
PSMB4	0.0468	0.0017	0.0362	0.0816	0.0034	0.0416	0.0548	0.0017	0.0309	0.1327	0.0034	0.0256
PSMB5	0.0379	0.0017	0.0454				0.0981	0.0034	0.0351	0.0427	0.0017	0.0403
PSMB6	0.1279	0.0057	0.0445	0.1142	0.0038	0.0332	0.0487	0.0019	0.0389	0.0486	0.0019	0.0389
PSMB7	0.1625	0.0048	0.0298	0.0714	0.0032	0.0451	0.1431	0.0065	0.0451	0.0288	0.0016	0.0557
PSMB8	0.3553	0.0162	0.0457	0.3186	0.0179	0.0562	0.3895	0.0179	0.0459	0.505	0.0179	0.0354
PSMD14	0	0	0.0048	0	0	0.0048	0	0	0.0048	0	0	0.0097
PSMD2	0.0264	0.001	0.0369	0.0335	0.001	0.029	0.1067	0.0024	0.0228	0.0451	0.0019	0.0432
PSME4	0.0496	0.002	0.0397	0.0712	0.003	0.0415	0.0457	0.0021	0.045	0.0571	0.0022	0.0388
PTGDS	0.1049	0.0071	0.0673	0.105	0.0071	0.0672	0.1189	0.0071	0.0594	0.159	0.0094	0.0593
PTN	0.0462	0.0026	0.0557	0.0702	0.0026	0.0367	0.0462	0.0026	0.0557	0.0702	0.0026	0.0367
PTPRD	0.0789	0.0041	0.0524	0.0746	0.0037	0.0493	0.0261	0.0011	0.0438	0.0755	0.0035	0.0467
PTPRF	0.0517	0.0023	0.0453	0.0351	0.0018	0.052	0.0506	0.0021	0.0412	0.0602	0.0031	0.052
PTPRJ	0.2715	0.0183	0.0675	0.254	0.0187	0.0735	0.2863	0.0187	0.0654	0.351	0.0214	0.0609
PTPRS	0.1789	0.015	0.0839	0.2072	0.0168	0.0812	0.186	0.018	0.0967	0.2234	0.018	0.0805
PURA	0.1303	0.0028	0.0212	0.1633	0.0028	0.0169	0	0	0.0136	0.6587	0.0028	0.0042
PYGB	0.3215	0.041	0.1276	0.3372	0.041	0.1216	0.3435	0.0513	0.1493	0.362	0.048	0.1326
QPCT	0.1519	0.0073	0.0482	0.2487	0.011	0.0442	0.1823	0.0068	0.0374	0.278	0.0123	0.0441
QSCN6	0.354	0.0159	0.0448	0.3553	0.0151	0.0425				0.2544	0.0174	0.0684
RAB10	0	0	0.0077	0	0	0.0155	0	0	0.0077	0	0	0.0155
RAB11B	0	0	0.0666	0	0	0.0807	0	0	0.0956	0	0	0.0736
RAB13	0	0	0.0684	0	0	0.0684	0	0	0.0764	0	0	0.0527
RAB14	0	0	0.028	0	0	0.0209	0	0	0.0209	0	0	0.0209
Rab18	0	0	0.0322	0	0	0.0322	0	0	0.0391	0.063	0.0037	0.0586
RAB1A	0.1135	0.0049	0.0435	0.1135	0.0049	0.0435	0.1135	0.0049	0.0435	0.1135	0.0049	0.0435
RAB1B	0	0	0.0429	0.0437	0.0022	0.0503	0.3097	0.0167	0.0538	0	0	0.0884
RAB27A	0.1048	0.0059	0.0561	0.0804	0.0039	0.0487	0.0276	0.002	0.0709	0.0796	0.0039	0.0491
RAB27B	0.2281	0.008	0.0349	0.2847	0.01	0.035	0.1896	0.008	0.0421	0.3848	0.008	0.0207
RAB2A	0	0	0.0069	0	0	0.0069				0	0	0.0069
RAB3B	0.0361	0.002	0.0551	0	0	0.0549	0	0	0.0621	0.0415	0.002	0.0479
RAB3D	0.0786	0.006	0.0763	0.0578	0.004	0.069	0.0731	0.004	0.0546	0.1171	0.0045	0.0385
RAB5B	0	0	0.0345	0	0	0.0274	0	0	0.0179	0	0	0.0205
RAB5C	0.0444	0.0018	0.04	0.0777	0.0036	0.0458	0.0688	0.0036	0.0517	0.0278	0.0018	0.0638
RAC1	0.3321	0.0064	0.0192	0.248	0.0064	0.0257	0.2479	0.0064	0.0257	0.3322	0.0064	0.0192
RAD23B	0.1603	0.0076	0.0477	0.1918	0.0099	0.0515	0.2265	0.0076	0.0337	0.1833	0.0087	0.0477
RALA	0	0	0.0623	0	0	0.0788	0.4518	0.0541	0.1197	0	0	0.0228
RALB	0.0548	0.0019	0.0353	0	0	0.0468	0.0543	0.0019	0.0359	0	0	0.0427
RAP1B	0	0	0.0324	0	0	0.0242	0	0	0.0407	0	0	0.0407
RBP4	0.0637	0.0043	0.0682	0.0639	0.0043	0.068	0.0701	0.0046	0.0659	0.0474	0.0043	0.0918
RDX	0.0276	0.0014	0.051	0.0329	0.0014	0.0427	0.3208	0.024	0.0747	0.0378	0.0014	0.0372
RELN	0.0452	0.0024	0.0526	0.088	0.0047	0.053	0.0485	0.0023	0.0481	0.0603	0.0028	0.0458
RHOA	0	0	0.0153	0	0	0.0153	0	0	0.0153	0	0	0.031
RNASE1	0.2198	0.017	0.0775	0.2116	0.0142	0.067	0.168	0.0113	0.0673	0.3601	0.017	0.0473
RNASE4	0.7984	0.0241	0.0302	0.694	0.0211	0.0303	0.5923	0.0241	0.0407	0.2238	0.0211	0.0943
RNASET2	0.3255	0.0404	0.1242	0.3076	0.0404	0.1313	0.3494	0.0386	0.1106	0.4083	0.0422	0.1034
RPLP0	0	0	0.0258	0	0	0.0258	0.0932	0.0028	0.0302	0	0	0.0171
RRBP1	0.2789	0.0207	0.0742	0.2667	0.0202	0.0758	0.247	0.0184	0.0747	0.2003	0.0174	0.0871
RTN4RL1	0.1079	0.0092	0.0852	0.1635	0.0123	0.0752	0.1508	0.014	0.0927	0.1217	0.0092	0.0755
RUVBL1	0	0	0.0511	0	0	0.0478	0	0	0.0543	0	0	0.051
RUVBL2	0.0269	0.0019	0.0719	0.0326	0.0019	0.0594	0.0238	0.0019	0.0813	0.0486	0.003	0.0621
s100A11	0	0	0.0428	0	0	0.0283	0	0	0.0143	0	0	0.0284
SCGB2A1	0.7923	0.0274	0.0346	1.1951	0.0415	0.0347	0.528	0.0275	0.052	0.3459	0.0182	0.0525
SCPEP1	0.1505	0.0058	0.0387	0.3026	0.0102	0.0338	0.1507	0.0058	0.0386	0.1379	0.0058	0.0422
SDC1	0.6646	0.0223	0.0335	0.2807	0.0097	0.0347	0.3196	0.0163	0.0511	0.919	0.0192	0.0209
SDCBP	0.0862	0.0029	0.0335	0.1009	0.0029	0.0286	0.113	0.0044	0.039	0.1126	0.0043	0.0384
SDCBP2	0.4472	0.0154	0.0343	0.2954	0.0154	0.052	0.1312	0.0076	0.0582	0.1653	0.0076	0.0462
SDK2												
SELENBP1	0.1246	0.0074	0.0591	0.1217	0.0082	0.0676	0.1363	0.0065	0.0478	0.1047	0.0074	0.0704
SEMA3C	0.0661	0.0034	0.0512	0.0742	0.0039	0.0532	0.0687	0.0034	0.0501	0.0722	0.0028	0.039
SEMA3F	0.0981	0.0063	0.0638	0.1073	0.0069	0.0644	0.1039	0.0063	0.0606	0.0809	0.0053	0.066

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
PPP2CA	0	0	0.048	0.0801	0.0042	0.053	0	0	0.0579	0	0	0.0784
PPP2R4	0.1528	0.0118	0.077	0.154	0.0106	0.0689	0.125	0.0082	0.0653	0.0959	0.0082	0.0859
PPP5C	0.0268	0.0026	0.0973	0.0199	0.0017	0.0872	0.0323	0.0026	0.0806	0.0246	0.0017	0.0707
PPT1	0.0719	0.0057	0.0794	0.0675	0.0057	0.0846	0.0539	0.0057	0.106	0.0718	0.0057	0.0796
PRCP	0.2337	0.0124	0.0529	0.2312	0.0115	0.0498	0.2019	0.0107	0.0527	0.3243	0.0124	0.0381
PRDX1	0.0354	0.0022	0.0617	0.0354	0.0022	0.0617	0.0833	0.0059	0.0713	0	0	0.0618
PRDX2	0	0	0.0796	0	0	0.072	0	0	0.0796	0.0236	0.0022	0.0952
PRDX4	0.1494	0.0067	0.0447	0.2476	0.0142	0.0575	0.1869	0.0083	0.0447	0.3402	0.0083	0.0245
PRDX5	0.3113	0.0203	0.0653	0.2494	0.0152	0.0609	0.3195	0.0196	0.0612	0.3176	0.0174	0.0547
PRDX6	0.117	0.0059	0.0508	0.0928	0.0059	0.0641	0.0928	0.0059	0.0641	0.0767	0.0059	0.0776
PRKACA	0.1415	0.0149	0.105	0.3089	0.0305	0.0986	0.1242	0.0149	0.1197	0.234	0.0374	0.1597
PRKAR1A	0.0135	0.0012	0.0856	0.0167	0.0012	0.0692	0.0353	0.0023	0.0654	0.0135	0.0012	0.0855
PRKAR2A	0.2779	0.0229	0.0825	0.2782	0.0252	0.0904	0.288	0.0251	0.0873	0.2784	0.0263	0.0944
PRKCSH	0.1133	0.0147	0.13	0.1426	0.0164	0.1151	0.1361	0.0172	0.1266	0.0984	0.0131	0.1331
PROM2	0.2819	0.0304	0.1077	0.2456	0.0286	0.1166	0.2894	0.0323	0.1115	0.263	0.0287	0.109
PROS1	0.2655	0.0184	0.0694	0.258	0.0198	0.0766	0.346	0.0247	0.0713	0.2947	0.0218	0.0738
PRSS22												
PRSS8	0.3474	0.0294	0.0846	0.4509	0.0314	0.0697	0.3815	0.0307	0.0805	0.4633	0.0383	0.0826
PSAP	0.0881	0.0067	0.0756	0.0803	0.0058	0.0725	0.0684	0.0055	0.0802	0.0847	0.0067	0.0786
PSAT1	0.102	0.0089	0.0874	0.1324	0.0107	0.0809	0.1123	0.0092	0.0816	0.1243	0.0095	0.0766
PSCA	0.1095	0.0187	0.171	0.128	0.0242	0.1889	0.1275	0.0242	0.1895	0.1427	0.0242	0.1696
PSMA1	0	0	0.0835	0	0	0.0717	0	0	0.0776	0	0	0.066
PSMA2	0	0	0.0547	0	0	0.0547	0.3562	0.0172	0.0484	0	0	0.0547
PSMA3	0	0	0.0607	0	0	0.0481	0.5132	0.0496	0.0967	0	0	0.0357
PSMA4	0	0	0.0973	0	0	0.1038	0	0	0.0979	0	0	0.0844
PSMA5	0.0368	0.0018	0.0492	0.0423	0.0018	0.0429	0	0	0.0309	0	0	0.0366
PSMA6	0	0	0.0238	0	0	0.0422	0	0	0.0298	0	0	0.0238
PSMA7	0.0253	0.0018	0.0705	0	0	0.0767	0	0	0.0705	0.0429	0.0036	0.083
PSMB1	0.115	0.0111	0.0967	0.1433	0.0111	0.0776				0.0717	0.0074	0.1031
PSMB2	0.1881	0.0168	0.0893	0.1631	0.0168	0.103	0.1889	0.0168	0.089	0.1313	0.0126	0.0958
PSMB4	0.0397	0.0034	0.0854	0.0558	0.0051	0.0913	0.0372	0.0034	0.0911	0.0599	0.0051	0.0852
PSMB5	0.0443	0.0034	0.0776				0.0773	0.0052	0.0668	0.0477	0.0034	0.0722
PSMB6	0.0778	0.0076	0.0978	0.0664	0.0057	0.0857	0.0413	0.0038	0.0918	0.0412	0.0038	0.092
PSMB7	0.052	0.0048	0.093	0.0327	0.0032	0.0985	0.0589	0.0065	0.1097	0.0132	0.0016	0.1215
PSMB8	0.2591	0.0146	0.0564	0.2427	0.0163	0.067	0.2869	0.0162	0.0565	0.3179	0.0146	0.0459
PSMD14	0	0	0.0294	0	0	0.0294	0	0	0.0295	0	0	0.0344
PSMD2	0.0132	0.001	0.074	0.0141	0.001	0.069	0.0371	0.0024	0.0658	0.0264	0.002	0.074
PSME4	0.0663	0.0039	0.0589	0.0829	0.0049	0.0589	0.0596	0.0037	0.0623	0.073	0.0037	0.0502
PTGDS	0.3475	0.0262	0.0753	0.3476	0.0262	0.0753	0.3482	0.0262	0.0752	0.4257	0.0286	0.0673
PTN	0.0341	0.0026	0.0755	0.046	0.0026	0.0559	0.0341	0.0026	0.0754	0.0341	0.0026	0.0754
PTPRD	0.039	0.0023	0.0587	0.0308	0.0018	0.0596	0.0759	0.0048	0.0635	0.0314	0.0016	0.0523
PTPRF	0.0502	0.0051	0.1012	0.0486	0.0051	0.1045	0.0473	0.0046	0.0971	0.0743	0.007	0.0945
PTPRJ	0.3596	0.0401	0.1116	0.3365	0.0397	0.1181	0.3694	0.041	0.1108	0.4029	0.0426	0.1057
PTPRS	0.0107	0.0012	0.1138	0.0273	0.0031	0.1116	0.0154	0.0019	0.1232	0.0127	0.0015	0.1172
PURA	0.0543	0.0014	0.0255	0.0653	0.0014	0.0212	0	0	0.0182	0.1647	0.0014	0.0084
PYGB	0.0314	0.0036	0.1158	0.0314	0.0036	0.1157	0.0657	0.0095	0.1448	0.0913	0.0112	0.123
QPCT	0.1221	0.011	0.0904	0.1708	0.0147	0.0863	0.115	0.0082	0.0713	0.1861	0.016	0.086
QSCN6	0.2314	0.0196	0.0846	0.229	0.0188	0.0821				0.2344	0.023	0.0981
RAB10	0	0	0.0179	0	0	0.0271	0	0	0.0179	0	0	0.0271
RAB11B	0	0	0.0879	0	0	0.1024	0	0	0.1031	0	0	0.0951
RAB13	0	0	0.0682	0	0	0.0682	0	0	0.0761	0	0	0.0842
RAB14	0	0	0.028	0	0	0.0209	0	0	0.0351	0	0	0.0209
Rab18	0	0	0.0322	0	0	0.0322	0	0	0.0391	0.063	0.0037	0.0586
RAB1A	0	0	0.0218	0	0	0.0218	0	0	0.0218	0	0	0.0218
RAB1B	0	0	0.1041	0.0196	0.0022	0.1121	0.144	0.0167	0.1157	0	0	0.0883
RAB27A	0.1247	0.0098	0.0787	0.1105	0.0078	0.071	0.0624	0.0059	0.0941	0.0546	0.0039	0.0716
RAB27B	0.0708	0.004	0.0563	0.106	0.006	0.0564	0.0627	0.004	0.0635	0.0955	0.004	0.0417
RAB2A	0	0	0.021	0	0	0.021				0	0	0.021
RAB3B	0.02	0.002	0.0993	0	0	0.099	0	0	0.1065	0.0236	0.002	0.0842
RAB3D	0.061	0.006	0.0983	0.0406	0.004	0.0983	0.0581	0.004	0.0688	0.0517	0.0045	0.0871
RAB5B	0.3568	0.0332	0.0929	0.3884	0.0332	0.0854	0.5208	0.0438	0.0841	0.3568	0.0332	0.0929
RAB5C	0.0781	0.0036	0.0456	0.0346	0.0018	0.0514	0.031	0.0018	0.0573	0.0512	0.0036	0.0695
RAC1	0	0	0.0259	0	0	0.0325	0	0	0.0325	0	0	0.0258
RAD23B	0.0427	0.0033	0.0765	0.0815	0.0066	0.0806	0.0595	0.0033	0.0548	0.0703	0.0044	0.062
RALA	0	0	0.0623	0	0	0.0788	0.3941	0.0541	0.1371	0	0	0.0228
RALB	0.0809	0.0057	0.07	0.0665	0.0049	0.0739	0.135	0.0076	0.0564	0.0598	0.0038	0.063
RAP1B	0	0	0.049	0	0	0.0406	0	0	0.0574	0	0	0.0574
RBP4												
RDX	0.0108	0.0007	0.065	0.0124	0.0007	0.0566	0.2887	0.0232	0.0805	0.0124	0.0007	0.0566
RELN	0.0554	0.0046	0.0837	0.0778	0.0068	0.0873	0.0594	0.0047	0.0787	0.0586	0.0049	0.0829
RHOA	0	0	0.039	0	0	0.039	0	0	0.039	0	0	0.0552
RNASE1	0.552	0.0527	0.0954	0.5229	0.0496	0.0949	0.4871	0.0465	0.0954	0.6281	0.0465	0.0741
RNASE4	0.2408	0.015	0.0622	0.1914	0.0119	0.0624	0.2041	0.015	0.0733	0.0924	0.012	0.1294
RNASET2	0.1436	0.0171	0.1189	0.1355	0.0171	0.126	0.1455	0.0154	0.1055	0.1503	0.0188	0.1253
RPLP0	0	0	0.0435	0	0	0.0435	0.0588	0.0028	0.0479	0	0	0.0346
RRBP1	0.0879	0.0086	0.0975	0.0959	0.0081	0.0847	0.0691	0.0063	0.0916	0.0683	0.0072	0.1057
RTN4RL1	0.1729	0.0248	0.1436	0.2268	0.0301	0.1327	0.2259	0.0355	0.1571	0.1859	0.0248	0.1333
RUVBL1	0	0	0.061	0	0	0.0644	0	0	0.071	0	0	0.0744
RUVBL2	0	0	0.1204	0	0	0.1138	0	0	0.1306	0.0082	0.001	0.1227
s100A11	0.0828	0.0126	0.1526	0.093	0.0126	0.1358	0.1057	0.0129	0.1219	0.0925	0.0126	0.1364
SCGB2A1	0.199	0.0512	0.2572	0.2357	0.0608	0.2581	0.1159	0.0322	0.2783	0.1144	0.0322	0.2812
SCPEP1	0.2259	0.0186	0.0825	0.2988	0.0231	0.0773	0.247	0.0186	0.0754	0.1926	0.0166	0.0863
SDC1	0.452	0.0374	0.0828	0.2342	0.0196	0.0838	0.2811	0.0306	0.1091	0.5183	0.0396	0.0765
SDCBP	0.1437	0.008	0.0555	0.1579	0.008	0.0505	0.1561	0.0096	0.0614	0.1608	0.0102	0.0631
SDCBP2	0.214	0.0218	0.1018	0.145	0.0186	0.1284	0.1311	0.0155	0.118	0.1434	0.0139	0.097
SDK2	0.0583	0.0062	0.1058	0.0537	0.0058	0.1072	0.0571	0.0064	0.1121	0.0635	0.0063	0.0989
SELENBP1	0.1485	0.0135	0.0909	0.1398	0.0144	0.1028	0.1214	0.0118	0.0971	0.1155	0.0131	0.1131
SEMA3C	0.0602	0.0039	0.0656	0.071	0.0045	0.0635	0.062	0.004	0.0648	0.0818	0.0045	0.0552
SEMA3F	0.0789	0.0074	0.094	0.0818	0.0081	0.0987	0.0665	0.0063	0.0947	0.0701	0.0065	0.0932

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
PPP2CA	0	0	0.063
PPP2R4	0.427	0.0576	0.1349
PPP5C	0.0588	0.0043	0.0739
PPT1	0.0913	0.008	0.0873
PRCP	0.4785	0.0424	0.0886
PRDX1	0.0476	0.0022	0.0459
PRDX2	0.1665	0.0227	0.1365
PRDX4	0.2834	0.0083	0.0295
PRDX5	0.101	0.0087	0.0859
PRDX6	0.065	0.0059	0.0915
PRKACA			
PRKAR1A	0.0167	0.0012	0.0692
PRKAR2A	0.2227	0.0229	0.1029
PRKCSH	0.1201	0.0174	0.1449
PROM2	0.3962	0.0502	0.1267
PROS1	0.2935	0.0204	0.0695
PRSS22			
PRSS8	0.3019	0.0341	0.1131
PSAP	0.1337	0.0115	0.0861
PSAT1	0.0973	0.0083	0.0854
PSCA	0.1771	0.0298	0.1682
PSMA1	0.1056	0.0082	0.0776
PSMA2	0	0	0.0869
PSMA3	0	0	0.0357
PSMA4	0.032	0.0033	0.1036
PSMA5	0	0	0.0429
PSMA6	0.325	0.015	0.0461
PSMA7	0.0494	0.0054	0.1083
PSMB1	0.096	0.0093	0.0965
PSMB2	0	0	0.1171
PSMB4	0.0186	0.0017	0.091
PSMB5	0.0667	0.0052	0.0775
PSMB6	0.022	0.0019	0.0859
PSMB7	0.0451	0.0032	0.0714
PSMB8	0.3172	0.0162	0.0512
PSMD14	0	0	0.0345
PSMD2	0.0276	0.002	0.0707
PSME4	0.0471	0.0028	0.0595
PTGDS	0.6495	0.0238	0.0366
PTN	0.0682	0.0051	0.0756
PTPRD	0.0668	0.0051	0.0756
PTPRF	0.0569	0.0057	0.1002
PTPRJ	0.3624	0.0432	0.1191
PTPRS	0.1148	0.0154	0.1345
PURA	0.3278	0.0042	0.0127
PYGB	0.2297	0.0439	0.191
QPCT	0.1342	0.011	0.0821
QSCN6	0.1633	0.0159	0.0972
RAB10	0	0	0.0089
RAB11B	0	0	0.1023
RAB13	0	0	0.0927
RAB14	0	0	0.0424
Rab18	0	0	0.0388
RAB1A	0.1914	0.0049	0.0258
RAB1B	0	0	0.1203
RAB27A	0.0417	0.0039	0.0938
RAB27B	0.0621	0.004	0.064
RAB2A	0	0	0.0139
RAB3B	0	0	0.084
RAB3D	0	0	0.0982
RAB5B	0.3884	0.0332	0.0854
RAB5C	0.0706	0.0053	0.0757
RAC1	0.1975	0.0064	0.0323
RAD23B	0.1059	0.0065	0.0618
RALA	0	0	0.0463
RALB	0.0386	0.0019	0.05
RAP1B	0	0	0.0324
RBP4			
RDX	0.0104	0.0007	0.0678
RELN	0.05	0.0043	0.0852
RHOA	0	0	0.039
RNASE1	0.5214	0.0418	0.0801
RNASE4	0.406	0.021	0.0517
RNASET2	0.2322	0.0439	0.1892
RPLP0	0	0	0.0435
RRBP1	0.1848	0.0205	0.1108
RTN4RL1	0.2052	0.0233	0.1133
RUVBL1	0	0	0.0678
RUVBL2	0.0175	0.0019	0.1104
s100A11	0.093	0.0126	0.1358
SCGB2A1	0.1378	0.0417	0.3027
SCPEP1	0.1936	0.0147	0.0757
SDC1	0.3568	0.029	0.0812
SDCBP	0.1494	0.0087	0.0582
SDCBP2	0.0711	0.0096	0.1344
SDK2			
SELENBP1	0.1308	0.0135	0.1031
SEMA3C	0.059	0.0048	0.0813
SEMA3F	0.07	0.0068	0.0977

Gene	CH_*ω*	CH_*Ka*	CH_*Ks*	GH_*ω*	GH_*Ka*	GH_*Ks*	GC_*ω*	GC_*Ka*	GC_*Ks*
SEMA7A	0.4677	0.0063	0.0136	0.2549	0.0053	0.021	0.3936	0.0104	0.0264
SEMG1	0.9024	0.0121	0.0134	0.8252	0.0299	0.0362	0.7572	0.0328	0.0433
SEMG2	0.714	0.0177	0.0248	0.6274	0.0158	0.0251	1.0356	0.0173	0.0167
SEPP1	0.5868	0.007	0.012						
SERPINA1	0.1502	0.0031	0.0209	0.3876	0.0094	0.0244	0.4325	0.0105	0.0243
SERPINA3	0.416	0.0108	0.0259	0.3317	0.0108	0.0325	0.4545	0.0118	0.0259
SERPINA4	0.1859	0.0028	0.0153	0.4592	0.0061	0.0132	0.1004	0.003	0.0302
SERPINA5	0.3831	0.0154	0.0401	0.2988	0.0075	0.0252	0.6523	0.0165	0.0252
SERPINA6	0.7122	0.0076	0.0106	0.4573	0.0065	0.0142	0.3049	0.0054	0.0178
SERPINB5	0.1134	0.0023	0.0203	0.0805	0.0023	0.0285	0.0703	0.0023	0.0327
SERPINB6	0.3691	0.01	0.0271	0.1772	0.0192	0.1082	0.2269	0.0279	0.1229
SERPINC1	0.1002	0.0019	0.0188	0.0741	0.002	0.0265	0.1985	0.0039	0.0198
SERPINF1	0.1432	0.0043	0.0297	0.2579	0.0085	0.0331	0.2152	0.0064	0.0297
SERPING1	0.486	0.0054	0.0111						
SERPINI1	0.2784	0.0031	0.0113	0.2781	0.0042	0.015	0.278	0.0031	0.0113
sez6L2	0.2102	0.0035	0.0165	0.0828	0.0015	0.0179	0.1264	0.003	0.0234
SFN	0	0	0.0116	0	0	0.0116	0	0	0.0058
SH3BGRL2	0	0	0.0142	0.2834	0.0041	0.0143	0.1403	0.0041	0.0289
SI	0.1244	0.0024	0.019	0.1752	0.0045	0.0255	0.1991	0.0053	0.0265
SIL1	0.1838	0.0039	0.021	0.2403	0.0058	0.0241	0.2139	0.0058	0.027
SLC15A2	0.1322	0.0018	0.0136	0.3101	0.0024	0.0078	0.1855	0.0018	0.0097
SLC1A1	0.3252	0.0042	0.013	0.1625	0.0025	0.0157	0.6545	0.0051	0.0078
SLC35F2	0.1069	0.0013	0.0122	0.1061	0.0026	0.0246	0.1918	0.0039	0.0205
SLC44A4	0.2206	0.0026	0.0116	0.152	0.0038	0.0248	0.1321	0.0026	0.0194
SLIT2	0.0508	0.0011	0.0223	0.1675	0.0026	0.0153	0.2342	0.0038	0.0164
SLPI	0.2933	0.0066	0.0226	1.1934	0.0133	0.0112	0.3878	0.0133	0.0343
SMOC2	0.0812	0.003	0.0368	0.1356	0.0038	0.0283	0.1122	0.003	0.0266
SMPD1	0.1705	0.0043	0.0253	0.0928	0.0022	0.0233	0.1546	0.0036	0.0233
smpdl3A	1.7518	0.0057	0.0033	0.7255	0.0057	0.0079	1.7517	0.0069	0.0039
SMPDL3B	0.1551	0.0029	0.0187	0.267	0.0058	0.0218	0.1963	0.0068	0.0346
SMS	0.1466	0.0012	0.0081	0.1241	0.0099	0.0799	0.1581	0.0112	0.0706
SOD1	0	0	0.0091	0.1569	0.0029	0.0183	0.1039	0.0029	0.0277
SOD3	0	0	0	0.3461	0.0026	0.0076	0.3461	0.0026	0.0076
SORD	0.5105	0.0076	0.0148	0.4148	0.0149	0.0359	0.371	0.0149	0.0402
SORL1	0.1018	0.0028	0.0272	0.1385	0.0041	0.0297	0.0888	0.003	0.0334
SORT1	0.1564	0.0021	0.0135	0.0694	0.0011	0.0153	0.0478	0.0011	0.0223
SPACA3	0.9784	0.0062	0.0064	0	0	0.0324	0.1596	0.0063	0.0394
SPINK2	0	0.0109	0	0	0.0054	0	0	0.0054	0
SPINT1	0	0	0.0157	0.5127	0.0067	0.0131	2.5841	0.0067	0.0026
SPINT3	0	0.0199	0	0.2929	0.0099	0.0338	0.2974	0.0099	0.0334
SPOCK3	0.1586	0.0029	0.018						
SPON2	0.2592	0.0041	0.0158						
ST14	0.106	0.0036	0.0339	0.1198	0.0045	0.0377	0.1715	0.0068	0.0397
STEAP2	0.2026	0.0036	0.0176	0.0609	0.001	0.0162	0.2046	0.002	0.0097
STXBP2	0.0989	0.0029	0.0298	0.1473	0.0039	0.0266	0.1314	0.0052	0.0393
SYT1	0	0	0.0142	0.0355	0.001	0.0287	0.0408	0.001	0.0251
SYT7	0.6459	0.0057	0.0088	0	0	0.0263	0.2406	0.0057	0.0237
TAGLN2	0	0	0.022	0	0	0	0	0	0.015
TALDO1	0.1555	0.0026	0.0168	0.1037	0.0013	0.0126	0.1856	0.0039	0.0211
TCP1	0	0	0.0075	0	0	0.0177	0	0	0.0101
TEX101	1.033	0.0102	0.0099	0.4577	0.0068	0.0149	0.2736	0.0068	0.025
TF	0.1866	0.0031	0.0167	0.0663	0.0012	0.0188	0.0995	0.0019	0.0188
TFPI2	0.0967	0.0018	0.0186	0.2316	0.0072	0.0312	0.4406	0.0054	0.0123
TFRC	0.608	0.0023	0.0038	0.1	0.0023	0.0229	0.1498	0.004	0.0268
TGFB1	0	0	0.0068	0	0	0.0171	0	0	0.0102
TGFB3	0	0	0.0069	0	0	0.0139	0	0	0.0139
TGFBR3	0.1423	0.0031	0.0217	0.0514	0.001	0.02	0.2064	0.0031	0.015
TGM4	1.5045	0.0064	0.0042	0.3943	0.0103	0.0261	0.4763	0.0103	0.0216
THBS1	0.1072	0.0011	0.0103	0.0334	0.0007	0.022	0.0569	0.0011	0.0194
THBS2	0.0652	0.0012	0.0187	0.0473	0.0012	0.0245	0.0988	0.0026	0.0262
THBS4	0.2277	0.0046	0.02	0.1486	0.0023	0.0152	0.2728	0.0052	0.0192
TIMP1	0.5615	0.0107	0.019						
TIMP2	0.1945	0.004	0.0205	0	0	0.0248	0.0662	0.0022	0.0332
TIMP3	0	0	0.0281	0	0	0.0353	0	0	0.0069
TKT	0.0561	0.0014	0.0248	0.0929	0.0021	0.0225	0.0842	0.0021	0.0248
TMC5	0.4369	0.0082	0.0189	0.3696	0.0073	0.0198	0.2805	0.0069	0.0245
TMEFF2	0	0	0.004	0	0	0.0048	0	0	0.0096
TMEM8	0.1579	0.0049	0.0311						
tmpRSS2	1.3496	0.0109	0.008	0.3068	0.0108	0.0353	0.3056	0.0117	0.0383
TNFSF10	0.2006	0.0046	0.0227	0.0895	0.0015	0.0169	0.5411	0.003	0.0056
TOLLIP	0.1659	0.002	0.0123	0.6264	0.0134	0.0214	0.4529	0.0158	0.0348
tor1B	0.1037	0.0013	0.0126	0	0	0.0084	0.3129	0.0013	0.0042
TP53I3	0.2264	0.0027	0.012	0.0845	0.0014	0.016	0.1128	0.0014	0.012
TPI1	0	0	0.0222	0.161	0.0036	0.0222	0.161	0.0036	0.0222
TPP2	0.0867	0.0014	0.0161	0	0	0.0185	0.0672	0.0014	0.0208
TPT1	0	0	0	0	0	0	0	0	0
TSG101	0	0	0.0036	0	0	0.0036	0	0	0
TSN	0	0	0.006	0	0	0.0121	0	0	0.006
TSNAX	0.2808	0.0015	0.0053	0	0	0.0106	0.0929	0.0015	0.0159
TSTA3	0.3816	0.0068	0.0179	0.3062	0.0055	0.0179	1.0777	0.0096	0.0089
TTR	0.344	0.0124	0.0361	0.7007	0.0124	0.0178	0.3442	0.0124	0.0361
TUBB1	0.1469	0.0019	0.0131	0.176	0.0029	0.0164	0.0585	0.001	0.0164
TWSG1	0	0.0019	0	0.2734	0.0019	0.007	0	0	0.007
TXN	0	0	0.0153	0	0	0	0	0	0
UBE2L3	0	0	0.0306	0	0	0.0517	0	0	0.0203
UBE2N	0	0	0						
UGCGL1	0.1814	0.0014	0.0078						
UGDH	0	0	0.0087	0.0606	0.0009	0.0146	0.0759	0.0009	0.0116
USP14	0	0	0.0124	0.2113	0.0026	0.0124	0.4243	0.0026	0.0062

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
SEMA7A	0.0577	0.0033	0.0578	0.127	0.0084	0.0658	0.1	0.006	0.0602
SEMG1	1.0231	0.0629	0.0614	1.0397	0.0639	0.0614	0.9221	0.0659	0.0715
SEMG2	0.5543	0.0301	0.0544	0.6432	0.0332	0.0516	0.5415	0.0315	0.0582
SEPP1	0.6854	0.0165	0.0241	0.5076	0.0164	0.0324			
SERPINA1	0.2475	0.0169	0.0681	0.2641	0.0179	0.068	0.3921	0.0222	0.0567
SERPINA3	0.5876	0.0311	0.053	0.6522	0.0301	0.0462	0.5376	0.0322	0.0598
SERPINA4	0.4243	0.0105	0.0247	0.2779	0.0095	0.0342	0.301	0.0101	0.0337
SERPINA5	0.2252	0.0153	0.0679	0.3239	0.0239	0.0738	0.235	0.0136	0.058
SERPINA6	0.3698	0.012	0.0323	0.3026	0.0109	0.0359	0.2548	0.012	0.047
SERPINB5	0.1131	0.0046	0.0408	0.0813	0.0023	0.0283	0.1025	0.0046	0.045
SERPINB6	0.0617	0.0023	0.0371	0.1874	0.0124	0.0662	0.1466	0.0216	0.1476
SERPINC1	0.0589	0.0028	0.0479	0.1138	0.0047	0.0414	0.0978	0.0039	0.0401
SERPINF1	0.1817	0.0117	0.0646	0.1408	0.0096	0.0682	0.1937	0.0139	0.0717
SERPING1	0.2526	0.0143	0.0566	0.2373	0.0108	0.0454			
SERPINI1	0.0721	0.0042	0.058	0.0579	0.0031	0.0541	0.0835	0.0042	0.0501
sez6L2	0.2588	0.0092	0.0356	0.2596	0.0107	0.0413	0.193	0.0077	0.0399
SFN	0.0426	0.0018	0.0414	0.0601	0.0018	0.0293	0.0499	0.0018	0.0354
SH3BGRL2	0	0	0.0142	0	0	0.0288	0.1403	0.0041	0.0289
SI	0.1894	0.0095	0.0502	0.1877	0.0098	0.052	0.203	0.0116	0.0571
SIL1	0.2985	0.018	0.0601	0.2843	0.018	0.0632	0.2816	0.0165	0.0585
SLC15A2	0.1359	0.0048	0.0356	0.1123	0.0042	0.0376	0.1757	0.0048	0.0275
SLC1A1	0.0286	0.0017	0.0591	0.0792	0.0042	0.0536	0.0452	0.0025	0.0562
SLC35F2	0.1925	0.0072	0.0371	0.1813	0.0052	0.0289	0.1574	0.0065	0.0416
SLC44A4	0.2564	0.0092	0.0357	0.2881	0.0093	0.0323	0.2774	0.0104	0.0376
SLIT2	0.0175	0.0009	0.0489	0.0298	0.0014	0.0479	0.0878	0.0036	0.0406
SLPI	0.3371	0.0235	0.0696	0.3179	0.0303	0.0952	0.3683	0.0303	0.0822
SMOC2									
SMPD1	0.1447	0.0065	0.0446	0.1855	0.0079	0.0427	0.1266	0.0043	0.0341
smpdl3A	0.2343	0.0086	0.0368	0.3169	0.0106	0.0333	0.2874	0.0092	0.0319
SMPDL3B	0.5804	0.0127	0.0218	0.3938	0.0136	0.0346	0.2837	0.0107	0.0377
SMS	0.0319	0.0012	0.037	0.0826	0.0024	0.0287	0.1318	0.0099	0.0752
SOD1	0.4366	0.0204	0.0466	0.3615	0.0204	0.0563	0.3508	0.0233	0.0664
SOD3	0.4364	0.0095	0.0217	0.4364	0.0095	0.0217	0.2723	0.0106	0.0388
SORD	0.265	0.0152	0.0574	0.3105	0.0178	0.0573	0.2617	0.0163	0.0624
SORL1	0.0767	0.0039	0.0504	0.0478	0.0025	0.0516	0.0785	0.0041	0.0519
SORT1	0.2074	0.0053	0.0256	0.1458	0.0042	0.0291	0.1302	0.0043	0.0327
SPACA3	0.8518	0.0274	0.0322	0.7549	0.0295	0.0391	0.465	0.0277	0.0595
SPINK2	1.0102	0.0196	0.0194	0.6698	0.013	0.0194	0.6698	0.013	0.0194
SPINT1	0.4723	0.0207	0.0439	0.6286	0.0208	0.033	0.7989	0.0242	0.0303
SPINT3	0.2897	0.0149	0.0514	0.2942	0.0149	0.0508	0.0572	0.0049	0.0865
SPOCK3	0.0868	0.0038	0.044	0.1398	0.0067	0.0478			
SPON2	0.2789	0.0124	0.0443	0.2286	0.0082	0.036			
ST14	0.1036	0.0072	0.0694	0.1185	0.0082	0.0694	0.1388	0.0091	0.0653
STEAP2	0.075	0.0027	0.0357	0.025	0.0009	0.0356	0.0302	0.001	0.0328
STXBP2	0.0444	0.0037	0.0828	0.0385	0.0037	0.0958	0.0816	0.0063	0.0767
SYT1	0.0283	0.001	0.0361	0.0316	0.001	0.0324	0.0566	0.002	0.0361
SYT7	0.0484	0.0019	0.0389	0.2115	0.0076	0.0358	0.0527	0.0019	0.0359
TAGLN2	0	0	0.0371	0	0	0.0448	0	0	0.0303
TALDO1	0.1541	0.0052	0.034	0.1838	0.0079	0.0428	0.1704	0.0065	0.0384
TCP1	0.0361	0.0016	0.0438	0.0384	0.0016	0.0412	0.034	0.0016	0.0465
TEX101	0.9411	0.0187	0.0199	0.8914	0.0222	0.0249	0.5352	0.0189	0.0353
TF	0.4781	0.025	0.0524	0.5221	0.025	0.048	0.4999	0.0251	0.0502
TFPI2	0.4065	0.0127	0.0312	0.8837	0.0109	0.0123	0.6613	0.0164	0.0248
TFRC	0.2462	0.0081	0.0327	0.267	0.0098	0.0367	0.1418	0.0069	0.0487
TGFB1	0.0219	0.0011	0.0525	0.0254	0.0011	0.0453	0.0235	0.0011	0.0489
TGFB3	0	0	0.0282	0	0	0.0282	0	0	0.0281
TGFBR3	0.0889	0.0036	0.0406	0.131	0.0046	0.0355	0.1071	0.0036	0.0337
TGM4	0.1524	0.0115	0.0755	0.1448	0.0102	0.0707	0.1745	0.0129	0.0738
THBS1	0.0484	0.0018	0.038	0.0581	0.0022	0.038	0.0246	0.0011	0.0447
THBS2	0.0549	0.0043	0.0776	0.0594	0.0047	0.0797	0.0576	0.0047	0.0808
THBS4	0.0495	0.0024	0.049	0.1046	0.0056	0.0538	0.0555	0.0024	0.0437
TIMP1	0.4023	0.0216	0.0536	0.4957	0.0216	0.0435			
TIMP2	0	0	0.0458	0.066	0.0024	0.0363	0	0	0.0553
TIMP3	0	0	0.0722	0	0	0.0425	0	0	0.0499
TKT	0.0363	0.0028	0.0768	0.0375	0.0028	0.0744	0.0397	0.0021	0.0527
TMC5	0.1975	0.01	0.0506	0.1929	0.0102	0.053	0.1699	0.0089	0.0525
TMEFF2	0.0508	0.0023	0.0454	0.0464	0.0023	0.0497	0.0541	0.0027	0.0493
TMEM8	0.1649	0.0127	0.0767	0.1274	0.0099	0.0773			
tmpRSS2	0.5784	0.0289	0.05	0.6496	0.0307	0.0472	0.4413	0.0246	0.0557
TNFSF10	0.0989	0.0047	0.0476	0.1773	0.0063	0.0354	0.2141	0.0063	0.0293
TOLLIP	0	0	0.0624	0.0359	0.002	0.057	0.1846	0.0134	0.0728
tor1B	0	0	0.0429	0.0339	0.0013	0.0385	0	0	0.0341
TP53I3	0.1677	0.0068	0.0405	0.1518	0.0068	0.0447	0.1108	0.0054	0.0491
TPI1	0	0	0.0393	0	0	0.0393	0.1281	0.0036	0.0279
TPP2	0	0	0.041	0.033	0.0016	0.0476	0	0	0.0434
TPT1	0	0	0	0	0	0	0	0	0
TSG101	0.0683	0.0023	0.033	0.0771	0.0023	0.0293	0.0771	0.0023	0.0293
TSN	0	0	0.0244	0	0	0.0306	0	0	0.0369
TSNAX	0	0	0.0213	0.0554	0.0015	0.0267	0	0	0.0213
TSTA3	0.1225	0.0096	0.0786	0.2145	0.0138	0.0642	0.1801	0.0124	0.0688
TTR	0.5214	0.0187	0.036	0.3414	0.0187	0.0548	0.5217	0.0187	0.0359
TUBB1	0.0839	0.0048	0.0573	0.0502	0.0029	0.0574	0.0631	0.0038	0.061
TWSG1	0.0674	0.0019	0.0284	0	0	0.0284	0	0	0.0356
TXN	0	0	0.0153	0	0	0.0308	0	0	0.0156
UBE2L3	0	0	0.0625	0	0	0.0306	0	0	0.0517
UBE2N	0	0	0.0093	0	0	0.0093			
UGCGL1	0.1215	0.0044	0.0365	0.1281	0.0041	0.0324			
UGDH	0	0	0.0235	0	0	0.0146	0.0334	0.0009	0.0265
USP14	0.069	0.0026	0.0378	0.0832	0.0026	0.0314	0.1667	0.0052	0.0314

Gene	giH_*ω*	giH_*Ka*	giH_*Ks*	giC_*ω*	giC_*Ka*	giC_*Ks*	giG_*ω*	giG_*Ka*	giG_*Ks*	giO_*ω*	giO_*Ka*	giO_*Ks*
SEMA7A	0.097	0.0067	0.0689	0.1569	0.0117	0.0747	0.1163	0.008	0.0691	0.1328	0.0074	0.0554
SEMG1	0.8538	0.0382	0.0447	0.9198	0.0411	0.0447	0.9412	0.058	0.0616	0.9877	0.0772	0.0781
SEMG2	0.8931	0.0498	0.0557	0.8191	0.053	0.0647	0.6993	0.05	0.0715	0.6946	0.0456	0.0656
SEPP1	0.4578	0.0226	0.0493	0.4545	0.0225	0.0494				0.4196	0.0225	0.0535
SERPINA1	0.5646	0.0249	0.0441	0.5911	0.026	0.044	0.6381	0.0304	0.0476	0.2942	0.0233	0.0792
SERPINA3	0.7147	0.0517	0.0724	0.8711	0.057	0.0654	0.6648	0.0528	0.0794	0.6869	0.0597	0.087
SERPINA4	0.4195	0.0211	0.0502	0.334	0.0201	0.0601	0.2804	0.0173	0.0618	0.4098	0.022	0.0537
SERPINA5	0.2087	0.0168	0.0805	0.3084	0.0248	0.0805	0.2287	0.0157	0.0687	0.21	0.018	0.0859
SERPINA6	0.3593	0.0197	0.0547	0.3655	0.0186	0.0508	0.3172	0.0197	0.0621	0.3276	0.0142	0.0432
SERPINB5	0.1074	0.0058	0.0537	0.106	0.0035	0.0326	0.0994	0.0058	0.058	0.2047	0.0058	0.0282
SERPINB6	0.1185	0.008	0.0677	0.2051	0.0184	0.0895	0.1518	0.0265	0.1745	0.1117	0.008	0.0719
SERPINC1	0.0984	0.0047	0.0479	0.1205	0.0052	0.043	0.1353	0.0059	0.0436	0.1177	0.0056	0.048
SERPINF1	0.1359	0.0122	0.0898	0.1086	0.0097	0.0898	0.1561	0.0147	0.0939	0.1366	0.0146	0.1072
SERPING1	0.2714	0.0164	0.0604	0.2613	0.0128	0.049				0.2608	0.0127	0.0487
SERPINI1	0.0745	0.0052	0.0703	0.0631	0.0042	0.0663	0.0841	0.0052	0.0622	0.1524	0.0052	0.0343
sez6L2	0.0824	0.0035	0.0419	0.0978	0.0049	0.0506	0.0426	0.002	0.0463	0.2	0.0077	0.0385
SFN	0	0	0.0413	0	0	0.0293	0	0	0.0353	0.0371	0.0018	0.0475
SH3BGRL2	0	0	0	0	0	0.0142	0.2834	0.0041	0.0143	0	0	0.0142
SI												
SIL1	0.2431	0.0207	0.0852	0.2148	0.0207	0.0966	0.2559	0.0213	0.0832	0.2834	0.0287	0.1012
SLC15A2	0.2308	0.0075	0.0326	0.1915	0.0072	0.0377	0.2839	0.0078	0.0276	0.1671	0.0066	0.0398
SLC1A1	0.065	0.0048	0.0744	0.1199	0.0077	0.0646	0.0857	0.0058	0.0677	0.0513	0.0048	0.0941
SLC35F2	0.0964	0.0036	0.037	0.0792	0.0026	0.033	0.0858	0.0039	0.0458	0.168	0.0066	0.039
SLC44A4	0.1901	0.0124	0.0652	0.1967	0.0126	0.0642	0.2197	0.0138	0.0628	0.2223	0.0128	0.0574
SLIT2	0.1016	0.0052	0.0515	0.1316	0.0064	0.0484	0.0876	0.0032	0.0366	0.1071	0.0061	0.0574
SLPI	0.7107	0.0408	0.0574	0.8243	0.0477	0.0578	0.685	0.0477	0.0697	0.2866	0.0235	0.0819
SMOC2	0.0286	0.0021	0.0748	0	0	0.0592	0	0	0.0669			
SMPD1	0.2798	0.0162	0.0579	0.2967	0.0174	0.0587	0.2649	0.0138	0.0519	0.3202	0.0152	0.0475
smpdl3A	0.2653	0.0125	0.0471	0.3315	0.0144	0.0436	0.2857	0.0138	0.0483	0.1339	0.0086	0.0645
SMPDL3B	0.2417	0.0146	0.0605	0.2108	0.0156	0.0741	0.2142	0.0137	0.0637	0.2525	0.0191	0.0756
SMS	0.3277	0.0198	0.0604	0.4058	0.021	0.0517	0.3054	0.0308	0.1009	0.3744	0.021	0.0561
SOD1	1.273	0.0352	0.0277	0.9488	0.0352	0.0371	0.8148	0.0382	0.0469	0.7288	0.0412	0.0566
SOD3	0.1516	0.0076	0.05	0.1516	0.0076	0.05	0.1249	0.0079	0.0633	0.2661	0.0133	0.05
SORD	0.2357	0.0159	0.0673	0.2746	0.0184	0.0672	0.2913	0.0221	0.0759	0.1798	0.0139	0.0775
SORL1	0.0959	0.0058	0.0606	0.0679	0.0043	0.0638	0.0904	0.0059	0.0654	0.0879	0.0048	0.0545
SORT1	0.1351	0.0045	0.0334	0.1115	0.0045	0.0405	0.0853	0.0035	0.0407	0.189	0.0066	0.0352
SPACA3	0.6556	0.0296	0.0452	0.6897	0.036	0.0522	0.4098	0.0299	0.0729	0.8227	0.0318	0.0386
SPINK2	0.6715	0.0229	0.0342	0.6762	0.023	0.034	0.5012	0.0171	0.0342	0.3207	0.0207	0.0647
SPINT1	0.4918	0.0143	0.0291	0.7792	0.0143	0.0184	1.1286	0.0177	0.0157	0.6087	0.0251	0.0412
SPINT3	1.1838	0.0199	0.0168	1.202	0.02	0.0166	0.598	0.0099	0.0166	0.2913	0.0174	0.0598
SPOCK3	0.086	0.0048	0.0556	0.1031	0.0057	0.0557				0.1169	0.0072	0.0614
SPON2	0.2015	0.0124	0.0614	0.1559	0.0082	0.0528				0.2083	0.011	0.0528
ST14	0.2045	0.016	0.0783	0.2112	0.0166	0.0784	0.2421	0.018	0.0742	0.1501	0.0129	0.0858
STEAP2	0.0995	0.0045	0.0449	0.0998	0.0045	0.0448	0.0604	0.002	0.0328	0.1096	0.0036	0.0326
STXBP2	0.0981	0.0081	0.0828	0.0876	0.0085	0.097	0.1328	0.0103	0.0779	0.0901	0.0085	0.0942
SYT1	0	0	0.0473	0	0	0.0435	0.0186	0.001	0.0548	0.0235	0.001	0.0435
SYT7	0.0673	0.0028	0.0413	0.2191	0.0085	0.0389	0.0675	0.0028	0.0413	0.1209	0.0047	0.039
TAGLN2	0.1767	0.0066	0.0373	0.2219	0.0066	0.0297	0.219	0.0067	0.0305	0.1085	0.0066	0.0608
TALDO1	0.1523	0.0068	0.0446	0.2023	0.0102	0.0504	0.1899	0.0085	0.0447	0.1369	0.0085	0.062
TCP1	0.0441	0.0016	0.0359	0.0476	0.0016	0.0333	0.0441	0.0016	0.0359	0.0441	0.0016	0.0359
TEX101	0.1876	0.0136	0.0723	0.2835	0.0205	0.0722	0.2197	0.0172	0.0781	0.3822	0.0256	0.0671
TF	0.6737	0.0395	0.0586	0.6051	0.0382	0.0631	0.6121	0.0366	0.0598	0.5391	0.0346	0.0641
TFPI2	0.2897	0.0131	0.0452	0.4411	0.0112	0.0254	0.3415	0.0131	0.0384	0.3412	0.0131	0.0384
TFRC	0.2295	0.0121	0.0528	0.2438	0.0139	0.0569	0.1683	0.011	0.0651	0.2206	0.0121	0.0549
TGFB1	0.0515	0.0035	0.0671	0.0578	0.0035	0.0597	0.0544	0.0035	0.0635	0.0409	0.0023	0.0562
TGFB3	0	0	0.0354	0	0	0.0354	0	0	0.0427	0	0	0.0282
TGFBR3	0.0935	0.0041	0.0442	0.146	0.0062	0.0424	0.1014	0.0041	0.0407	0.1285	0.0057	0.0442
TGM4	0.315	0.0173	0.055	0.3189	0.016	0.0503	0.2896	0.0187	0.0646	0.1559	0.0122	0.078
THBS1	0.0514	0.0026	0.0501	0.044	0.0022	0.0501	0.0323	0.0018	0.057	0.0509	0.0022	0.0434
THBS2	0.1259	0.0103	0.0816	0.1328	0.0123	0.0926	0.1189	0.0113	0.0947	0.1295	0.0129	0.0994
THBS4	0.0662	0.0038	0.0567	0.1148	0.0069	0.0597	0.0792	0.0042	0.0533	0.042	0.0025	0.0601
TIMP1												
TIMP2	0.0513	0.004	0.0771	0.0698	0.006	0.0858	0.023	0.0022	0.0955	0.032	0.0024	0.0748
TIMP3	0.0971	0.0041	0.0426	0.2969	0.0041	0.0139	0.1967	0.0041	0.021	0.1471	0.0041	0.0281
TKT	0.0345	0.0029	0.0846	0.0355	0.0029	0.0821	0.0368	0.0022	0.0594	0.0227	0.0015	0.0643
TMC5	0.387	0.0201	0.052	0.3561	0.0199	0.0558	0.338	0.0182	0.0539	0.2536	0.0181	0.0713
TMEFF2	0.0402	0.0012	0.0286	0.0351	0.0012	0.0328	0.0456	0.0013	0.0293	0.084	0.0035	0.0412
TMEM8	0.2437	0.0218	0.0894	0.1901	0.0188	0.099				0.1925	0.0162	0.0841
tmpRSS2	0.535	0.0334	0.0625	0.5231	0.0343	0.0656	0.3868	0.027	0.0697	0.4019	0.0271	0.0675
TNFSF10	0.2352	0.0122	0.0519	0.4015	0.0137	0.0342	0.4025	0.0138	0.0342	0.4024	0.0142	0.0353
TOLLIP	0	0	0.0789	0.0244	0.002	0.0838	0.1559	0.0134	0.0862	0	0	0.1013
tor1B	0.0913	0.0039	0.043	0.1358	0.0052	0.0386	0.1148	0.0039	0.0342	0.0695	0.0039	0.0565
TP53I3	0.1518	0.0068	0.0447	0.1672	0.0068	0.0406	0.1487	0.0054	0.0366	0.044	0.0027	0.0616
TPI1	0	0	0.0508	0	0	0.0509	0.0909	0.0036	0.0393	0	0	0.0451
TPP2	0.087	0.0031	0.0362	0.1145	0.0045	0.0398	0.0931	0.0031	0.0338	0.067	0.0031	0.047
TPT1	0.4292	0.0187	0.0435	0.4292	0.0187	0.0435	0.4292	0.0187	0.0435	0.4292	0.0187	0.0435
TSG101	0	0	0.033	0	0	0.0292	0	0	0.0292	0.0509	0.0023	0.0443
TSN	0	0	0.0369	0	0	0.0432	0	0	0.0495	0	0	0.0244
TSNAX	0.0685	0.003	0.0432	0.0913	0.0044	0.0487	0.0685	0.003	0.0432	0.092	0.003	0.0322
TSTA3	0.1384	0.0082	0.0595	0.1787	0.0124	0.0692	0.1593	0.011	0.069	0.0495	0.0041	0.0831
TTR	0.3455	0.0156	0.0452	0.1934	0.0124	0.0643	0.3456	0.0156	0.0451	0.5831	0.0156	0.0268
TUBB1	0.1129	0.0063	0.0555	0.0894	0.0048	0.0539	0.1147	0.0058	0.0504	0.0733	0.0058	0.0788
TWSG1	0.09	0.0019	0.0213	0	0	0.0212	0	0	0.0284	0	0	0.0357
TXN	0	0	0.0468	0	0	0.0631	0	0	0.0478	0	0	0.063
UBE2L3	0.1325	0.0112	0.0847	0.2165	0.0112	0.0518	0.1525	0.0112	0.0736	0.2726	0.0112	0.0412
UBE2N	0	0	0.0188	0	0	0.0188				0	0	0.0093
UGCGL1	0.09	0.0034	0.0376	0.0873	0.0031	0.0355				0.1152	0.0044	0.0385
UGDH	0.0607	0.0009	0.0146	0.076	0.0009	0.0116	0.101	0.0018	0.0175	0.0431	0.0009	0.0205
USP14	0	0	0.0373	0	0	0.0304	0.0937	0.0028	0.0304	0.0934	0.0028	0.0304

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
SEMA7A	0.0897	0.0084	0.0932	0.1349	0.0134	0.0993	0.1039	0.0097	0.0935	0.1048	0.009	0.0861
SEMG1	0.8436	0.08	0.0949	0.8015	0.0806	0.1005	0.9503	0.1002	0.1055	0.9351	0.1112	0.119
SEMG2	1.072	0.0733	0.0684	1.1561	0.0804	0.0696	0.9734	0.0765	0.0785	1.197	0.0762	0.0637
SEPP1	0.6989	0.033	0.0472	0.5683	0.0317	0.0558				0.687	0.0354	0.0515
SERPINA1	0.4869	0.0407	0.0835	0.4842	0.0413	0.0852	0.5351	0.0435	0.0813	0.3202	0.0341	0.1066
SERPINA3	0.5919	0.0565	0.0955	0.6028	0.0576	0.0955	0.5708	0.0586	0.1027	0.4988	0.0524	0.105
SERPINA4	0.1778	0.0172	0.0967	0.1332	0.0143	0.1074	0.1506	0.0142	0.0946	0.1867	0.0181	0.0972
SERPINA5	0.3245	0.0318	0.098	0.3897	0.0413	0.1061	0.3569	0.0307	0.0859	0.3214	0.032	0.0997
SERPINA6	0.3311	0.0297	0.0896	0.3345	0.0286	0.0854	0.3057	0.0297	0.0972	0.283	0.0241	0.0853
SERPINB5	0.0861	0.0058	0.0669	0.076	0.0034	0.0454	0.0807	0.0058	0.0713	0.1171	0.0058	0.0492
SERPINB6	0.1139	0.015	0.1316	0.1699	0.0232	0.1365	0.1392	0.0327	0.2346	0.087	0.0127	0.1456
SERPINC1	0.4765	0.0505	0.106	0.5707	0.0525	0.092	0.5239	0.0541	0.1033	0.5103	0.0518	0.1015
SERPINF1	0.1317	0.021	0.1595	0.1347	0.0188	0.1398	0.153	0.0232	0.1516	0.1567	0.0264	0.1687
SERPING1	0.2951	0.0355	0.1203	0.3027	0.0339	0.112				0.3626	0.0341	0.094
SERPINI1	0.1427	0.0094	0.0662	0.1687	0.0105	0.0622	0.1988	0.0116	0.0582	0.2505	0.0116	0.0461
sez6L2	0.0566	0.004	0.0698	0.0748	0.0054	0.0727	0.0353	0.0025	0.0698	0.1562	0.0092	0.0589
SFN	0.0141	0.0018	0.1248	0.0159	0.0018	0.1113	0.015	0.0018	0.118	0.0299	0.0035	0.1183
SH3BGRL2	0	0	0.0438	0	0	0.059	0.0691	0.0041	0.0593	0	0	0.0438
SI	0.3005	0.0234	0.0778	0.3146	0.024	0.0763	0.2959	0.0264	0.0891	0.332	0.0244	0.0733
SIL1	0.1547	0.0146	0.0941	0.1402	0.0146	0.1039	0.1444	0.0146	0.1008	0.1928	0.0214	0.1112
SLC15A2	0.218	0.0109	0.0499	0.1972	0.0115	0.0583	0.2528	0.0121	0.0479	0.1809	0.0109	0.0603
SLC1A1	0.1095	0.0072	0.066	0.155	0.0098	0.0632	0.113	0.0081	0.0716	0.0971	0.0072	0.0745
SLC35F2	0.0907	0.0095	0.1052	0.0657	0.0065	0.0996	0.0754	0.0079	0.1042	0.136	0.0143	0.1055
SLC44A4	0.1859	0.0152	0.0815	0.196	0.0154	0.0787	0.1973	0.0165	0.0835	0.1874	0.0155	0.0827
SLIT2	0.0369	0.0032	0.0872	0.0529	0.0044	0.0829	0.0773	0.0053	0.0681	0.0456	0.0041	0.0906
SLPI	0.5218	0.0599	0.1149	0.4691	0.0669	0.1427	0.5212	0.067	0.1286	0.3664	0.0423	0.1154
SMOC2	0.0848	0.0092	0.1081	0.0446	0.0048	0.107	0.096	0.0092	0.0954			
SMPD1	0.1935	0.0141	0.0727	0.1869	0.0141	0.0754	0.1793	0.0119	0.0666	0.1953	0.0133	0.0682
smpdl3A	0.2227	0.0193	0.0866	0.2567	0.0213	0.0828	0.2398	0.0219	0.0915	0.1747	0.0164	0.0937
SMPDL3B	0.5117	0.0518	0.1013	0.4523	0.0508	0.1123	0.4534	0.0508	0.112	0.5275	0.0544	0.1032
SMS	0.0329	0.0024	0.0726	0.0562	0.0036	0.0636	0.1195	0.0124	0.1038	0.0604	0.0036	0.0593
SOD1	0.6688	0.0443	0.0663	0.5814	0.0443	0.0762	0.5461	0.0473	0.0866	0.5203	0.0504	0.0968
SOD3	0.3723	0.027	0.0724	0.3723	0.027	0.0724	0.3105	0.0323	0.1041	0.399	0.0289	0.0725
SORD	0.2299	0.0243	0.1057	0.2305	0.0243	0.1056	0.2267	0.0265	0.1171	0.2165	0.0198	0.0913
SORL1	0.0726	0.0068	0.093	0.0578	0.0056	0.0963	0.0695	0.007	0.1002	0.0775	0.0065	0.0837
SORT1	0.0842	0.0053	0.0629	0.0795	0.0053	0.0666	0.0673	0.0043	0.0633	0.1292	0.0074	0.0575
SPACA3	0.8053	0.0535	0.0664	0.7815	0.0578	0.0739	0.5646	0.054	0.0956	0.9344	0.0556	0.0596
SPINK2	1.5409	0.1396	0.0906	1.5514	0.1398	0.0901	1.4677	0.133	0.0906	1.0279	0.1154	0.1123
SPINT1	0.2195	0.0194	0.0884	0.2736	0.0194	0.071	0.3097	0.0228	0.0738	0.307	0.0311	0.1013
SPINT3	2.4932	0.0638	0.0256	2.5323	0.064	0.0253	1.0623	0.0641	0.0603	0.9601	0.0667	0.0695
SPOCK3	0.0604	0.0038	0.0632	0.0995	0.0067	0.0672				0.0906	0.0057	0.0632
SPON2	0.2342	0.0193	0.0825	0.2056	0.0151	0.0737				0.2585	0.0179	0.0694
ST14	0.1261	0.0149	0.1178	0.1569	0.0176	0.112	0.1319	0.0162	0.1225	0.1204	0.0132	0.11
STEAP2	0.0486	0.0033	0.067	0.069	0.0044	0.063	0.0326	0.0022	0.067	0.0589	0.0033	0.0554
STXBP2	0.0801	0.0089	0.1115	0.0752	0.0093	0.1237	0.1103	0.0112	0.1012	0.0754	0.0093	0.1234
SYT1	0	0	0.0586	0	0	0.051	0.0146	0.001	0.0702	0.0174	0.001	0.0586
SYT7	0.0518	0.0029	0.0568	0.1658	0.0091	0.0546	0.0491	0.003	0.0602	0.0815	0.005	0.0613
TAGLN2	0	0	0.076	0	0	0.0841	0	0	0.0699	0	0	0.1006
TALDO1	0.0866	0.0052	0.0604	0.0864	0.0052	0.0605	0.1167	0.0065	0.0561	0.0752	0.0052	0.0695
TCP1	0.0277	0.0016	0.0572	0.0291	0.0016	0.0545	0.0264	0.0016	0.0599	0.0264	0.0016	0.0599
TEX101	0.5569	0.0349	0.0627	0.5486	0.0403	0.0735	0.5415	0.037	0.0684	0.6126	0.0385	0.0628
TF	0.4192	0.0413	0.0985	0.4058	0.04	0.0985	0.4024	0.0387	0.0962	0.3522	0.041	0.1163
TFPI2	0.4093	0.0302	0.0739	0.5281	0.0284	0.0538	0.4324	0.0275	0.0636	0.4805	0.0322	0.0669
TFRC	0.1478	0.0247	0.1673	0.1555	0.0262	0.1685	0.1296	0.0235	0.1817	0.1134	0.021	0.1851
TGFB1	0	0	0.083	0	0	0.0784	0	0	0.0878	0	0	0.0832
TGFB3	0.0377	0.0011	0.0282	0.0377	0.0011	0.0282	0.03	0.0011	0.0353	0.03	0.0011	0.0354
TGFBR3	0.1223	0.0101	0.0826	0.1633	0.0125	0.0763	0.1342	0.0101	0.0753	0.1477	0.0117	0.079
TGM4	0.3672	0.0285	0.0776	0.3648	0.0265	0.0727	0.3615	0.03	0.0829	0.254	0.0232	0.0915
THBS1	0.0329	0.0033	0.1008	0.0301	0.0029	0.0979	0.0252	0.0026	0.1022	0.0387	0.0037	0.095
THBS2	0.0528	0.0066	0.1247	0.0641	0.0082	0.1279	0.0561	0.0074	0.1314	0.0697	0.0092	0.132
THBS4	0.1087	0.0086	0.0793	0.1332	0.0117	0.0876	0.117	0.0091	0.0776	0.1012	0.0075	0.0746
TIMP1	0.642	0.0346	0.0539	0.7062	0.0309	0.0437				1.1366	0.0383	0.0337
TIMP2	0	0	0.0756	0.0697	0.0047	0.068	0	0	0.1102	0	0	0.0848
TIMP3	0	0	0.0722	0	0	0.0572	0	0	0.0648	0	0	0.0425
TKT	0.0328	0.0042	0.1282	0.0321	0.0042	0.1309	0.0311	0.0035	0.1125	0.0261	0.0028	0.1071
TMC5	0.2764	0.0244	0.0885	0.2661	0.024	0.0902	0.2665	0.0239	0.0898	0.2118	0.0201	0.0949
TMEFF2	0.0311	0.0012	0.037	0.0279	0.0012	0.0412	0.0301	0.0013	0.0443	0.084	0.0035	0.0412
TMEM8	0.1952	0.0271	0.1387	0.1841	0.0261	0.1419				0.173	0.0223	0.1291
tmpRSS2	0.5019	0.0604	0.1203	0.4854	0.0609	0.1255	0.4368	0.0546	0.125	0.4177	0.0541	0.1295
TNFSF10	0.1673	0.0169	0.1008	0.2437	0.0215	0.0883	0.2248	0.0184	0.0819	0.2088	0.019	0.0912
TOLLIP	0.0118	0.0016	0.1365	0.0264	0.0041	0.1552	0.1038	0.0155	0.1496	0.0097	0.0016	0.1669
tor1B	0.0643	0.0039	0.061	0.0927	0.0052	0.0565	0.0755	0.0039	0.052	0.0493	0.0039	0.0795
TP53I3	0.3576	0.0213	0.0595	0.3331	0.0213	0.0638	0.2913	0.0199	0.0684	0.1873	0.0143	0.0766
TPI1	0.0847	0.009	0.1057	0.0847	0.009	0.1058	0.096	0.009	0.0933	0.1028	0.009	0.0871
TPP2	0.1733	0.0137	0.0792	0.177	0.0152	0.0856	0.1788	0.0137	0.0768	0.1492	0.0137	0.092
TPT1	0	0	0.0385	0	0	0.0385	0	0	0.0385	0	0	0.0385
TSG101	0	0	0.0405	0	0	0.0368	0	0	0.0368	0.0508	0.0023	0.0444
TSN	0	0	0.0431	0	0	0.0494	0	0	0.0559	0	0	0.0305
TSNAX	0.0738	0.0044	0.0602	0.0902	0.0059	0.0658	0.062	0.0044	0.0717	0.0815	0.0044	0.0546
TSTA3	0.139	0.011	0.079	0.2179	0.0151	0.0695	0.1987	0.0138	0.0693	0.0778	0.0069	0.0882
TTR	0.4258	0.0315	0.0739	0.3343	0.0314	0.094	0.4261	0.0315	0.0739	0.3423	0.0187	0.0547
TUBB1	0.0518	0.0058	0.1117	0.0322	0.0038	0.1195	0.0333	0.0038	0.1157	0.0416	0.0048	0.1158
TWSG1	0.0331	0.0019	0.0579	0	0	0.0577	0	0	0.0653	0	0	0.0729
TXN	1.0814	0.0165	0.0152	0.5352	0.0165	0.0308	1.0786	0.0168	0.0156	0.5356	0.0165	0.0307
UBE2L3	0	0	0.0625	0	0	0.0306	0	0	0.0306	0	0	0.0411
UBE2N	0	0	0.0284	0	0	0.0284				0	0	0.0188
UGCGL1	0.0942	0.0085	0.0901	0.0934	0.0082	0.0879				0.0958	0.0085	0.0883
UGDH	0.0382	0.0027	0.0694	0.0442	0.0027	0.06	0.0534	0.0035	0.0663	0.042	0.0027	0.0632
USP14	0	0	0.0377	0	0	0.0281	0.0835	0.0026	0.0313	0.069	0.0026	0.0378

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
SEMA7A	0.1263	0.0097	0.0769
SEMG1	0.9098	0.0765	0.0841
SEMG2	1.2127	0.0823	0.0679
SEPP1	0.5657	0.0366	0.0647
SERPINA1	0.4572	0.0363	0.0794
SERPINA3	0.7298	0.0816	0.1119
SERPINA4	0.2441	0.0293	0.1202
SERPINA5	0.2395	0.0279	0.1164
SERPINA6	0.3068	0.0286	0.0932
SERPINB5	0.1532	0.0069	0.0452
SERPINB6	0.0811	0.0115	0.1417
SERPINC1	0.4953	0.0538	0.1087
SERPINF1	0.1406	0.024	0.1706
SERPING1	0.301	0.0322	0.1069
SERPINI1	0.2169	0.0126	0.0582
sez6L2	0.0528	0.0035	0.0654
SFN	0.0169	0.0018	0.1047
SH3BGRL2	0	0	0.0438
SI			
SIL1	0.2377	0.023	0.0968
SLC15A2	0.2637	0.0124	0.047
SLC1A1	0.0696	0.0068	0.0974
SLC35F2	0.1064	0.0107	0.101
SLC44A4	0.1435	0.0149	0.1038
SLIT2	0.0941	0.0087	0.092
SLPI	0.5183	0.0528	0.1019
SMOC2	0.0392	0.0039	0.0996
SMPD1	0.2111	0.017	0.0807
smpdl3A	0.2074	0.0198	0.0955
SMPDL3B	0.4409	0.0508	0.1153
SMS	0.2831	0.0224	0.079
SOD1	0.3026	0.0262	0.0867
SOD3	0.2625	0.0269	0.1026
SORD	0.1481	0.0185	0.1248
SORL1	0.077	0.0062	0.0801
SORT1	0.0907	0.0064	0.0702
SPACA3	0.6424	0.0469	0.073
SPINK2	1.2116	0.1399	0.1155
SPINT1	0.2761	0.022	0.0796
SPINT3	1.493	0.0639	0.0428
SPOCK3	0.0709	0.0048	0.0674
SPON2	0.1833	0.0152	0.0828
ST14	0.1482	0.0171	0.1154
STEAP2	0.0632	0.0033	0.0516
STXBP2	0.0636	0.0059	0.0934
SYT1	0	0	0.0663
SYT7	0.1035	0.0059	0.0569
TAGLN2	0.0652	0.0066	0.1012
TALDO1	0.079	0.0068	0.0859
TCP1	0.0322	0.0016	0.0491
TEX101	0.9378	0.0438	0.0467
TF	0.4221	0.0462	0.1093
TFPI2	0.4349	0.0284	0.0652
TFRC	0.1456	0.0272	0.1867
TGFB1	0.028	0.0028	0.1018
TGFB3	0.03	0.0011	0.0354
TGFBR3	0.1482	0.0101	0.0682
TGM4	0.4012	0.0265	0.0661
THBS1	0.028	0.0029	0.1052
THBS2	0.0998	0.0145	0.1452
THBS4	0.113	0.0099	0.0876
TIMP1			
TIMP2	0.0228	0.0023	0.1027
TIMP3	0.0971	0.0041	0.0426
TKT	0.0198	0.0022	0.1108
TMC5	0.3369	0.0304	0.0903
TMEFF2	0.0703	0.0023	0.0328
TMEM8	0.2133	0.0287	0.1347
tmpRSS2	0.4176	0.0536	0.1285
TNFSF10	0.2251	0.0184	0.0818
TOLLIP	0.0136	0.0016	0.1186
tor1B	0.0987	0.0079	0.0797
TP53I3	0.2365	0.0171	0.0723
TPI1	0.0901	0.009	0.0995
TPP2	0.2172	0.0169	0.078
TPT1	0.2943	0.0187	0.0635
TSG101	0	0	0.052
TSN	0	0	0.0305
TSNAX	0.0959	0.0074	0.0774
TSTA3	0.0586	0.0055	0.0935
TTR	0.6251	0.0283	0.0453
TUBB1	0.0565	0.0067	0.1194
TWSG1	0	0	0.0504
TXN	0.2618	0.0165	0.0629
UBE2L3	0.1792	0.0112	0.0626
UBE2N	0	0	0.0284
UGCGL1	0.0902	0.0079	0.0878
UGDH	0.0267	0.0018	0.0662
USP14	0	0	0.0373

Gene	CH_ω	CH_Ka	CH_Ks	GH_ω	GH_Ka	GH_Ks	GC_ω	GC_Ka	GC_Ks
VAMP2	0	0	0.0119	0	0	0.0241	0	0	0.012
VAMP8	0	0	0.0295	0	0	0.0295	0	0	0.0295
VAT1	1.2271	0.0081	0.0066	0.5811	0.0058	0.0099	0.4659	0.0046	0.0099
VCL	0	0	0.0048	0	0	0.0109	0	0	0.0084
VCP	0	0	0.028	0	0	0.0174	0	0	0.0245
VPS28	0.0627	0.0019	0.0303	0.0617	0.004	0.0651	0.1034	0.006	0.0583
VTN	0.1517	0.0027	0.0181	0.3805	0.0096	0.0253	0.3558	0.0067	0.0189
VWA1									
VWF	0.1941	0.0044	0.0224						
WFDC2	0	0	0.0113	0	0	0.0228	0	0	0.0113
WFDC8	0.3159	0.0106	0.0337	0.3535	0.0071	0.02	0.3967	0.0106	0.0268
WFDC9	0	0.0146	0	0	0.0146	0	0	0	0
XPNPEP1	0.038	0.0007	0.0179	0.0232	0.0007	0.0293	0	0	0.0247
YWHAB	0	0	0.0124	0	0	0.0124	0	0	0.0062
YWHAE	0	0	0.0059	0	0	0.0178	0	0	0.0118
YWHAG	0	0	0.0122	0	0	0.0245	0	0	0.0122
YWHAQ	0	0	0.006	0	0	0.012	0	0	0.006
YWHAZ	0	0	0.0061	0	0	0.0061	0	0	0
ZPBP	0.4698	0.0076	0.0161	0.1389	0.0063	0.0452	0.2388	0.0088	0.0369

Gene	OH_ω	OH_Ka	OH_Ks	OC_ω	OC_Ka	OC_Ks	OG_ω	OG_Ka	OG_Ks
VAMP2	0	0	0.0365	0	0	0.0241	0	0	0.0365
VAMP8	0	0	0.0605	0	0	0.0296	0	0	0.0605
VAT1	0.3084	0.0105	0.034	0.3059	0.0093	0.0305	0.1862	0.007	0.0376
VCL	0.08	0.002	0.0244	0.0843	0.002	0.0231	0.08	0.002	0.0244
VCP	0	0	0.0316	0	0	0.0388	0	0	0.0245
VPS28	0.1037	0.0126	0.1212	0.1273	0.0145	0.1141	0.165	0.0174	0.1056
VTN	0.4397	0.0175	0.0399	0.4742	0.0152	0.0321	0.4127	0.0179	0.0434
VWA1									
VWF	0.1637	0.0089	0.0543	0.1764	0.0097	0.0548			
WFDC2	0.3839	0.018	0.0469	0.5159	0.018	0.0349	0.78	0.018	0.0231
WFDC8	0.4216	0.0176	0.0418	0.4756	0.0199	0.0418	0.5302	0.0176	0.0333
WFDC9	0.8271	0.0296	0.0358	0.6953	0.0246	0.0354	0.6953	0.0246	0.0354
XPNPEP1	0.0298	0.0014	0.0457	0.0176	0.0007	0.0386	0.0142	0.0007	0.048
YWHAB	0	0	0.0577	0	0	0.0445	0	0	0.0511
YWHAE	0	0	0.0118	0	0	0.0059	0	0	0.0178
YWHAG	0	0	0.0435	0	0	0.0435	0	0	0.0564
YWHAQ	0	0	0.0243	0	0	0.0181	0	0	0.0243
YWHAZ	0	0	0.0123	0	0	0.0061	0	0	0.0061
ZPBP	0.3677	0.0135	0.0366	0.3911	0.0186	0.0475	0.2072	0.0168	0.0813

Gene	giH_ω	giH_Ka	giH_Ks	giC_ω	giC_Ka	giC_Ks	giG_ω	giG_Ka	giG_Ks	giO_ω	giO_Ka	giO_Ks
VAMP2	0	0	0.0618	0	0	0.049	0	0	0.0618	0	0	0.0241
VAMP8	0	0	0.0602	0	0	0.0295	0	0	0.0602	0	0	0.0605
VAT1	0.3116	0.0116	0.0372	0.281	0.0104	0.0371	0.2178	0.0081	0.0373	0.1826	0.0082	0.0447
VCL	0.0545	0.0014	0.0263	0.0573	0.0014	0.025	0.0519	0.0014	0.0276	0.0946	0.0035	0.0368
VCP	0.0441	0.0016	0.0372	0.0369	0.0016	0.0445	0.0548	0.0016	0.03	0.0489	0.0016	0.0336
VPS28	0.0808	0.0101	0.1252	0.0605	0.0076	0.1253	0.1706	0.0162	0.0949	0.1689	0.0233	0.138
VTN	0.519	0.0301	0.058	0.5281	0.0264	0.05	0.5228	0.0288	0.0551	0.5499	0.0276	0.0502
VWA1	0.2544	0.0145	0.0568									
VWF												
WFDC2	0.1519	0.0108	0.071	0.1837	0.0108	0.0587	0.2315	0.0108	0.0466	0.3026	0.0198	0.0655
WFDC8	0.5312	0.0288	0.0542	0.4998	0.0306	0.0612	0.61	0.0288	0.0472	0.2613	0.0199	0.0762
WFDC9	1.1097	0.0196	0.0177	0.278	0.0049	0.0175	0.278	0.0049	0.0175	0.5558	0.0297	0.0535
XPNPEP1	0.0283	0.0014	0.048	0.0187	0.0007	0.0363	0.0135	0.0007	0.0504	0	0	0.0528
YWHAB	0	0	0.0711	0	0	0.0577	0	0	0.0644	0	0	0.038
YWHAE	0.095	0.0017	0.0178	0.071	0.0017	0.0238	0.0469	0.0017	0.0361	0.0566	0.0017	0.0299
YWHAG	0	0	0.0791	0	0	0.0791	0	0	0.0867	0	0	0.0945
YWHAQ	0.4813	0.0179	0.0371	0.5799	0.0179	0.0308	0.4813	0.0179	0.0371	0.7279	0.0179	0.0245
YWHAZ	0	0	0.0123	0	0	0.0061	0	0	0.0061	0	0	0.0123
ZPBP	0.3442	0.0126	0.0367	0.4474	0.0164	0.0368	0.173	0.0101	0.0582	0.3899	0.0186	0.0476

Gene	MH_ω	MH_Ka	MH_Ks	MC_ω	MC_Ka	MC_Ks	MG_ω	MG_Ka	MG_Ks	MO_ω	MO_Ka	MO_Ks
VAMP2	0	0	0.0618	0	0	0.049	0	0	0.0618	0	0	0.0241
VAMP8	0	0	0.0922	0	0	0.0602	0	0	0.0923	0	0	0.0927
VAT1	0.1779	0.021	0.1182	0.1741	0.0199	0.114	0.1481	0.0175	0.1184	0.1476	0.0176	0.119
VCL	0.0383	0.002	0.0509	0.0393	0.002	0.0497	0.0403	0.002	0.0484	0.0767	0.0039	0.0509
VCP	0.0106	0.0005	0.0517	0.0089	0.0005	0.061	0.0105	0.0005	0.0517	0.0106	0.0005	0.0517
VPS28	0.039	0.0076	0.1956	0.0507	0.0095	0.188	0.0663	0.0121	0.1826	0.0841	0.0165	0.1959
VTN	0.4619	0.0417	0.0904	0.4297	0.0388	0.0904	0.4122	0.0425	0.1031	0.4253	0.0364	0.0856
VWA1	0.164	0.0223	0.136									
VWF	0.1562	0.0174	0.1115	0.1683	0.0184	0.1092				0.1637	0.0177	0.1083
WFDC2	0.2238	0.0329	0.1472	0.2463	0.0329	0.1338	0.2733	0.0329	0.1206	0.2982	0.0403	0.1353
WFDC8	0.6712	0.0646	0.0963	0.5815	0.0646	0.1112	0.6237	0.0646	0.1037	0.4513	0.0545	0.1208
WFDC9	0.6193	0.0632	0.102	0.4716	0.0476	0.101	0.4716	0.0476	0.101	0.7379	0.0741	0.1004
XPNPEP1	0.0474	0.0027	0.0575	0.0371	0.002	0.0551	0.0328	0.002	0.0623	0.0189	0.0014	0.0721
YWHAB	0	0	0.0642	0	0	0.051	0	0	0.0576	0	0	0.0444
YWHAE	0.1428	0.0017	0.0118	0.2867	0.0017	0.0059	0.0948	0.0017	0.0178	0.1428	0.0017	0.0118
YWHAG	0	0	0.1034	0	0	0.0897	0	0	0.1034	0	0	0.0966
YWHAQ	0.1166	0.0036	0.0305	0.1464	0.0036	0.0243	0.1166	0.0036	0.0305	0.1166	0.0036	0.0305
YWHAZ	0	0	0.0123	0	0	0.0061	0	0	0.0061	0	0	0.0123
ZPBP	0.3311	0.0184	0.0556	0.3291	0.019	0.0578	0.2406	0.0203	0.0843	0.3411	0.0237	0.0696

Gene	Mgi_*ω*	Mgi_*Ka*	Mgi_*Ks*
VAMP2	0	0	0.0241
VAMP8	0	0	0.0602
VAT1	0.1072	0.014	0.1305
VCL	0.0641	0.0035	0.0543
VCP	0.0381	0.0022	0.0576
VPS28	0.0543	0.0127	0.2331
VTN	0.5425	0.0506	0.0933
VWA1	0.175	0.0214	0.1223
VWF			
WFDC2	0.2413	0.0292	0.1209
WFDC8	0.4156	0.0552	0.1328
WFDC9	0.5248	0.0426	0.0811
XPNPEP1	0.0202	0.0014	0.0672
YWHAB	0	0	0.0576
YWHAE	0.113	0.0034	0.03
YWHAG	0	0	0.1181
YWHAQ	0.4947	0.0215	0.0435
YWHAZ	0	0	0.0123
ZPBP	0.2834	0.0152	0.0536

Control estimates of pairwise *ω, Ka,* and *Ks*

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
ABCB11	0.2331	0.006	0.026	0.1866	0.0037	0.0196	0.2112	0.0086	0.0409	0.1616	0.0071	0.0438
ABCD3	0	0	0.0135	0.4029	0.0094	0.0233	0.1396	0.004	0.0285	0.0299	0.0013	0.0444
ABHD10	0	0	0.0045	0.1044	0.0029	0.0277	0.2628	0.0072	0.0276	0.1413	0.0072	0.0513
ABHD4	0	0	0.029	0	0	0.0247	0.1601	0.0071	0.0446	0.0715	0.0052	0.0723
ACCN1	0	0	0.0113				0.0428	0.0019	0.0444	0.4012	0.0467	0.1165
ACOT12	0.1666	0.0039	0.0236	0.1667	0.0039	0.0236	0.2758	0.0095	0.0343	0.2187	0.0139	0.0633
ACSM1				0.4667	0.0069	0.0147	0.3705	0.0216	0.0582			
ADAM29	0.2552	0.0114	0.0448	0.3217	0.0073	0.0228	0.3797	0.0168	0.0443	0.3639	0.015	0.0412
ADAM9	0.1495	0.0011	0.0071	0.149	0.0016	0.0107	0.0983	0.0027	0.027	0.1401	0.0053	0.038
ADAMTS8	0.2222	0.005	0.0227				0.2072	0.0086	0.0414			
ADAT2	0.1496	0.0023	0.0153	0.3002	0.0023	0.0076	0.148	0.0046	0.0309	0.4015	0.0092	0.0229
ADH1A	0.3941	0.0059	0.015	0.4097	0.0642	0.1566	0.1804	0.0118	0.0656	0.2168	0.0148	0.0682
ADNP2	0.0721	0.0008	0.0109	0.1083	0.0016	0.015	0.1173	0.0055	0.0472	0.1832	0.0091	0.0497
ADRA1B	0.459	0.012	0.0262	0.1379	0.0035	0.0253	0.0766	0.0017	0.0228	0.1651	0.0091	0.0553
AGAP10	0.7679	0.0266	0.0347				0.7887	0.0542	0.0687	0.8982	0.0604	0.0673
AGGF1	0.852	0.0054	0.0064	0.6204	0.006	0.0096	0.2171	0.0084	0.0389	0.2629	0.0089	0.0338
AGPAT2	0.2455	0.0072	0.0293	0.3306	0.0183	0.0555	0.2654	0.013	0.0489	0.2253	0.0149	0.0661
AHSA1	0.3011	0.0013	0.0043	0	0	0.0173	0.1192	0.0026	0.0216	0.0747	0.0013	0.0172
ALDH1A3	0.0531	0.0009	0.0162	0.2399	0.0026	0.0108	0.1716	0.0082	0.048	0.1446	0.0058	0.0402
ALKBH3	0	0	0.0202	0.0603	0.0015	0.0254				0.0905	0.0077	0.0848
ALOX15	0.0732	0.0013	0.0184	0.4664	0.0312	0.0669	0.0826	0.0064	0.0776	0.1993	0.017	0.0853
AMBN	0.3201	0.001	0.0031	0.5276	0.0079	0.0149	0.2832	0.009	0.0317	1.7472	0.0271	0.0155
ANGEL2	0	0	0.0056	0.1481	0.0008	0.0056	0.0963	0.0042	0.0432	0.0583	0.0017	0.0285
ANKRD52	0.2563	0.0025	0.0098	0.0566	0.0009	0.0152	0.0168	0.0004	0.0247	0.2895	0.0121	0.0418
ANO1	0.1104	0.0027	0.0244	0.0728	0.0023	0.0316	0.105	0.0066	0.063	0.0743	0.0065	0.0878
APC2	0.1858	0.0049	0.0265	0.2005	0.0054	0.0269	0.2352	0.0137	0.0583	0.1581	0.0106	0.067
APOBEC1	1.1436	0.0073	0.0064				0.3867	0.0204	0.0526	0.2297	0.0185	0.0805
ARCN1	0	0	0.0028	0	0	0.0056	0.0269	0.0009	0.0316	0.0273	0.001	0.0355
ARHGAP19	0.0428	0.0009	0.0207	0.0855	0.0018	0.0206	0.1389	0.0056	0.0405	0.1353	0.0044	0.0327
ARHGAP4	0.038	0.0005	0.012	0.0852	0.0018	0.0215	0.2393	0.0119	0.0499	0.6108	0.0921	0.1508
ARHGEF25	0.083	0.0007	0.0087							0.3627	0.008	0.022
ARL6IP1	0	0	0.007	-1	0.0027	0	0.1224	0.0043	0.0355	0.077	0.0022	0.0282
ARV1	0.1442	0.0039	0.0268	0.4278	0.0048	0.0112	0.2429	0.0096	0.0396	0.2834	0.008	0.0282
ASB1	0	0	0.0197	0	0	0.0292	0.0328	0.0027	0.082	0.0476	0.0027	0.0565
ASCC3	0.2453	0.002	0.008	0.121	0.0014	0.0114	0.0945	0.0024	0.0254	0.0769	0.0026	0.0332
ASH2L	0.2013	0.0014	0.0069	0.076	0.0015	0.0193	0.1243	0.0038	0.0306	0.0559	0.0028	0.0496
ASPH	0.3598	0.0057	0.0158	0.2232	0.004	0.0179	0.1172	0.004	0.034	0.1177	0.0057	0.0485
ATAD2	0.2936	0.0041	0.0138				0.2128	0.0059	0.0279	0.2249	0.0063	0.028
ATAD5	0.6879	0.0063	0.0091	0.5584	0.0048	0.0086	0.4455	0.0146	0.0329	0.4709	0.0164	0.0348
ATG16L1	0.0779	0.0007	0.0093	0.1242	0.0014	0.0116	0.1078	0.0043	0.0403	0.0606	0.0029	0.0485
ATP10D	0.1622	0.0024	0.0151	0.2582	0.0049	0.0189	0.254	0.0103	0.0406	0.2114	0.0105	0.0495
ATP5H	0	0	0	0	0	0	0.3622	0.0107	0.0295	0.1071	0.0053	0.0498
B4GALT5	0.0596	0.0011	0.0188	0	0	0.0307	0.072	0.0023	0.0318	0.0533	0.0022	0.0421
BCCIP	-1	0.0054	0	1.0642	0.0109	0.0102	0.4449	0.0166	0.0373	0.6739	0.0247	0.0367
BCL9L	0.1867	0.0032	0.017	0.0759	0.0023	0.0301	0.1187	0.0042	0.0352	0.1063	0.0049	0.0464
BET1	0	0	0	0	0	0.0125	0	0	0.0149	0.2972	0.0037	0.0125
BLNK	0.2329	0.0029	0.0124	0.3901	0.0147	0.0376	0.1275	0.0048	0.0378	0.2831	0.0103	0.0365
BROX	0.1482	0.0021	0.0143				0.1262	0.0032	0.0252	0.1975	0.0042	0.0215
C10orf11	0.0777	0.0022	0.0287	0.9336	0.008	0.0086	0.187	0.0067	0.0359	0.4678	0.0203	0.0434
C11orf20	0.6138	0.0044	0.0072	0.0662	0.0044	0.0665	0.2411	0.0088	0.0365	0.6994	0.1026	0.1466
C11orf40	1.7451	0.0174	0.01	1.5495	0.0155	0.01				1.1032	0.1536	0.1392
C11orf80	0.3452	0.0084	0.0242	0.6725	0.0125	0.0187				0.5659	0.0567	0.1002
C11orf84	0.1116	0.0026	0.0237	0.1988	0.0071	0.0356	0.1267	0.0083	0.0652	0.6463	0.2314	0.358
C12orf5	0.9026	0.0049	0.0054	0.149	0.0016	0.0108	0.6538	0.0363	0.0556	0.3769	0.0081	0.0216
C14orf180	0.5344	0.0119	0.0222	2.4179	0.0178	0.0074	0.6588	0.0223	0.0339	1.3329	0.0299	0.0224
C14orf181	-1	0.0028	0				1.0767	0.0232	0.0215	0.7056	0.0201	0.0285
C17orf51	0.1729	0.002	0.0118				0.8927	0.0394	0.0441	0.5201	0.0533	0.1024
C19orf47	0.3422	0.0032	0.0093	0.4113	0.0064	0.0156	0.0963	0.0043	0.0443	0.0194	0.0012	0.0609
C19orf68	0.7794	0.0402	0.0515	0.1454	0.0026	0.0179	0.0734	0.0043	0.0591	0.1192	0.008	0.0667
C1orf101	1.4059	0.0087	0.0062	0.2323	0.0075	0.0323	0.3899	0.0217	0.0555	0.4001	0.0234	0.0586
C1orf187	0.3401	0.0026	0.0076	0.2349	0.0065	0.0277	0.3325	0.0129	0.0389	0.1315	0.0077	0.0589
C1orf27	-1	0.0019	0	0.5854	0.0038	0.0065	0.7319	0.0048	0.0065	0.1284	0.0038	0.0297
C1orf43	0.6454	0.0035	0.0054	0	0	0.0164	0	0	0.0275	0.1055	0.0035	0.0332
C1QTNF7	0	0	0.0094	0.4912	0.0046	0.0094	0.0804	0.0031	0.0383	0.145	0.0077	0.0533
C20orf160	0	0	0.01				0.1735	0.0055	0.0316	0.0425	0.0016	0.0378
C21orf59	0.1282	0.0037	0.029				0.0988	0.0067	0.0678	0.0576	0.0052	0.0905
C22orf41	0.2537	0.0048	0.019	0.061	0.0048	0.0792	0.1667	0.0097	0.0582			
C4orf31	0.0245	0.0008	0.0313	0.0182	0.0008	0.042	0.0685	0.0031	0.0447	0.1282	0.0054	0.0419
C4orf33	0.6954	0.0108	0.0156	0.551	0.0086	0.0157	0.2699	0.0174	0.0645	0.348	0.0196	0.0563
C4orf7	0.3249	0.0053	0.0163				0.7525	0.0377	0.0502	1.3382	0.0662	0.0495
C7orf60	-1	0.0021	0	0.2928	0.0011	0.0036	0.0638	0.0021	0.0335	0.1161	0.0021	0.0184
C8orf39	-1	0.0044	0	-1	0.0088	0	-1	0.009	0	2.3328	0.0155	0.0067
C8orf40	0	0	0.0148	0	0	0	0	0	0.0148	0	0	0.0452
C9orf142	0.755	0.0057	0.0075	0.3699	0.0068	0.0184	0.2618	0.0114	0.0434	0.6654	0.0206	0.0309
C9orf46	0	0	0.013	0	0	0.0263				0.0524	0.0035	0.0677
C9orf9	0.3741	0.0203	0.0542	0.1381	0.0027	0.0193	0.1079	0.0053	0.0495	0.1811	0.0107	0.0594
CA10	0	0	0.0091	0.071	0.0017	0.0246	0	0	0.0276	0	0	0.0659
CA5A	1.0845	0.0101	0.0093	0.3362	0.0188	0.056						
CACNG6	0.255	0.0036	0.014	0.5899	0.0213	0.0361				0.3422	0.0185	0.0541
CAPN11	0.922	0.0089	0.0097	0.4113	0.0098	0.0239	0.25	0.0101	0.0405	0.3663	0.0285	0.0778
CAPN7	0.1168	0.0011	0.0091	0.289	0.0029	0.0101	0.0769	0.0021	0.0276	0.1403	0.0051	0.036
CAPS2	0.4384	0.0085	0.0193	0.3554	0.0077	0.0217				0.3654	0.0274	0.0749
CARD11	0.0304	0.0008	0.0249	0.4711	0.0237	0.0502	0.031	0.0019	0.0612	0.0569	0.0038	0.0666
CASP8	0.1374	0.0022	0.0157	0.0451	0.0015	0.0322	0.1627	0.0065	0.04	0.2222	0.0098	0.0441
CAV1	0	0	0.0173	0	0	0.026	0.0456	0.0024	0.0531	0.0457	0.0024	0.053
CCDC115	0	0	0.0071	0	0	0.0142	0.2939	0.0128	0.0434	0.3541	0.0128	0.0361
CCDC132	0.3258	0.0036	0.0109	0.0927	0.001	0.0104	0.1249	0.0048	0.0387	0.0346	0.0014	0.0401
CCDC157	1.907	0.0102	0.0054				0.4111	0.0156	0.0379	0.5277	0.0243	0.0461
CCDC36	0.3769	0.0058	0.0154	0.5675	0.0116	0.0205	0.7264	0.0168	0.0231	0.9511	0.022	0.0231
CCDC68	-1	0.0025	0	1.6506	0.0077	0.0046	0.3411	0.0064	0.0187	0.6679	0.0168	0.0252
CCDC69	0.2005	0.003	0.0147	0.1502	0.003	0.0197	0.2969	0.0119	0.04	0.3604	0.0163	0.0453
CCDC73	0.3634	0.0039	0.0107	0.7085	0.0156	0.0221	0.8043	0.0146	0.0181	0.4103	0.0154	0.0377
CCDC82	0.1986	0.0031	0.0155	0.7707	0.0079	0.0102	0.8742	0.0163	0.0187	0.4673	0.0172	0.0368
CCL24	0.4166	0.015	0.0361				0.3605	0.0265	0.0736	0.622	0.0329	0.0529
CCNB1	-1	0.001	0				0.6235	0.0061	0.0098	0.1954	0.0072	0.0368
CCRL1	0.293	0.0037	0.0127	0.1955	0.0025	0.0127	0.2009	0.0087	0.0433	0.1607	0.0062	0.0387
CD2AP	0.1738	0.0027	0.0157	0.2279	0.0041	0.018	0.2447	0.0089	0.0365	0.2801	0.0089	0.0319
CD300C	0.4477	0.0163	0.0364	0.4553	0.017	0.0374	0.6753	0.0412	0.0611			
CD69	0.2715	0.0021	0.0079				0.2674	0.0086	0.0322	0.2286	0.0151	0.0661
CDC20	0.6483	0.0036	0.0055	0	0	0.0165	0.0356	0.0009	0.0249	0.0289	0.0009	0.0307
CDC23	0.0605	0.0007	0.0121				0.0713	0.0018	0.0256	0.072	0.0026	0.0355
CDC37	0.0363	0.0013	0.037	0	0	0.0394	0.0156	0.0013	0.0827	0	0	0.0881
CDCA2	0.3911	0.0055	0.0142				0.3971	0.019	0.0478	0.5291	0.0229	0.0433
CDCA3	-1	0.0034	0	0.2333	0.0046	0.0197	0.346	0.0068	0.0196			
CDK13	0.1231	0.0009	0.0072	0.1578	0.0013	0.0085	0.0779	0.0015	0.0194	0.057	0.0014	0.024
CDK9	0	0	0.0235	0	0	0.0196	0.0576	0.0026	0.0453	0	0	0.0648
CDT1	0.225	0.0079	0.0352	0.2757	0.0088	0.0319	0.2437	0.0264	0.1084	0.2308	0.0239	0.1037

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
ABCB11	0.2396	0.0203	0.0845	0.1384	0.0033	0.0241	0.1261	0.0058	0.046	0.1999	0.0106	0.0528
ABCD3	0.0647	0.0053	0.0821	0.2866	0.0098	0.0342	0.1214	0.0041	0.0342	0.0301	0.0014	0.0459
ABHD10	0.2076	0.0116	0.0561	0.1257	0.0029	0.023	0.3164	0.0072	0.0229	0.1559	0.0072	0.0465
ABHD4	0.0681	0.0065	0.095	0	0	0.0289	0.1601	0.0071	0.0446	0.1028	0.0052	0.0503
ACCN1	0.0447	0.0034	0.0763				0.0428	0.0019	0.0444	0.4009	0.0467	0.1166
ACOT12	0.1093	0.0107	0.0976	0.1794	0.0047	0.0263	0.2764	0.0103	0.0371	0.2673	0.0158	0.0593
ACSM1	0.4655	0.0506	0.1087									
ADAM29	0.444	0.0475	0.1071	0.3264	0.0146	0.0448	0.3218	0.0154	0.0478	0.2864	0.016	0.0557
ADAM9	0.1526	0.0101	0.0664	0.3739	0.0027	0.0071	0.1594	0.0037	0.0233	0.1865	0.0064	0.0342
ADAMTS8	0.0968	0.0071	0.0732				0.1479	0.0071	0.0478			
ADAT2	0.0784	0.0069	0.0879	0	0	0.023	0.0743	0.0023	0.0308	0.3023	0.0069	0.0228
ADH1A	0.2786	0.0269	0.0966	0.4202	0.0657	0.1564	0.2474	0.0142	0.0575	0.3537	0.0184	0.052
ADNP2	0.0684	0.0075	0.1099	0.1297	0.0024	0.0188	0.124	0.0063	0.051	0.1622	0.0091	0.0562
ADRA1B	0.0716	0.0035	0.0488	0.2921	0.0138	0.0473	0.2696	0.0121	0.0447	0.1485	0.0114	0.077
AGAP10	0.6321	0.0784	0.1241				0.95	0.0564	0.0594	0.9634	0.0616	0.0639
AGGF1	0.2275	0.0115	0.0507	0.3128	0.0053	0.0169	0.1982	0.009	0.0456	0.2333	0.0095	0.0408
AGPAT2	0.2443	0.0204	0.0837	0.4003	0.025	0.0624	0.1579	0.0102	0.0647	0.1567	0.0123	0.0787
AHSA1	0.0243	0.0013	0.053	0.0998	0.0013	0.0129	0.2246	0.0039	0.0172	0.2003	0.0026	0.0129
ALDH1A3	0.0734	0.0078	0.1062	0.1062	0.0017	0.0163	0.1697	0.0093	0.0546	0.1096	0.0058	0.053
ALKBH3				0.1011	0.0015	0.0151				0.0905	0.0077	0.0848
ALOX15	0.2455	0.0257	0.1046	0.5299	0.0305	0.0575	0.0964	0.0064	0.0665	0.1881	0.0156	0.0831
AMBN	0.9652	0.0474	0.0491	0.5888	0.0068	0.0116	0.2802	0.008	0.0284	2.1064	0.0261	0.0124
ANGEL2	0.0962	0.0043	0.0451	0.1481	0.0008	0.0056	0.0963	0.0042	0.0432	0.0484	0.0017	0.0343
ANKRD52	0.0077	0.0004	0.0551	0.2561	0.0026	0.0101	0.1059	0.0021	0.0198	0.353	0.0139	0.0393
ANO1	0.0752	0.0097	0.129	0.0417	0.0014	0.0338	0.0889	0.0058	0.0657	0.0661	0.0057	0.0857
APC2	0.0935	0.0129	0.1374	0.1969	0.008	0.0404	0.2301	0.0166	0.0721	0.1561	0.0123	0.0788
APOBEC1	0.319	0.0279	0.0875				0.2785	0.0166	0.0596	0.1679	0.0147	0.0878
ARCN1	0.0487	0.0026	0.0525	0	0	0.0028	0.0297	0.0009	0.0287	0.0301	0.001	0.0322
ARHGAP19	0.1329	0.0089	0.0667	0.0247	0.0009	0.0358	0.0827	0.0047	0.0568	0.0737	0.0035	0.0481
ARHGAP4	0.1249	0.0138	0.1108	0.0601	0.0014	0.0228	0.2145	0.0114	0.0532	0.601	0.0916	0.1524
ARHGEF25	0.2309	0.0153	0.0663							0.4138	0.0073	0.0175
ARL6IP1	0.0866	0.0043	0.0502	0.3168	0.0027	0.0085	0.1015	0.0043	0.0428	0.0613	0.0022	0.0354
ARV1	0.1616	0.0112	0.0694	0.7273	0.0097	0.0133	0.24	0.0097	0.0404	0.2879	0.0097	0.0336
ASB1	0.0318	0.004	0.1269	0	0	0.0207	0.0346	0.0027	0.0777	0.0611	0.0027	0.044
ASCC3	0.0824	0.0046	0.0555	0.1699	0.0022	0.0127	0.118	0.003	0.0254	0.0965	0.0033	0.0346
ASH2L	0.0525	0.0042	0.0794	0	0	0.012	0.0999	0.0023	0.0228	0.0328	0.0014	0.0423
ASPH	0.2035	0.0152	0.0748	0.3391	0.0074	0.0218	0.1947	0.0074	0.0379	0.1798	0.0093	0.0517
ATAD2	0.211	0.0111	0.0524				0.13	0.0041	0.0312	0.1909	0.006	0.0313
ATAD5	0.4563	0.0265	0.0582	0.699	0.0053	0.0076	0.5097	0.0154	0.0302	0.5534	0.0178	0.0322
ATG16L1	0.0674	0.0051	0.0753	0.062	0.0007	0.0116	0.0897	0.0036	0.0403	0.0454	0.0022	0.0486
ATP10D	0.2372	0.0182	0.0769	0.1508	0.0024	0.0161	0.179	0.0083	0.0463	0.1669	0.0086	0.0516
ATP5H	0.165	0.0134	0.0813	0	0	0	0.3622	0.0107	0.0295	0.1071	0.0053	0.0498
B4GALT5	0.0208	0.0011	0.054	0.0943	0.0012	0.013	0.2922	0.0034	0.0118	0.1487	0.0034	0.0227
BCCIP	0.4237	0.0246	0.0582	1.3294	0.0136	0.0102	0.5564	0.0208	0.0373	0.7101	0.0261	0.0367
BCL9L	0.0858	0.0056	0.0653	0.1119	0.0034	0.0304	0.1314	0.0048	0.0363	0.1063	0.0054	0.0511
BET1	-1	0.0074	0	0	0	0.0125	0	0	0.0149	0.2972	0.0037	0.0125
BLNK	0.1435	0.0097	0.0675	0.3634	0.0137	0.0376	0.1018	0.0039	0.0379	0.2112	0.0092	0.0437
BROX	0.0829	0.0042	0.0511				0.1774	0.0032	0.0179	0.2974	0.0042	0.0143
C10orf11	0.1927	0.0112	0.0583	0.3089	0.0053	0.0172	0.1244	0.0045	0.0359	0.4678	0.0203	0.0434
C11orf20	0.5428	0.0301	0.0555	0.1494	0.0088	0.059	0.5629	0.0143	0.0255	0.8112	0.1089	0.1343
C11orf40				0.92	0.0124	0.0134				1.0639	0.1602	0.1505
C11orf80				0.5162	0.009	0.0175				0.5568	0.0612	0.11
C11orf84	0.0733	0.0071	0.0964	0.1669	0.0053	0.0318	0.1094	0.0066	0.0607	0.6665	0.2627	0.3942
C12orf5	0.2959	0.0197	0.0664	0.3968	0.0065	0.0163	0.6167	0.0403	0.0653	0.4816	0.013	0.0271
C14orf180	1.1852	0.1156	0.0976	0.8035	0.0239	0.0298	0.6874	0.0284	0.0414	0.7972	0.0361	0.0453
C14orf181							1.0727	0.023	0.0214	0.6014	0.0171	0.0284
C17orf51							0.6456	0.0371	0.0574	0.4374	0.051	0.1165
C19orf47	0.121	0.0107	0.0884	0.772	0.0096	0.0125	0.1817	0.0075	0.0411	0.0826	0.0047	0.0573
C19orf68	0.1068	0.0118	0.1105	1.0954	0.0488	0.0445	0.465	0.0419	0.0901	0.6105	0.0638	0.1045
C1orf101	0.7348	0.0625	0.085	0.3515	0.0111	0.0315	0.4668	0.0259	0.0555	0.5011	0.0293	0.0585
C1orf187	0.1407	0.013	0.0921	0.2353	0.0065	0.0277	0.333	0.0129	0.0388	0.1414	0.0077	0.0547
C1orf27	0.2629	0.0105	0.0401	0.5862	0.0038	0.0065	0.733	0.0048	0.0065	0.1286	0.0038	0.0297
C1orf43	0.022	0.0018	0.0797	0.1598	0.0035	0.022	0.1057	0.0035	0.0332	0.1806	0.007	0.0389
C1QTNF7	0.0785	0.0062	0.0787	-1	0.0046	0	0.1079	0.0031	0.0286	0.1784	0.0077	0.0433
C20orf160	0.6522	0.0942	0.1445				0.1989	0.0055	0.0276	0.0425	0.0016	0.0378
C21orf59	0.053	0.0067	0.1266				0.1001	0.006	0.0595	0.0545	0.0045	0.082
C22orf41	0.0974	0.0097	0.0997	0	0	0.0588	0.1258	0.0048	0.0384			
C4orf31	0.0856	0.0069	0.0807	0.0364	0.0015	0.042	0.0857	0.0038	0.0447	0.1378	0.0061	0.0446
C4orf33	0.3026	0.0196	0.0648	0.2067	0.0065	0.0314	0.2436	0.0197	0.0808	0.2154	0.0175	0.081
C4orf7	4.444	0.0728	0.0164				0.9749	0.0322	0.0331	2.2074	0.072	0.0326
C7orf60	0.0226	0.0012	0.0537	0.2923	0.0011	0.0037	0.0637	0.0021	0.0335	0.1159	0.0021	0.0184
C8orf39	-1	0.0223	0	-1	0.0044	0	-1	0.0045	0	1.6614	0.0111	0.0067
C8orf40	0	0	0.061	0	0	0.0148	0	0	0.0299	0	0	0.061
C9orf142	0.2524	0.0159	0.0631	0.1852	0.0057	0.0305	0.1833	0.0085	0.0463	0.1468	0.0056	0.0385
C9orf46	0.1044	0.0071	0.068	0	0	0.0398				0.0432	0.0035	0.082
C9orf9	0.215	0.0244	0.1133	0.3243	0.0176	0.0541	0.3981	0.0258	0.0647	0.4208	0.0314	0.0746
CA10	0	0	0.037	0.095	0.0017	0.0184	0	0	0.037	0	0	0.0758
CA5A				0.3529	0.0236	0.0669						
CACNG6	1.2867	0.018	0.014	0.4299	0.0213	0.0496				0.2609	0.0185	0.071
CAPN11	0.2413	0.0249	0.1032	0.373	0.0126	0.0339	0.2288	0.0119	0.0522	0.3362	0.0256	0.0762
CAPN7	0.0658	0.0047	0.0713	0.2893	0.0017	0.006	0.0824	0.0021	0.0258	0.1168	0.004	0.0342
CAPS2	0.4492	0.0398	0.0887	0.4789	0.0118	0.0246				0.3775	0.0306	0.081
CARD11	0.01	0.0012	0.1196	0.5261	0.0237	0.045	0.0365	0.0019	0.0519	0.0619	0.0038	0.0613
CASP8	0.2967	0.0231	0.0777	0.136	0.0044	0.0321	0.2176	0.0087	0.04	0.2225	0.0098	0.044
CAV1	0	0	0.044	0	0	0.0439	0.0456	0.0024	0.053	0.0339	0.0024	0.0715
CCDC115	0.3161	0.0232	0.0734	0	0	0.0071	0.3545	0.0128	0.036	0.4448	0.0128	0.0287
CCDC132	0.0335	0.0018	0.0532	0.2088	0.0029	0.0139	0.1645	0.0066	0.0403	0.0777	0.0032	0.0418
CCDC157	0.3724	0.028	0.0752				0.3796	0.0139	0.0366	0.5348	0.0237	0.0443
CCDC36	0.4697	0.0253	0.0538	0.4958	0.0102	0.0205	0.6623	0.0153	0.0231	0.8864	0.0205	0.0231
CCDC68	0.3223	0.0154	0.0478	1.0985	0.0051	0.0046	0.3411	0.0064	0.0187	0.5555	0.014	0.0252
CCDC69	0.2249	0.0149	0.0661	0.1999	0.0029	0.0148	0.3387	0.0119	0.035	0.4047	0.0163	0.0403
CCDC73	0.5748	0.0289	0.0504	0.9007	0.0157	0.0174	1.0135	0.015	0.0148	0.4605	0.0159	0.0345
CCDC82	0.739	0.0451	0.061	0.2126	0.0044	0.0206	0.4688	0.0132	0.0281	0.2952	0.0139	0.0471
CCL24	0.4905	0.0572	0.1167				0.4396	0.0266	0.0605	0.766	0.0323	0.0422
CCNB1	0.1528	0.0061	0.0399				0.5192	0.0051	0.0098	0.1674	0.0062	0.0368
CCRL1	0.3977	0.0188	0.0473	0.1463	0.0012	0.0085	0.127	0.005	0.039	0.1443	0.005	0.0344
CD2AP	0.2463	0.0173	0.0701	0.1215	0.0014	0.0112	0.2084	0.0062	0.0296	0.2467	0.0062	0.025
CD300C	0.9038	0.0752	0.0832	0.3796	0.0193	0.0508	0.5553	0.0414	0.0745			
CD69	0.4513	0.0374	0.0828				0.2685	0.0065	0.024	0.225	0.0129	0.0575
CDC20	0.0228	0.0018	0.0775	0.3229	0.0036	0.011	0.2297	0.0044	0.0194	0.1999	0.0045	0.0223
CDC23	0.0585	0.004	0.0689				0.06	0.0015	0.0244	0.0691	0.0022	0.0317
CDC37	0	0	0.1728	0.0507	0.0019	0.0375	0	0	0.0578	0	0	0.099
CDCA2	0.3508	0.0292	0.0832				0.3438	0.0185	0.0539	0.455	0.0225	0.0493
CDCA3	0.1704	0.0068	0.0397	0.3499	0.0069	0.0197	0.5195	0.0102	0.0196			
CDK13	0.0889	0.0027	0.0299	0.1753	0.0017	0.0096	0.0995	0.0021	0.0213	0.0747	0.0017	0.0229
CDK9	0	0	0.0901	0	0	0.0275	0.0477	0.0026	0.0547	0	0	0.0733
CDT1	0.2103	0.0287	0.1365	0.1694	0.0093	0.0547	0.22	0.0253	0.1152	0.2034	0.023	0.1128

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
ABCB11	0.2379	0.0207	0.087	0.1619	0.0062	0.0381	0.1856	0.0081	0.0439	0.241	0.0178	0.0741
ABCD3	0.0615	0.0055	0.09	0.3196	0.0137	0.0428	0.1654	0.0108	0.0653	0.1519	0.0151	0.0995
ABHD10	0.2272	0.0116	0.0512	0.2175	0.0102	0.0467	0.1535	0.0102	0.0661	0.1723	0.0131	0.076
ABHD4	0.0716	0.0065	0.0904	0.1421	0.0072	0.0503	0.0948	0.0052	0.0546	0.0682	0.0065	0.0948
ACCN1	0.0447	0.0034	0.0763									
ACOT12	0.1376	0.0131	0.0949	0.3239	0.0103	0.0317	0.2807	0.0154	0.055	0.1517	0.0131	0.0861
ACSM1				0.4502	0.0239	0.0532				0.5273	0.0531	0.1007
ADAM29	0.438	0.0498	0.1137	0.4162	0.0184	0.0443	0.4419	0.0182	0.0412	0.5144	0.0523	0.1016
ADAM9	0.1793	0.0112	0.0625	0.0786	0.0021	0.027	0.126	0.0048	0.038	0.1533	0.0096	0.0626
ADAMTS8	0.0936	0.006	0.0641									
ADAT2	0.0525	0.0046	0.0875	0.0994	0.0023	0.023	0.4551	0.0069	0.0152	0.058	0.0046	0.0792
ADH1A	0.3677	0.0293	0.0798	0.3682	0.0719	0.1952	0.4382	0.0725	0.1654	0.37	0.0765	0.2067
ADNP2	0.0684	0.0075	0.1099	0.1511	0.0069	0.0459	0.2227	0.0102	0.0459	0.0874	0.0094	0.1076
ADRA1B	0.1931	0.0138	0.0715	0.1052	0.0035	0.0332	0.1729	0.0114	0.0661	0.1251	0.0061	0.0489
AGAP10	0.7187	0.0811	0.1128									
AGGF1	0.1894	0.0109	0.0576	0.2186	0.0083	0.0379	0.2956	0.0095	0.0321	0.2426	0.0123	0.0507
AGPAT2	0.2159	0.0217	0.1007	0.3013	0.0238	0.079	0.2193	0.026	0.1184	0.327	0.0351	0.1072
AHSA1	0.0533	0.0026	0.0484	0.1192	0.0026	0.0216	0.0747	0.0013	0.0172	0.0243	0.0013	0.053
ALDH1A3	0.0672	0.0069	0.1032	0.2361	0.0113	0.0481	0.1455	0.0068	0.0466	0.0865	0.0087	0.1002
ALKBH3							0.1087	0.0092	0.0848			
ALOX15	0.2578	0.0264	0.1023	0.3259	0.0376	0.1152	0.3705	0.0478	0.1291	0.3859	0.0552	0.143
AMBN	1.0112	0.0464	0.0459	0.3876	0.011	0.0285	1.5515	0.0309	0.0199	1.0519	0.0497	0.0472
ANGEL2	0.1033	0.0043	0.042	0.1341	0.005	0.0372	0.0875	0.0025	0.0285	0.1341	0.0052	0.0389
ANKRD52	0.045	0.0021	0.0472	0.0211	0.0004	0.0204	0.3086	0.0125	0.0407	0.009	0.0004	0.0488
ANO1	0.0732	0.0089	0.1217	0.0796	0.0055	0.0696	0.0611	0.0053	0.087	0.0625	0.0082	0.1305
APC2	0.1065	0.0153	0.1435	0.2421	0.0155	0.064	0.1461	0.011	0.0755	0.1017	0.014	0.1375
APOBEC1	0.2541	0.0241	0.0949									
ARCN1	0.0517	0.0026	0.0495	0.033	0.0009	0.0258	0.0301	0.001	0.0322	0.0517	0.0026	0.0495
ARHGAP19	0.0857	0.0071	0.0829	0.0856	0.0037	0.0437	0.0741	0.0026	0.0357	0.1013	0.0071	0.0699
ARHGAP4	0.1201	0.0133	0.1108	0.2419	0.0125	0.0515	0.6251	0.0926	0.1481	0.129	0.0131	0.1017
ARHGEF25	0.2373	0.0145	0.0613									
ARL6IP1	0.0754	0.0043	0.0576	0.2083	0.0054	0.0259	0.1575	0.0027	0.0171	0.1554	0.0054	0.0348
ARV1	0.1477	0.0107	0.0722	0.5139	0.0145	0.0281	0.7611	0.0128	0.0168	0.2791	0.0161	0.0575
ASB1	0.0388	0.004	0.1042	0.0293	0.0028	0.0958	0.0471	0.0028	0.0595	0.0314	0.0042	0.134
ASCC3	0.0955	0.0054	0.0562	0.097	0.0026	0.0267	0.0811	0.0028	0.0339	0.0883	0.0048	0.054
ASH2L	0.0387	0.0028	0.0718	0.0912	0.0024	0.0266	0.0314	0.0015	0.0466	0.0406	0.0029	0.0722
ASPH	0.2103	0.0175	0.083	0.158	0.0057	0.0359	0.1468	0.0074	0.0503	0.2086	0.0169	0.0809
ATAD2	0.2047	0.0107	0.0525									
ATAD5	0.4901	0.0272	0.0556	0.4712	0.0151	0.0321	0.4988	0.0168	0.0337	0.5484	0.0268	0.0489
ATG16L1	0.0577	0.0043	0.0753	0.1144	0.0043	0.0379	0.0637	0.0029	0.0461	0.0695	0.0051	0.0729
ATP10D	0.1954	0.0162	0.083	0.3359	0.0077	0.023	0.2851	0.0077	0.0271	0.2683	0.0178	0.0664
ATP5H	0.165	0.0134	0.0813	0.3622	0.0107	0.0295	0.1071	0.0053	0.0498	0.165	0.0134	0.0813
B4GALT5	0.0655	0.0022	0.0343	0.1125	0.0025	0.0218	0.0618	0.0025	0.0397	0.0229	0.0012	0.0534
BCCIP	0.4705	0.0274	0.0583	0.4026	0.0194	0.0482	0.5511	0.0261	0.0474	0.377	0.0261	0.0691
BCL9L	0.0998	0.0062	0.0616	0.0983	0.0042	0.043	0.0878	0.0047	0.0535	0.0624	0.0048	0.0772
BET1	-1	0.0074	0	0	0	0.0301	0.1474	0.0037	0.0252	0.5972	0.0074	0.0125
BLNK	0.1001	0.0068	0.0675	0.2446	0.0156	0.0639	0.3104	0.0226	0.0727	0.2174	0.0206	0.0946
BROX	0.0829	0.0042	0.0511									
C10orf11	0.1539	0.009	0.0583	0.4129	0.0107	0.0259	0.854	0.0297	0.0348	0.2544	0.0134	0.0526
C11orf20	0.6204	0.0362	0.0583	0.2245	0.0133	0.0591	0.6697	0.1066	0.1592	0.3673	0.0348	0.0946
C11orf40							1.0898	0.1647	0.1512			
C11orf80							0.5924	0.0571	0.0964			
C11orf84	0.0636	0.0066	0.1043	0.1021	0.0059	0.0577	0.689	0.2281	0.3311	0.079	0.0083	0.1044
C12orf5	0.3408	0.0247	0.0723	0.6809	0.038	0.0558	0.4505	0.0097	0.0216	0.3861	0.0213	0.0552
C14orf180	1.2304	0.1245	0.1012	0.8285	0.0345	0.0416	1.4031	0.0422	0.0301	1.2642	0.1305	0.1033
C14orf181												
C17orf51												
C19orf47	0.1128	0.0096	0.0851	0.1348	0.0064	0.0475	0.0915	0.0059	0.0648	0.1399	0.0128	0.0918
C19orf68	0.3731	0.051	0.1367	0.0626	0.0026	0.0415	0.1354	0.0073	0.0538	0.1396	0.0133	0.0954
C1orf101	0.7282	0.0637	0.0875	0.3593	0.0218	0.0606	0.3573	0.0241	0.0675	0.6528	0.0618	0.0947
C1orf187	0.1478	0.013	0.0877	0.3471	0.018	0.0519	0.1497	0.0114	0.0764	0.1459	0.0164	0.1124
C1orf27	0.2633	0.0105	0.04	0.5117	0.0067	0.0131	0.1573	0.0057	0.0365	0.2659	0.0125	0.0469
C1orf43	0.0615	0.0053	0.0858	0	0	0.0109	0.2137	0.0035	0.0164	0.0284	0.0018	0.0619
C1QTNF7	0.0904	0.0062	0.0684	0.0537	0.0015	0.0286	0.1421	0.0062	0.0434	0.0675	0.0046	0.0686
C20orf160	0.3442	0.0295	0.0857									
C21orf59	0.0506	0.006	0.1176									
C22orf41	0.0612	0.0048	0.0789	0.0483	0.0048	0.1				0.0335	0.0048	0.1441
C4orf31	0.092	0.0077	0.0835	0.0484	0.0023	0.0474	0.0972	0.0046	0.0473	0.0734	0.0061	0.0836
C4orf33	0.2152	0.0174	0.0811	0.3654	0.0174	0.0477	0.318	0.0152	0.0479	0.3177	0.0152	0.0479
C4orf7	4.8044	0.0787	0.0164									
C7orf60	0.0452	0.0024	0.0538	0.0286	0.0011	0.0373	0.0482	0.0011	0.0222	0.0208	0.0012	0.0583
C8orf39	-1	0.0178	0	-1	0.009	0	2.331	0.0155	0.0067	-1	0.0223	0
C8orf40	0	0	0.0771	0	0	0.0148	0	0	0.0452	0	0	0.061
C9orf142	0.1623	0.0142	0.0874	0.2164	0.0136	0.0631	0.4087	0.0205	0.0502	0.2603	0.0182	0.07
C9orf46	0.0861	0.0071	0.0824				0.0368	0.0035	0.0965	0.0732	0.0071	0.097
C9orf9	0.3285	0.0425	0.1295	0.1624	0.008	0.0494	0.2272	0.0135	0.0593	0.2155	0.0244	0.1131
CA10	0	0	0.037	0.04	0.0017	0.0436	0.021	0.0017	0.0831	0.0349	0.0017	0.0501
CA5A												
CACNG6	0.5096	0.0144	0.0283				0.3439	0.0298	0.0867	0.6025	0.0341	0.0566
CAPN11	0.2481	0.0252	0.1017	0.3005	0.0141	0.047	0.4104	0.0339	0.0826	0.2503	0.0283	0.1129
CAPN7	0.0679	0.0047	0.0691	0.1191	0.0029	0.0244	0.1677	0.005	0.0295	0.0926	0.0058	0.063
CAPS2	0.473	0.0427	0.0902				0.4075	0.031	0.0762	0.4346	0.0408	0.0938
CARD11	0.0107	0.0012	0.1121	0.323	0.0248	0.0769	0.3048	0.0266	0.0872	0.1809	0.0254	0.1406
CASP8	0.2662	0.0253	0.095	0.2697	0.0079	0.0294	0.3166	0.0148	0.0467	0.3744	0.0282	0.0752
CAV1	0	0	0.044	0.0552	0.0024	0.0439	0.039	0.0024	0.0621	0	0	0.0349
CCDC115	0.353	0.0232	0.0657	0.2939	0.0128	0.0434	0.3541	0.0128	0.0361	0.3161	0.0232	0.0734
CCDC132	0.0651	0.0036	0.0548	0.1331	0.0043	0.032	0.0151	0.0005	0.0333	0.0209	0.001	0.0461
CCDC157	0.39	0.0286	0.0733									
CCDC36	0.4418	0.0238	0.0539	0.5418	0.0153	0.0283	0.7252	0.0205	0.0283	0.3774	0.0223	0.0592
CCDC68	0.3223	0.0154	0.0478	0.3818	0.009	0.0235	0.8384	0.0168	0.0201	0.3416	0.018	0.0528
CCDC69	0.2432	0.0148	0.061	0.3361	0.0126	0.0375	0.3986	0.0171	0.0429	0.2454	0.0156	0.0636
CCDC73	0.5627	0.0302	0.0537	1.1097	0.0254	0.0229	0.6272	0.0265	0.0423	0.6643	0.041	0.0617
CCDC82	0.6192	0.0418	0.0676	0.7707	0.0159	0.0206	0.3658	0.015	0.0409	0.6326	0.0449	0.071
CCL24	0.5992	0.0614	0.1024									
CCNB1	0.1272	0.0051	0.0399									
CCRL1	0.3692	0.0175	0.0475	0.1592	0.0062	0.0389	0.1083	0.0037	0.0343	0.3432	0.0163	0.0474
CD2AP	0.2409	0.0152	0.0629	0.2061	0.0075	0.0366	0.2359	0.0075	0.032	0.2531	0.0165	0.0654
CD300C	0.7534	0.0829	0.11	0.861	0.0546	0.0634				1.0264	0.0889	0.0866
CD69	0.3835	0.0351	0.0916									
CDC20	0.0744	0.0053	0.0717	0.0459	0.0009	0.0193	0.0354	0.0009	0.025	0.0248	0.0018	0.0715
CDC23	0.0564	0.0037	0.0649									
CDC37	0.0078	0.0013	0.1729	0.0229	0.0018	0.0789	0	0	0.1255	0	0	0.1925
CDCA2	0.3248	0.0287	0.0883									
CDCA3	0.1703	0.0068	0.0397	0.3478	0.0115	0.0332				0.1695	0.0115	0.068
CDK13	0.0779	0.0027	0.0341	0.1197	0.0028	0.0232	0.0853	0.0021	0.0244	0.0988	0.0035	0.0353
CDK9	0	0	0.0901	0.0522	0.0026	0.05	0	0	0.069	0	0	0.0945
CDT1	0.2052	0.0263	0.1281	0.2005	0.0231	0.1152	0.176	0.021	0.1192	0.1704	0.0239	0.1401

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
ABCB11	0.2327	0.0105	0.045	0.2481	0.0201	0.0811	0.254	0.0195	0.0767
ABCD3	0.0776	0.004	0.0513	0.084	0.0073	0.087	0.0549	0.0053	0.0967
ABHD10	0.2355	0.0087	0.037	0.2822	0.0131	0.0464	0.1671	0.0102	0.0609
ABHD4	0.0636	0.0036	0.0561	0.0288	0.0018	0.062	0.043	0.0039	0.0902
ACCN1	0.4198	0.0544	0.1297	0.0845	0.0057	0.0677	0.379	0.0504	0.1329
ACOT12	0.3085	0.0178	0.0579	0.1736	0.0155	0.089	0.2266	0.0199	0.0877
ACSM1				0.4632	0.0526	0.1135			
ADAM29	0.3789	0.0153	0.0403	0.4603	0.0461	0.1001	0.4589	0.0471	0.1026
ADAM9	0.0933	0.0037	0.0398	0.1383	0.0088	0.0636	0.1319	0.0104	0.0789
ADAMTS8				0.0969	0.0076	0.0788			
ADAT2	1.2217	0.0092	0.0075	0.1264	0.0069	0.0546	0.1856	0.0116	0.0623
ADH1A	0.2094	0.019	0.0907	0.2515	0.0312	0.1241	0.3697	0.0336	0.0908
ADNP2	0.2107	0.0083	0.0395	0.0806	0.0075	0.0933	0.1211	0.0103	0.0851
ADRA1B	0.2132	0.0103	0.0482	0.0677	0.0035	0.0516	0.1473	0.0103	0.0698
AGAP10	0.6961	0.0529	0.076	0.6799	0.074	0.1088	0.6617	0.0828	0.1252
AGGF1	0.326	0.0095	0.0292	0.2518	0.0128	0.0506	0.2163	0.0115	0.0532
AGPAT2	0.0657	0.0049	0.0744	0.1263	0.0129	0.1022	0.1082	0.0111	0.1026
AHSA1	0.0597	0.0013	0.0216	0.0673	0.0039	0.0575	0.0589	0.0026	0.0438
ALDH1A3	0.1066	0.0044	0.0414	0.0774	0.0082	0.1064	0.0528	0.0058	0.1101
ALKBH3									
ALOX15	0.1527	0.0132	0.0866	0.2511	0.026	0.1036	0.2992	0.0313	0.1045
AMBN	1.0682	0.0303	0.0284	0.962	0.0508	0.0528	1.1722	0.048	0.0409
ANGEL2	0.1114	0.0042	0.0373	0.1014	0.0052	0.0514	0.1032	0.0043	0.0421
ANKRD52	0.3181	0.0117	0.0367	0	0	0.0472	0.2031	0.0119	0.0584
ANO1	0.0907	0.0073	0.081	0.0924	0.0107	0.1156	0.0879	0.0099	0.1128
APC2	0.1818	0.0128	0.0704	0.1393	0.021	0.1507	0.1056	0.0155	0.147
APOBEC1	0.2798	0.0166	0.0594	0.2982	0.026	0.0873	0.1957	0.0185	0.0945
ARCN1	0.0426	0.0019	0.0455	0.0527	0.0034	0.0647	0.0794	0.0039	0.0489
ARHGAP19	0.1503	0.0066	0.0437	0.1196	0.0103	0.0865	0.1537	0.0098	0.0635
ARHGAP4	0.6544	0.1101	0.1683	0.187	0.0176	0.094	0.347	0.054	0.1555
ARHGEF25							0.2705	0.0154	0.0569
ARL6IP1	0.0433	0.0022	0.0501	0.0596	0.0043	0.0728	0.0333	0.0022	0.0651
ARV1	0.1417	0.0048	0.0338	0.1065	0.008	0.0751	0.1007	0.0064	0.0634
ASB1	0	0	0.0733	0.0093	0.0013	0.1453	0.0141	0.0013	0.0952
ASCC3	0.09	0.0026	0.0288	0.0766	0.004	0.0527	0.0843	0.0044	0.0519
ASH2L	0.0745	0.0023	0.0306	0.0519	0.0038	0.0734	0.0361	0.0028	0.0769
ASPH	0.1952	0.0074	0.0378	0.2652	0.0169	0.0637	0.2191	0.0186	0.085
ATAD2	0.2417	0.006	0.0247	0.1929	0.0095	0.0491	0.1954	0.0098	0.0503
ATAD5	0.4429	0.021	0.0474	0.4264	0.0311	0.0731	0.4621	0.0279	0.0604
ATG16L1	0.1012	0.0044	0.0436	0.0785	0.0065	0.0831	0.0505	0.0044	0.0874
ATP10D	0.2013	0.0089	0.0443	0.2325	0.0179	0.0771	0.2221	0.0175	0.0786
ATP5H	0.4067	0.0161	0.0396	0.2664	0.0188	0.0707	0.2049	0.0189	0.092
B4GALT5	0.0824	0.0023	0.0278	0.0286	0.0011	0.04	0.0294	0.0011	0.0382
BCCIP	0.4154	0.011	0.0265	0.1785	0.0096	0.0539	0.6119	0.0143	0.0234
BCL9L	0.1382	0.0063	0.0453	0.1036	0.0067	0.0648	0.1133	0.0069	0.0612
BET1	0.1491	0.0045	0.0301	0.302	0.0045	0.0149	0.8961	0.0112	0.0125
BLNK	0.244	0.012	0.0491	0.1173	0.0087	0.0742	0.2729	0.0164	0.06
BROX	0.1264	0.0032	0.0251	0.067	0.0032	0.0474	0.0723	0.0042	0.0586
C10orf11	0.4392	0.0158	0.0359	0.0682	0.0045	0.0657	0.2766	0.0203	0.0736
C11orf20	0.8843	0.1076	0.1216	0.7197	0.0347	0.0482	0.8533	0.126	0.1477
C11orf40									
C11orf80									
C11orf84	0.6894	0.2315	0.3358	0.0981	0.0094	0.0963	0.6354	0.2291	0.3605
C12orf5	0.7528	0.0415	0.0552	0.5962	0.0501	0.0841	0.3241	0.0214	0.066
C14orf180	0.7045	0.0406	0.0576	1.1483	0.1223	0.1065	0.9586	0.1188	0.1239
C14orf181	1.6133	0.0347	0.0215						
C17orf51	0.5676	0.0695	0.1225						
C19orf47	0.0221	0.0012	0.0535	0.0788	0.0064	0.0812	0.0595	0.0059	0.0996
C19orf68	0.1304	0.01	0.0763	0.118	0.0129	0.1094	0.1511	0.0183	0.1214
C1orf101	0.559	0.0281	0.0503	0.8526	0.0686	0.0805	1.0395	0.064	0.0616
C1orf187	0.2691	0.0182	0.0675	0.2316	0.0234	0.1012	0.1757	0.0136	0.0774
C1orf27	0.2911	0.0067	0.0231	0.3357	0.0135	0.0401	0.218	0.0125	0.0572
C1orf43	0.2137	0.0035	0.0164	0.0284	0.0018	0.0619	0.0258	0.0018	0.0679
C1QTNF7	0.0729	0.0046	0.0634	0.0451	0.0031	0.0684	0.1049	0.0077	0.0737
C20orf160	0.0366	0.0015	0.0404	0.0865	0.0064	0.0739	0.0699	0.0067	0.0955
C21orf59	0.0169	0.0015	0.088	0.0337	0.003	0.0882	0.0149	0.0015	0.0996
C22orf41				0	0	0.1209			
C4orf31	0.1891	0.0069	0.0365	0.0886	0.0069	0.0779	0.1146	0.0092	0.0805
C4orf33	0.4125	0.0197	0.0476	0.4307	0.0241	0.0559	0.4396	0.0174	0.0396
C4orf7	0.9857	0.0661	0.0671	1.7915	0.0905	0.0505	1.8161	0.1062	0.0585
C7orf60	0	0	0.0373	0	0	0.0677	0	0	0.0491
C8orf39	1.0078	0.0067	0.0067	-1	0.0135	0	3.0176	0.0201	0.0066
C8orf40	0	0	0.061	0	0	0.0771	0	0	0.0771
C9orf142	0.2725	0.0136	0.0501	0.1956	0.0136	0.0698	0.3259	0.0228	0.0701
C9orf46							0.0315	0.0035	0.1122
C9orf9	0.1086	0.0053	0.0493	0.2331	0.0189	0.0809	0.1821	0.0175	0.0963
CA10	0	0	0.0758	0	0	0.0465	0	0	0.0858
CA5A									
CACNG6							0.5218	0.0311	0.0596
CAPN11	0.2996	0.0211	0.0704	0.1871	0.0219	0.1168	0.2998	0.0352	0.1173
CAPN7	0.0862	0.0032	0.037	0.035	0.0023	0.0669	0.0479	0.0035	0.0734
CAPS2							0.3419	0.0234	0.0685
CARD11	0.0591	0.0042	0.0706	0.0199	0.0024	0.121	0.0274	0.0036	0.1319
CASP8	0.3616	0.0144	0.0397	0.3734	0.0291	0.0778	0.3497	0.0309	0.0884
CAV1	0.0536	0.0048	0.0905	0.0929	0.0024	0.0261	0.0299	0.0024	0.081
CCDC115	0.1542	0.0102	0.0662	0.1965	0.0206	0.1048	0.2125	0.0206	0.0969
CCDC132	0.123	0.0046	0.0371	0.09	0.0048	0.0536	0.0257	0.0014	0.054
CCDC157	0.4693	0.0203	0.0433	0.3215	0.0255	0.0794	0.3646	0.0305	0.0836
CCDC36	0.7703	0.0197	0.0256	0.5128	0.0227	0.0443	0.4658	0.0275	0.0591
CCDC68	0.5154	0.0182	0.0354	0.2902	0.0167	0.0577	0.3562	0.0239	0.0672
CCDC69	0.4631	0.0163	0.0352	0.3269	0.0148	0.0454	0.3144	0.0193	0.0614
CCDC73	0.7263	0.0188	0.0259	0.736	0.0334	0.0454	0.6366	0.0333	0.0523
CCDC82	0.3815	0.0114	0.03	0.7088	0.0386	0.0545	0.5946	0.0408	0.0685
CCL24	0.5519	0.0441	0.08	0.5677	0.0655	0.1154	0.5261	0.0613	0.1165
CCNB1	0.2702	0.0072	0.0266	0.2048	0.0061	0.0298	0.1012	0.0051	0.0507
CCRL1	0.1647	0.005	0.0301	0.2876	0.015	0.0521	0.3895	0.015	0.0385
CD2AP	0.2509	0.0069	0.0273	0.2256	0.0158	0.0703	0.2421	0.0158	0.0654
CD300C				0.8738	0.0696	0.0797			
CD69	0.2939	0.0195	0.0663	0.4153	0.0419	0.1008	0.3599	0.0463	0.1288
CDC20	0	0	0.0222	0.0142	0.0009	0.0625	0.0118	0.0009	0.0749
CDC23	0.0817	0.0022	0.0268	0.0563	0.0037	0.065	0.0627	0.0044	0.0701
CDC37	0.013	0.0013	0.0992	0.0093	0.0013	0.1393	0	0	0.116
CDCA2	0.5037	0.0255	0.0507	0.3972	0.0343	0.0864	0.4835	0.035	0.0724
CDCA3				0.3029	0.0136	0.0449			
CDK13	0.0448	0.0014	0.0317	0.0809	0.0028	0.034	0.0451	0.0019	0.0423
CDK9	0.0352	0.0026	0.0742	0.0295	0.0026	0.0884	0	0	0.0993
CDT1	0.2169	0.0271	0.1248	0.1731	0.0292	0.169	0.1572	0.0239	0.1519

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
CEACAM6	0.1107	0.0039	0.0354	0.7801	0.142	0.182	0.3249	0.0278	0.0856	0.5439	0.0935	0.1718
CEBPZ	0.628	0.0056	0.009	0.5362	0.0032	0.006	0.2778	0.0089	0.032	0.1949	0.0081	0.0416
CENPT	1.1706	0.0106	0.0091	1.6847	0.0114	0.0068	0.5052	0.0247	0.0488	0.63	0.0327	0.0519
CEP78	0.2176	0.0036	0.0167	0.3834	0.0036	0.0095	0.3755	0.0154	0.041	0.3888	0.0122	0.0315
CES5A	0.2283	0.0077	0.0339	0.6762	0.0248	0.0366	0.3316	0.018	0.0542	0.3171	0.0176	0.0554
CHL1	0.1197	0.0032	0.0267	0.0899	0.0028	0.0316	0.1759	0.0071	0.0404	0.1664	0.0082	0.0492
CHM	0.4359	0.002	0.0045	2.0445	0.0046	0.0023				0.2877	0.0086	0.03
CHMP5	0	0	0.0211	0	0	0.0211	0	0	0.0356	0	0	0.0355
CHRDL2	0.045	0.001	0.0217	0.1047	0.0029	0.0281	0.0666	0.0049	0.0737	0.3824	0.0325	0.0851
CHST2	0	0	0.0118	0	0	0.0166	0.169	0.0069	0.041	0.1312	0.0035	0.0263
CHST4	0.3059	0.0034	0.0111	0.1216	0.0023	0.0186	0.3443	0.0177	0.0515	0.1675	0.0103	0.0614
CISH	0.3503	0.0016	0.0047	0.524	0.0049	0.0094	0.1968	0.0066	0.0335	0.3022	0.0116	0.0384
CLCN4				0	0	0.0182	0	0	0.0559	0.0116	0.0006	0.0501
CLEC4E	-1	0.0059	0	1.116	0.0079	0.007	0.3806	0.0138	0.0362	0.832	0.0179	0.0215
CLK4	0	0	0.017	0.0566	0.002	0.0348	0.0256	0.0009	0.0343	0.0585	0.0026	0.045
CMBL	0	0	0.0316	0	0	0.0252	0.0783	0.0035	0.0448	0.1721	0.0088	0.0512
CNPY1	0.5242	0.0093	0.0178	0.2613	0.0046	0.0178	0.2592	0.0093	0.0359	0.3897	0.014	0.036
CNTFR				0.0682	0.0012	0.0177	0.028	0.0012	0.0435	0.217	0.0076	0.035
CNTN6	0.1954	0.003	0.0153	0.0896	0.0021	0.0237	0.2023	0.0068	0.0337	0.2795	0.0103	0.037
COL20A1	0.3697	0.009	0.0243	0.2134	0.0065	0.0303	0.2311	0.0187	0.081	0.2099	0.019	0.0906
COL5A2	0.0538	0.0006	0.0114	0	0	0.0164	0.0157	0.0006	0.039	0.1023	0.0036	0.0351
COPS4	0.0583	0.001	0.0169				0.0485	0.001	0.0204	0.0358	0.0011	0.0297
COQ3	-1	0.0072	0	3.484	0.0146	0.0042	0.7584	0.0188	0.0247	0.4936	0.02	0.0405
CORO1C	0.0404	0.0009	0.0225	0.1426	0.0018	0.0127	0.1422	0.0018	0.0128	0	0	0.0434
COX5B	-1	0.0142	0	-1	0.0071	0	0.1927	0.0089	0.0461	0.8872	0.0179	0.0201
CPA5	0.2018	0.006	0.0299	0.2252	0.0091	0.0402	0.0838	0.006	0.0721	0.1636	0.0141	0.0865
CPB2	0.591	0.0041	0.0069	0.3519	0.0062	0.0175	0.4393	0.0124	0.0282	0.4557	0.0145	0.0318
CPT1B	0.6152	0.0023	0.0037	0.2686	0.004	0.0148	0.0998	0.0045	0.0454	0.1143	0.0066	0.0579
CWC22	0.1525	0.0023	0.0154	0.2081	0.0045	0.0215	0.1158	0.0049	0.0427	0.215	0.0092	0.0428
CXCR5	0.3424	0.0024	0.0071	0.0564	0.0012	0.0214	0.1021	0.0048	0.0473	0.1323	0.0073	0.0549
CYLC1	0.5365	0.0026	0.0049				0.7375	0.0232	0.0315	0.6051	0.0322	0.0532
CYP3A5	0.4577	0.0026	0.0057	0.2798	0.0118	0.0423	0.1806	0.0052	0.029	0.2972	0.0167	0.0561
CYP4F11	0.1268	0.0042	0.033	0.1734	0.0067	0.0387	0.1795	0.0114	0.0632	0.1641	0.0135	0.0822
CYTH1	0	0	0.0197	0.0701	0.0011	0.0157	0	0	0.0357	0	0	0.0501
DACT2	0.3874	0.0101	0.026	0.3911	0.0123	0.0315	0.452	0.03	0.0663			
DARC	0.371	0.0041	0.0111	0.8042	0.018	0.0223	0.4127	0.0124	0.03	0.5314	0.0183	0.0344
DBX1	0.4519	0.0064	0.0142	0.488	0.0174	0.0356	0.2978	0.0149	0.0501	0.3971	0.0133	0.0335
DCAF12L2	0.1143	0.0019	0.017	0.0681	0.0019	0.0286	0.341	0.0627	0.1839	0.0558	0.0029	0.0524
DCAF4L1	0.2425	0.0034	0.0139				0.1445	0.0056	0.0388	0.3556	0.0113	0.0317
DCAF5	0.0901	0.0009	0.0104	0.14	0.0019	0.0133	0.0637	0.003	0.0476	0.087	0.0033	0.0377
DCAF7	0	0	0.017	0	0	0.017	0	0	0.0522	0	0	0.0477
DCTN6	0	0	0.0075	0	0	0.0247	0.1536	0.0023	0.0151	0	0	0.0243
DDB2	0	0	0.0066	0.103	0.001	0.01	0.1013	0.0041	0.0406	0.0835	0.0052	0.0617
DDHD2	0	0	0.0041	0	0	0.0139	0.2369	0.0055	0.0232	0.4765	0.0079	0.0167
DDTL	0	0	0.0112	0	0	0.0262	0.5339	0.0206	0.0385			
DEF8	0.5098	0.0156	0.0306	0.138	0.0034	0.0249	0.072	0.0052	0.0717	0.0966	0.0086	0.0894
DEFB103A	0.3331	0.0068	0.0204	0.1629	0.0068	0.0415	0	0	0.0632	0	0	0.0415
DEFB110	-1	0.0257	0	1	0.0257	0.0257	2.2486	0.0289	0.0128	-1	0.0258	0
DENND4B	0.1831	0.0012	0.0067	0.1502	0.003	0.0201	0.1389	0.0055	0.0396	0.1881	0.0068	0.0362
DERL1	0	0	0.0056	0	0	0.0056	0.1569	0.0018	0.0112	0	0	0.0226
DGAT1	0	0	0.0149	0.6917	0.0437	0.0632	0.2066	0.0084	0.0407			
DHRS7	0.1077	0.0013	0.0122	0	0	0	0.1822	0.0053	0.0289	0.192	0.0039	0.0204
DHTKD1	0.2876	0.0057	0.02	0.3311	0.0077	0.0232	0.2144	0.0101	0.047	0.2043	0.0128	0.0625
DIRC2	0.2358	0.0019	0.008	0.0349	0.0009	0.0272	0.0634	0.0019	0.0299	0.1759	0.0039	0.0219
DLEC1	0.3155	0.0064	0.0203	0.2967	0.0081	0.0274	0.2621	0.0107	0.0408	0.3937	0.0171	0.0434
DLX6	0	0	0	-1	0.0033	0	0	0	0.006	0.895	0.0053	0.0059
DMGDH	0.1574	0.002	0.0129	0.1748	0.0025	0.0145	0.2018	0.0046	0.0227	0.2472	0.01	0.0403
DNAI2	0.0763	0.0029	0.0375	0.1408	0.0068	0.0482	0.1015	0.0058	0.0572	0.1914	0.0195	0.1019
DNAJC17	0.3112	0.0029	0.0093	0	0	0.0282	0.1696	0.0073	0.0428	0.0436	0.0017	0.04
DNAJC24	0	0	0	0	0	0	0	0	0.0325	0.1332	0.0058	0.0435
DNAJC30	0.3603	0.004	0.0112	1.4506	0.0081	0.0056	0.4918	0.0153	0.0311	0.6147	0.0246	0.04
DNAJC5G	1.1338	0.0184	0.0162	-1	0.012	0	0.8513	0.0278	0.0327	0.7459	0.0602	0.0808
DRAP1	0.0764	0.0021	0.0281	-1	0.0046	0	0.2086	0.012	0.0577			
DSCR3	0.0444	0.0015	0.0335	0.0519	0.0015	0.0286	0.1212	0.0089	0.0738	0.0651	0.0045	0.0688
DUSP1	0	0	0.0189	0	0	0.0322	0	0	0.0383	0	0	0.0718
EBI3	0.3506	0.004	0.0113				0.1256	0.011	0.0873	0.4667	0.0221	0.0473
ECEL1	0.1518	0.0037	0.0246	0.1637	0.0034	0.0211	0.1241	0.0058	0.0464	0.0928	0.0052	0.0562
EFS	0.1428	0.0025	0.0174	0.1903	0.0041	0.0217	0.4155	0.01	0.024	0.2784	0.0091	0.0328
EIF2C2	0.0511	0.001	0.0199	0.0359	0.001	0.0285	0.07	0.0033	0.0466	0.0091	0.0005	0.0599
EIF2C4	0	0	0				0	0	0.0183	0	0	0.0301
ELF4	0.2674	0.0072	0.0268	0.0431	0.0007	0.0158	0.0733	0.002	0.0278	0.3554	0.0162	0.0455
ENOPH1	0	0	0.0109	0	0	0.0165	0	0	0.022	0	0	0.0277
EPB41L1	0.0389	0.0005	0.0128	0.0206	0.0005	0.0242	0.0926	0.0035	0.0383	0.0954	0.0055	0.0578
EPB49	0	0	0.0033	0	0	0.0066	0	0	0.02	0.0296	0.0011	0.0372
EPHB3	0.0438	0.0009	0.0204	0	0	0.0245				0.0179	0.0009	0.0498
EPSTI1	0.5845	0.0106	0.0182	0.8783	0.016	0.0182	0.3665	0.015	0.0409	0.8017	0.0235	0.0294
EPT1	0	0	0.0145	0.0631	0.0011	0.0181	0.1043	0.0034	0.0329	0.0566	0.0023	0.0404
ERC1	0.2021	0.0019	0.0095				0.0309	0.0012	0.0374	0.0796	0.0036	0.0451
ERCC3	0.3636	0.0033	0.0091	0.0295	0.0006	0.0204	0.0185	0.0011	0.0599	0.1166	0.0067	0.0573
EXD1	1.8178	0.0046	0.0025	0.9128	0.0052	0.0057	0.4099	0.0115	0.0281	0.9046	0.0205	0.0226
EXPH5	0.5259	0.0059	0.0112	0.4407	0.0057	0.013	0.4549	0.0157	0.0345	0.465	0.0237	0.051
FAAH2	0.4242	0.0067	0.0157	0.2452	0.0058	0.0237	0.2362	0.0075	0.0317	0.3726	0.0135	0.0363
FAM103A1	0.2609	0.0036	0.0138	0.1292	0.0036	0.0279	0.0634	0.0036	0.0569	0.0634	0.0036	0.0569
FAM111A	2.4305	0.0126	0.0052	0.8042	0.0084	0.0104	1.1879	0.0425	0.0358			
FAM120A	0	0	0.0122	0.2878	0.003	0.0106	0.5319	0.02	0.0376	0.0146	0.0004	0.0272
FAM126B	0	0	0.0051	0.5952	0.0248	0.0417	0.0402	0.0008	0.0208	0.0805	0.0017	0.0208
FAM131A	0	0	0.0185				0.0988	0.0032	0.0327	0.1918	0.0081	0.0422
FAM165B	0	0	0.0265				0.1653	0.0231	0.1399	0.1621	0.023	0.142
FAM167A	0.1626	0.0042	0.0257	0.1297	0.0042	0.0322	0.1691	0.0147	0.087	0.1338	0.0126	0.0941
FAM55B	0.9046	0.01	0.0111				0.3888	0.0131	0.0337	0.4336	0.0172	0.0397
FAM64A	1.3765	0.0153	0.0111	0.6852	0.0076	0.0111	0.4813	0.0191	0.0397	0.8505	0.0191	0.0225
FANCG	0.2824	0.0029	0.0103	0.1762	0.0022	0.0124	0.7042	0.0088	0.0124	0.8868	0.09	0.1015
FBL	0	0	0.004	0	0	0.0201	0.0348	0.0014	0.0406	0.1077	0.0088	0.0821
FBXL12	0	0	0.0195	0.0789	0.0028	0.0355	0.0218	0.0014	0.0641	0	0	0.0559
FBXO22	0.634	0.0022	0.0035	0.6345	0.0022	0.0034	0.187	0.0066	0.0352	0.1032	0.0044	0.0425
FCRL2	0.78	0.0149	0.0191	0.5446	0.0153	0.028	0.5549	0.0191	0.0344	0.499	0.0243	0.0487
FGF2	0.5757	0.0048	0.0084	0.1273	0.0018	0.0141	0.1418	0.0048	0.034	0.2257	0.0097	0.043
FGGY	0.2111	0.0031	0.0145				0.1558	0.0062	0.0395	0.1204	0.0038	0.0319
FKRP	0.2526	0.0037	0.0148	0.0288	0.0009	0.0324	0.1055	0.0056	0.0532	0.1032	0.0048	0.0464
FLT3	1.4551	0.0043	0.003	0.3988	0.0048	0.012	0.2269	0.0065	0.0288	0.1574	0.007	0.0443
FMO6P	0.4166	0.015	0.0361				0.3605	0.0265	0.0736	0.716	0.0293	0.0409
FOLR2	0.1612	0.005	0.0312	0.2682	0.007	0.0261	0.1084	0.0084	0.0775	0.105	0.0067	0.0639
FOSB	0	0	0	0	0	0.0038	0	0	0.0151	0	0	0.019
FTSJ2	0.672	0.0073	0.0109	0.1637	0.0073	0.0446	0.2838	0.011	0.0388	0.2075	0.0165	0.0798
FXYD3	-1	0.0051	0	0.4665	0.0154	0.0331	0.2868	0.0259	0.0904	0.7387	0.0371	0.0502
FZR1	0.1351	0.0022	0.0164	0.0237	0.0009	0.0383	0.0726	0.0059	0.0817	0	0	0.0967
G6PC	0.2095	0.0025	0.0118	0.8285	0.0109	0.0131				0.1522	0.0099	0.0652

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
CEACAM6	0.9179	0.0643	0.07	0.6967	0.1385	0.1988	0.3333	0.024	0.072	0.5229	0.0902	0.1726
CEBPZ	0.2849	0.0183	0.0642	0.7168	0.0065	0.009	0.3551	0.0113	0.0319	0.2647	0.0101	0.0383
CENPT	0.6962	0.0306	0.0439	0.7669	0.0122	0.0159	0.5377	0.0263	0.049	0.5737	0.0326	0.0569
CEP78	0.2011	0.0129	0.0641	0.3053	0.0035	0.0116	0.2436	0.0058	0.024	0.3814	0.0073	0.0191
CES5A	0.2436	0.0172	0.0708	0.6779	0.0248	0.0366	0.291	0.018	0.0619	0.268	0.0176	0.0657
CHL1	0.2303	0.019	0.0823	0.0817	0.0032	0.039	0.1335	0.0067	0.0505	0.1376	0.0078	0.0568
CHM	0.2349	0.013	0.0553	0.5821	0.004	0.0068				0.2293	0.008	0.0347
CHMP5	0	0	0.0501	0	0	0.014	0	0	0.0283	0	0	0.0283
CHRDL2	0.0692	0.0088	0.1277	0.1053	0.002	0.0186	0.0586	0.0039	0.067	0.4023	0.0315	0.0783
CHST2	0.0656	0.0052	0.0791	0	0	0.0191	0.1799	0.0069	0.0385	0.1201	0.0035	0.0287
CHST4	0.2231	0.0183	0.082	0.0506	0.0011	0.0224	0.2996	0.0166	0.0554	0.1224	0.008	0.0653
CISH	0.2103	0.0167	0.0793	0.4648	0.0066	0.0142	0.2148	0.0083	0.0385	0.3064	0.0133	0.0433
CLCN4	0.1071	0.0115	0.1071									
CLEC4E	0.4316	0.0526	0.1219	0.8411	0.0059	0.007	0.3278	0.0118	0.036	0.7432	0.0159	0.0214
CLK4	0.0851	0.0035	0.0413	0.0638	0.002	0.0309	0.0285	0.0009	0.0308	0.0636	0.0026	0.0414
CMBL	0.2327	0.0214	0.0918	0	0	0.0316	0.0884	0.0043	0.0481	0.1906	0.0107	0.0561
CNPY1	0.3916	0.014	0.0358	0.128	0.0046	0.0362	0.1693	0.0093	0.0549	0.2545	0.014	0.055
CNTFR	0.1043	0.0073	0.0698									
CNTN6	0.1804	0.0111	0.0617	0.1356	0.0034	0.0251	0.2135	0.0081	0.038	0.2925	0.0112	0.0384
COL20A1				0.4328	0.0099	0.0229	0.2745	0.0199	0.0723	0.2573	0.0208	0.081
COL5A2	0.0728	0.0042	0.0575	0.0418	0.0006	0.0147	0.0345	0.0012	0.0356	0.1401	0.0042	0.03
COPS4	0.0999	0.0059	0.0595				0	0	0.0169	0.0359	0.0011	0.0297
COQ3	0.4485	0.0296	0.0659	2.2087	0.0092	0.0042	0.5608	0.0139	0.0247	0.3727	0.0151	0.0405
CORO1C	0.043	0.0018	0.0423	0.0313	0.0009	0.029	0.0313	0.0009	0.029	0	0	0.0475
COX5B	1.0004	0.0512	0.0512	-1	0.0071	0	0.2781	0.0143	0.0513	0.8893	0.0179	0.0201
CPA5	0.1484	0.0172	0.1161	0.3018	0.0111	0.0368	0.1244	0.0081	0.0649	0.1874	0.0162	0.0864
CPB2	0.4709	0.0324	0.0688	0.2343	0.0041	0.0175	0.3657	0.0103	0.0282	0.3902	0.0124	0.0318
CPT1B	0.1692	0.0137	0.081	0.3589	0.004	0.0111	0.1091	0.0045	0.0416	0.1244	0.0066	0.0533
CWC22	0.1807	0.0121	0.0668	0.1314	0.0031	0.0233	0.0862	0.0035	0.0409	0.1895	0.0078	0.041
CXCR5	0.2009	0.0134	0.0665	0.0563	0.0012	0.0214	0.1021	0.0048	0.0474	0.1323	0.0073	0.0549
CYLC1	0.6223	0.0486	0.078				0.8293	0.0229	0.0276	0.724	0.0319	0.0441
CYP3A5	0.4725	0.0418	0.0885	0.2578	0.0109	0.0424	0.1497	0.0044	0.0291	0.2802	0.0158	0.0563
CYP4F11	0.2621	0.0418	0.1594	0.1781	0.0059	0.033	0.177	0.0122	0.069	0.175	0.0144	0.082
CYTH1	0	0	0.1037	0.0398	0.0011	0.0277	0	0	0.0398	0	0	0.0501
DACT2	0.2743	0.0333	0.1215	0.3131	0.0114	0.0364	0.4771	0.0317	0.0664			
DARC	0.4289	0.0413	0.0963	0.6326	0.0166	0.0262	0.3242	0.011	0.0339	0.4388	0.0169	0.0384
DBX1	0.1833	0.0194	0.1061	0.7311	0.0226	0.0309	0.2965	0.016	0.054	0.396	0.0143	0.036
DCAF12L2	0.04	0.0049	0.1217	0	0	0.017	0.3354	0.0606	0.1806	0.021	0.001	0.0465
DCAF4L1	0.1034	0.0079	0.0761				0.1685	0.009	0.0534	0.2689	0.0124	0.0461
DCAF5	0.1245	0.007	0.0565	0.2366	0.0028	0.0119	0.082	0.004	0.0493	0.1074	0.0042	0.0392
DCAF7	0.0208	0.0013	0.0612	0	0	0.017	0	0	0.0477	0	0	0.0477
DCTN6	0	0	0.0703	0	0	0.0331	0.1019	0.0023	0.0227	0	0	0.0326
DDB2	0.1295	0.0062	0.0477	0.3104	0.001	0.0033	0.1221	0.0041	0.0337	0.0835	0.0052	0.0617
DDHD2	0.2054	0.0092	0.0447	0	0	0.0139	0.2372	0.0055	0.0232	0.4771	0.008	0.0167
DDTL	0.8548	0.1152	0.1348	0	0	0.013	0.6997	0.0237	0.0339			
DEF8	0.0353	0.0038	0.1084	0.3481	0.0156	0.0448	0.2643	0.0173	0.0656	0.2512	0.0209	0.0832
DEFB103A	0	0	0.158	0.2169	0.0136	0.0628	0.0798	0.0068	0.0849	0.108	0.0068	0.0628
DEFB110	-1	0.0389	0	0.5008	0.0128	0.0255	0.4952	0.0127	0.0257	-1	0.0128	0
DENND4B	0.1008	0.0058	0.058	0.1837	0.0033	0.0182	0.1581	0.0058	0.0368	0.1931	0.0068	0.0352
DERL1	0.0384	0.0018	0.0458	0	0	0	0.315	0.0018	0.0056	0	0	0.0169
DGAT1	0.1881	0.0166	0.088	0.768	0.047	0.0611	0.2404	0.009	0.0373			
DHRS7	0.3432	0.0172	0.05	0.103	0.0014	0.0138	0.1583	0.0066	0.0417	0.1195	0.004	0.0331
DHTKD1	0.1312	0.0144	0.1096	0.1721	0.0048	0.0278	0.1203	0.0062	0.0518	0.1466	0.0099	0.0672
DIRC2	0.0514	0.0029	0.0555	0.05	0.0009	0.0189	0.0875	0.0019	0.0217	0.2827	0.0039	0.0136
DLEC1	0.2231	0.0173	0.0777	0.3241	0.0081	0.0251	0.281	0.0115	0.0409	0.4024	0.0171	0.0424
DLX6	0	0	0.0116	-1	0.0033	0	0	0	0.006	0.895	0.0053	0.0059
DMGDH	0.145	0.0092	0.0634	0.1047	0.0015	0.0146	0.1461	0.0036	0.0244	0.2215	0.0089	0.0403
DNAI2	0.151	0.0167	0.1107	0.1816	0.0059	0.0327	0.1079	0.0058	0.0538	0.2226	0.0195	0.0877
DNAJC17	0.0696	0.0072	0.1042	0.1548	0.0029	0.0187	0.3074	0.0102	0.0331	0.1848	0.0052	0.0284
DNAJC24	0.1765	0.0204	0.1156	0	0	0	0	0	0.0325	0.1332	0.0058	0.0435
DNAJC30	0.5075	0.0416	0.0819	0.2394	0.004	0.0169	0.2618	0.0112	0.0428	0.4746	0.0246	0.0519
DNAJC5G	0.6742	0.0362	0.0537	0.5578	0.012	0.0214	0.5644	0.0279	0.0494	0.637	0.0644	0.1012
DRAP1	0.0269	0.0021	0.0799	0.233	0.0068	0.0294	0.2514	0.0145	0.0578			
DSCR3	0.0353	0.0045	0.1267	0	0	0.0142	0.1085	0.0074	0.0687	0.0509	0.003	0.0586
DUSP1	0	0	0.0997	0	0	0.0256	0	0	0.0318	0	0	0.065
EBI3	0.3742	0.0344	0.092				0.1892	0.0165	0.0873	0.5481	0.0266	0.0485
ECEL1	0.0338	0.0049	0.1447	0.1522	0.0037	0.0246	0.1081	0.0056	0.0519	0.0967	0.0057	0.0585
EFS	0.2212	0.0201	0.0907	0.1263	0.0033	0.0262	0.3208	0.0091	0.0285	0.1983	0.0083	0.0419
EIF2C2	0	0	0.0927	0	0	0.0217	0.0793	0.0033	0.0411	0.01	0.0005	0.0543
EIF2C4	0	0	0.0301				0	0	0.0183	0	0	0.0302
ELF4	0.1038	0.0055	0.0526	0.197	0.0065	0.0329	0.159	0.0078	0.0494	0.4011	0.0224	0.056
ENOPH1	0.1342	0.0068	0.0503	0	0	0.0165	0	0	0.022	0	0	0.0277
EPB41L1	0.0391	0.003	0.0766	0	0	0.0177	0.1031	0.0035	0.0344	0.0983	0.005	0.0509
EPB49	0.0134	0.0012	0.092	0	0	0.0099	0	0	0.0234	0.0271	0.0011	0.0406
EPHB3	0.0159	0.0014	0.089	0.0386	0.0009	0.0231				0.0369	0.0018	0.0484
EPSTI1	0.4181	0.0351	0.0838	0.3248	0.0095	0.0294	0.2362	0.0101	0.0428	0.5136	0.017	0.0332
EPT1	0.0578	0.0034	0.0595	0.3185	0.0011	0.0036	0.1896	0.0034	0.0181	0.0898	0.0023	0.0255
ERC1	0.0102	0.0013	0.1258				0.0369	0.0015	0.0416	0.0804	0.004	0.0496
ERCC3	0.0107	0.0011	0.1034	0.071	0.0021	0.0303	0.0484	0.0033	0.0685	0.1163	0.0072	0.0617
EXD1	0.3297	0.0216	0.0655	0.6049	0.0052	0.0085	0.3236	0.01	0.0308	0.741	0.0188	0.0254
EXPH5	0.36	0.0263	0.0731	0.6249	0.0073	0.0117	0.5033	0.0172	0.0341	0.4984	0.0252	0.0506
FAAH2	0.1864	0.0142	0.0763	0.5263	0.0125	0.0238	0.4468	0.0142	0.0319	0.8092	0.0194	0.024
FAM103A1	0.0853	0.0036	0.0423	0	0	0.0138	0	0	0.0423	0	0	0.0423
FAM111A	0.9285	0.0512	0.0552	0.9421	0.0098	0.0104	1.0051	0.0399	0.0397			
FAM120A	0.0297	0.0012	0.0419	0.168	0.003	0.0182	0.5125	0.02	0.039	0.0118	0.0004	0.0335
FAM126B	0.0227	0.0008	0.0368	0.5262	0.0248	0.0471	0.0402	0.0008	0.0208	0.0805	0.0017	0.0208
FAM131A	0.0973	0.0085	0.0873				0.0763	0.0032	0.0423	0.1559	0.0081	0.0519
FAM165B	0.1084	0.0153	0.1411				0.2106	0.0231	0.1097	0.2067	0.023	0.1114
FAM167A				0	0	0.0191	0.1437	0.0105	0.0729	0.1589	0.0105	0.0659
FAM55B	0.343	0.0226	0.066				0.3585	0.01	0.0279	0.3356	0.0133	0.0395
FAM64A	0.8267	0.0395	0.0478	0.512	0.0114	0.0223	0.3719	0.0191	0.0514	0.6779	0.023	0.0339
FANCG	0.3474	0.0184	0.053	0.1511	0.0022	0.0145	0.5468	0.0102	0.0187	0.8152	0.0885	0.1085
FBL	0.1023	0.0092	0.0903	0	0	0.0161	0.0388	0.0014	0.0365	0.114	0.0088	0.0775
FBXL12	0.017	0.0015	0.0897	0.089	0.0028	0.0315	0.0205	0.0014	0.0683	0	0	0.0518
FBXO22	0.1647	0.0088	0.0534	0.316	0.0022	0.0069	0.1694	0.0066	0.0389	0.0949	0.0044	0.0462
FCRL2	0.487	0.047	0.0966	0.5027	0.0148	0.0295	0.5473	0.0172	0.0315	0.4811	0.0234	0.0487
FGF2				0.5088	0.0072	0.0141	0.2834	0.0097	0.0341	0.3384	0.0146	0.0431
FGGY	0.1308	0.0104	0.0798				0.0731	0.0031	0.0421	0.0624	0.0023	0.0369
FKRP	0.0618	0.0084	0.1364	0.1247	0.0047	0.0375	0.1603	0.0094	0.0585	0.1577	0.0084	0.0533
FLT3	0.2348	0.0153	0.0653	0.5329	0.0048	0.009	0.2573	0.0074	0.0288	0.1772	0.0079	0.0443
FMO6P	0.4905	0.0572	0.1167				0.4396	0.0266	0.0605	0.9472	0.0287	0.0303
FOLR2	0.1607	0.0169	0.1051	0.0531	0.0017	0.0329	0.0396	0.0033	0.0845	0.0236	0.0017	0.0707
FOSB	0.039	0.0013	0.0345	0	0	0.0038	0	0	0.0151	0	0	0.019
FTSJ2	0.1692	0.0166	0.0978	0.2195	0.0073	0.0333	0.2658	0.0073	0.0275	0.189	0.0128	0.0679
FXYD3	0.832	0.0419	0.0503	0.627	0.0207	0.033	0.2155	0.0194	0.0899	0.6339	0.0317	0.0501
FZR1	0	0	0.1183	0.144	0.0033	0.0231	0.0365	0.0022	0.0612	0.0258	0.0022	0.0859
G6PC	0.1278	0.0099	0.0777	1.2511	0.0109	0.0087				0.1633	0.0099	0.0608

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
CEACAM6	0.7306	0.0613	0.0839	0.8025	0.1529	0.1906	0.7237	0.2189	0.3025	0.9644	0.1709	0.1772
CEBPZ	0.3372	0.0216	0.0641	0.2519	0.0081	0.0321	0.2105	0.0081	0.0385	0.2716	0.0175	0.0643
CENPT	0.5853	0.0314	0.0536	0.4386	0.0247	0.0562	0.4925	0.0292	0.0593	0.5748	0.0301	0.0524
CEP78	0.2337	0.01	0.0427	0.3044	0.0088	0.0288	0.442	0.0095	0.0214	0.2856	0.0128	0.0448
CES5A	0.2375	0.0181	0.0763	0.6189	0.0338	0.0547	0.537	0.0342	0.0638	0.4577	0.0345	0.0753
CHL1	0.2012	0.0182	0.0904	0.1408	0.0071	0.0504	0.1379	0.0082	0.0593	0.2006	0.0189	0.0944
CHM	0.2228	0.0123	0.0553				0.2465	0.008	0.0323	0.1905	0.011	0.0576
CHMP5	0	0	0.0427	0	0	0.0283	0	0	0.0283	0	0	0.0427
CHRDL2	0.063	0.0078	0.1238	0.0976	0.0059	0.0605	0.4285	0.0336	0.0785	0.0789	0.0089	0.1124
CHST2	0.0635	0.0052	0.0817	0.1427	0.0069	0.0485	0.1024	0.0035	0.0337	0.0596	0.0052	0.087
CHST4	0.2206	0.0172	0.0778	0.389	0.0154	0.0397	0.1618	0.008	0.0494	0.2172	0.016	0.0737
CISH	0.2172	0.0184	0.0845	0.1899	0.0083	0.0435	0.2743	0.0133	0.0484	0.2041	0.0184	0.0899
CLCN4				0	0	0.0521	0.0126	0.0006	0.0463	0.1127	0.0115	0.1018
CLEC4E	0.4172	0.0506	0.1212	0.3156	0.0138	0.0437	0.5522	0.0159	0.0288	0.4041	0.0526	0.1302
CLK4	0.0931	0.0035	0.0377	0.0763	0.003	0.0388	0.0898	0.0049	0.0549	0.1169	0.0059	0.0507
CMBL	0.2417	0.0238	0.0984	0.1107	0.0035	0.0317	0.2318	0.0088	0.038	0.2744	0.0214	0.0779
CNPY1	0.2558	0.014	0.0548	0.0844	0.0046	0.0549	0.1691	0.0093	0.055	0.17	0.0093	0.0548
CNTFR				0	0	0.036	0.2038	0.0064	0.0313	0.092	0.0061	0.0659
CNTN6	0.1826	0.0122	0.0668	0.1367	0.0064	0.0468	0.2073	0.0099	0.0477	0.1421	0.0107	0.0753
COL20A1				0.2605	0.0192	0.0737	0.2381	0.02	0.0838			
COL5A2	0.0898	0.0048	0.0539	0.019	0.0006	0.0322	0.1267	0.0036	0.0283	0.0866	0.0042	0.0484
COPS4	0.0888	0.005	0.0558									
COQ3	0.3806	0.0248	0.0652	0.7595	0.0159	0.021	0.3672	0.0173	0.0471	0.3564	0.0267	0.0748
CORO1C	0.0154	0.0009	0.0591	0.0945	0.0018	0.0192	0	0	0.0475	0.0326	0.0018	0.0557
COX5B	1.0028	0.0512	0.0511	0.1387	0.0071	0.0512	0.5323	0.0107	0.0201	0.8573	0.0437	0.051
CPA5	0.1702	0.0188	0.1103	0.1396	0.0091	0.0651	0.1986	0.0172	0.0866	0.1853	0.0198	0.1068
CPB2	0.3822	0.0292	0.0765	0.3167	0.0124	0.0391	0.2899	0.0124	0.0427	0.3674	0.0324	0.0882
CPT1B	0.1781	0.0137	0.077	0.1128	0.0051	0.0453	0.15	0.008	0.0531	0.1714	0.0131	0.0767
CWC22	0.1548	0.0106	0.0687	0.1221	0.0042	0.0347	0.2441	0.0085	0.0348	0.1748	0.0109	0.0622
CXCR5	0.2009	0.0134	0.0665	0.0658	0.0036	0.055	0.0965	0.006	0.0627	0.182	0.0121	0.0667
CYLC1	0.6696	0.0487	0.0727									
CYP3A5	0.4601	0.0409	0.0888	0.2238	0.0136	0.0607	0.2925	0.0256	0.0875	0.4539	0.0492	0.1083
CYP4F11	0.2666	0.0425	0.1596	0.1792	0.0126	0.0705	0.1726	0.0152	0.0881	0.2664	0.0425	0.1597
CYTH1	0	0	0.1081	0.0309	0.0011	0.0356	0.0226	0.0014	0.0606	0.0098	0.0011	0.1126
DACT2	0.3062	0.0385	0.1257	0.4932	0.0272	0.0552				0.2913	0.0328	0.1126
DARC	0.3957	0.0398	0.1007	0.6367	0.0228	0.0359	0.6942	0.024	0.0345	0.4219	0.0434	0.1029
DBX1	0.1888	0.0209	0.1106	0.4537	0.0302	0.0666	0.5394	0.0286	0.053	0.2908	0.0355	0.122
DCAF12L2	0.0253	0.0029	0.1153	0.3355	0.0606	0.1806	0.021	0.001	0.0464	0.0253	0.0029	0.1153
DCAF4L1	0.0985	0.009	0.0914									
DCAF5	0.1373	0.008	0.0581	0.0914	0.004	0.0442	0.1074	0.0042	0.0392	0.1148	0.007	0.0613
DCAF7	0.0225	0.0013	0.0567	0	0	0.0522	0	0	0.0477	0.0208	0.0013	0.0612
DCTN6	0	0	0.0786	0.0596	0.0025	0.0413	0	0	0.0538	0	0	0.0761
DDB2	0.1295	0.0062	0.0477	0.1015	0.0036	0.0355	0.0729	0.0046	0.0635	0.1143	0.0057	0.0495
DDHD2	0.2056	0.0092	0.0447	0.1843	0.0061	0.0332	0.3146	0.0088	0.0281	0.1658	0.0095	0.0574
DDTL	0.8694	0.1158	0.1332	0.2435	0.0096	0.0394				0.8401	0.1323	0.1574
DEF8	0.1568	0.0179	0.1139	0.0502	0.0034	0.0685	0.0724	0.0069	0.0953	0.0442	0.0048	0.1083
DEFB103A	0.0511	0.0068	0.1323	0.107	0.0068	0.0632	0.1629	0.0068	0.0415	0.0427	0.0067	0.158
DEFB110	-1	0.0258	0	0.2447	0.0127	0.0521	0.5122	0.0128	0.025	1.0183	0.0258	0.0253
DENND4B	0.1187	0.0065	0.0544	0.1357	0.0053	0.0391	0.2103	0.009	0.0428	0.1272	0.0074	0.0581
DERL1	0.044	0.0018	0.0399	0.315	0.0018	0.0056	0	0	0.0169	0.044	0.0018	0.0399
DGAT1	0.2087	0.0176	0.0845	0.6382	0.0518	0.0812				0.5478	0.0631	0.1152
DHRS7	0.2734	0.0173	0.0632	0.1303	0.0043	0.0326	0.0613	0.0014	0.0231	0.383	0.0143	0.0373
DHTKD1	0.1054	0.0122	0.1154	0.2008	0.0091	0.0454	0.1667	0.0118	0.0707	0.1316	0.0149	0.1136
DIRC2	0.0607	0.0029	0.047	0.023	0.0009	0.0412	0.0871	0.0029	0.0332	0.0342	0.0019	0.0556
DLEC1	0.2525	0.0187	0.0741	0.3276	0.012	0.0367	0.4478	0.0171	0.0381	0.2529	0.0186	0.0736
DLX6	0	0	0.0116	0.6198	0.0037	0.006	1.5031	0.0088	0.0058	0.2961	0.0034	0.0115
DMGDH	0.1125	0.0071	0.0634	0.1564	0.0041	0.026	0.2248	0.0094	0.042	0.1253	0.0082	0.0652
DNAI2	0.1504	0.0175	0.1164	0.225	0.0091	0.0405	0.2123	0.0205	0.0967	0.1366	0.0188	0.1376
DNAJC17	0.1085	0.0102	0.0937	0.138	0.0073	0.0526	0.0381	0.0017	0.0459	0.0734	0.0073	0.0988
DNAJC24	0.1765	0.0204	0.1156	0	0	0.0254	0.1334	0.0069	0.0516	0.15	0.0208	0.1385
DNAJC30	0.4406	0.0416	0.0944	0.4147	0.0153	0.0369	0.5815	0.0267	0.0459	0.5206	0.0459	0.0881
DNAJC5G	0.5806	0.0411	0.0707	0.6591	0.0211	0.032	0.7276	0.072	0.099	0.561	0.0366	0.0652
DRAP1	0.0386	0.0043	0.1114	0.2531	0.0146	0.0575				0.0818	0.0068	0.0837
DSCR3	0.0245	0.003	0.1212	0.1172	0.0074	0.0635	0.0557	0.003	0.0535	0.0257	0.003	0.1158
DUSP1	0	0	0.0927	0	0	0.0322	0	0	0.0658	0	0	0.0939
EBI3	0.4336	0.0399	0.092									
ECEL1	0.0316	0.0047	0.1475	0.0994	0.0046	0.0463	0.0678	0.0041	0.0598	0.0315	0.0043	0.1356
EFS	0.2062	0.0193	0.0934	0.3801	0.0108	0.0284	0.2386	0.01	0.0418	0.2307	0.0209	0.0907
EIF2C2	0	0	0.089	0.076	0.0033	0.0429	0.01	0.0005	0.0543	0	0	0.0871
EIF2C4	0	0	0.0304									
ELF4	0.1744	0.0072	0.0411	0.0571	0.0014	0.0238	0.4158	0.0155	0.0372	0.1079	0.0048	0.0443
ENOPH1	0.109	0.0068	0.062	0	0	0.0276	0	0	0.0333	0.1204	0.0068	0.0561
EPB41L1	0.0358	0.0025	0.0696	0.084	0.0036	0.0423	0.0842	0.005	0.0595	0.0305	0.0025	0.0819
EPB49	0.0128	0.0012	0.0964	0	0	0.0268	0.025	0.0011	0.0441	0.0128	0.0012	0.0963
EPHB3	0.0209	0.0019	0.0906				0.019	0.0009	0.047	0.0172	0.0014	0.0825
EPSTI1	0.3447	0.0304	0.0883	0.3109	0.0133	0.0429	0.6426	0.0214	0.0332	0.4092	0.0362	0.0884
EPT1	0.0778	0.0034	0.0441	0.2102	0.0046	0.0218	0.1176	0.0034	0.0292	0.0956	0.0046	0.048
ERC1	0.0101	0.0013	0.1275									
ERCC3	0.0332	0.0033	0.1001	0.0099	0.0006	0.0607	0.1372	0.0066	0.0484	0.0061	0.0006	0.0987
EXD1	0.3152	0.0216	0.0685	0.4103	0.013	0.0317	0.7138	0.0196	0.0275	0.3054	0.0227	0.0742
EXPH5	0.3916	0.0278	0.071	0.441	0.015	0.0341	0.4788	0.0235	0.0492	0.3767	0.0273	0.0725
FAAH2	0.2745	0.021	0.0766	0.2914	0.0117	0.0401	0.3856	0.0164	0.0426	0.2158	0.0184	0.0854
FAM103A1	0	0	0.0279	0	0	0.0569	0	0	0.0569	0	0	0.0423
FAM111A	0.8995	0.052	0.0578	0.8186	0.0359	0.0439				0.7025	0.0446	0.0635
FAM120A	0.0249	0.0012	0.05	0.5696	0.0235	0.0412	0.1116	0.0035	0.0311	0.0964	0.0044	0.0453
FAM126B	0.0227	0.0008	0.0368	0.4027	0.0257	0.0638	0.4792	0.0265	0.0554	0.3422	0.0257	0.075
FAM131A	0.0868	0.0085	0.0978									
FAM165B	0.1382	0.0153	0.1107									
FAM167A				0.1313	0.0105	0.0798	0.1207	0.0105	0.0868			
FAM55B	0.2606	0.0187	0.0718									
FAM64A	0.7481	0.0427	0.0571	0.297	0.0153	0.0514	0.4499	0.0152	0.0339	0.5865	0.0353	0.0602
FANCG	0.2741	0.0169	0.0618	0.4562	0.0095	0.0208	0.8053	0.0893	0.1109	0.3206	0.0177	0.0551
FBL	0.0975	0.0092	0.0948	0.0388	0.0014	0.0366	0.114	0.0088	0.0775	0.0974	0.0093	0.0952
FBXL12	0.0179	0.0015	0.085	0.0492	0.0042	0.0856	0.0649	0.0035	0.054	0	0	0.0995
FBXO22	0.1537	0.0088	0.0572	0.1411	0.0055	0.0388	0.0845	0.0033	0.0389	0.1539	0.0088	0.0571
FCRL2	0.5362	0.0559	0.1042	0.53	0.0186	0.0351	0.4051	0.0166	0.041	0.5495	0.0577	0.105
FGF2				0.1882	0.0072	0.0382	0.262	0.0127	0.0483			
FGGY	0.0904	0.0072	0.0798									
FKRP	0.0791	0.0113	0.1424	0.095	0.0066	0.069	0.0893	0.006	0.0671	0.0559	0.0084	0.151
FLT3	0.2237	0.0153	0.0686	0.1833	0.007	0.0381	0.1381	0.0074	0.0538	0.1987	0.0149	0.075
FMO6P	0.5992	0.0614	0.1024									
FOLR2	0.1048	0.0118	0.1124	0.0641	0.0052	0.0818	0.0655	0.0035	0.0533	0.1102	0.0123	0.1114
FOSB	0.039	0.0013	0.0345	0	0	0.019	0	0	0.0228	0.035	0.0013	0.0384
FTSJ2	0.1497	0.0128	0.0857	0.2179	0.011	0.0504	0.2063	0.0165	0.0801	0.1683	0.0165	0.0982
FXYD3	0.7289	0.0366	0.0502	0.5906	0.0393	0.0665	0.7359	0.0371	0.0504	1.4198	0.0472	0.0333
FZR1	0.0205	0.0022	0.1081	0.1152	0.007	0.0609	0.0107	0.0009	0.0847	0.0097	0.0009	0.0938
G6PC	0.1358	0.0099	0.0732				0.3027	0.0191	0.0632	0.3047	0.0192	0.0629

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
CEACAM6	0.6435	0.1021	0.1587	0.9158	0.0642	0.0701	0.9001	0.1339	0.1487
CEBPZ	0.1637	0.0081	0.0495	0.3157	0.0208	0.0658	0.2265	0.0183	0.081
CENPT	0.5015	0.0279	0.0557	0.5256	0.0342	0.0651	0.6382	0.0378	0.0593
CEP78	0.4122	0.0161	0.039	0.2246	0.0167	0.0745	0.2211	0.0122	0.0554
CES5A	0.3921	0.0248	0.0633	0.2926	0.024	0.0821	0.3393	0.0236	0.0695
CHL1	0.1705	0.006	0.0353	0.2584	0.0178	0.0689	0.2267	0.0173	0.0762
CHM							0.2186	0.0137	0.0625
CHMP5	0	0	0.014	0	0	0.0428	0	0	0.0427
CHRDL2	0.3218	0.0295	0.0917	0.0449	0.0057	0.1274	0.2241	0.035	0.1563
CHST2	0.148	0.0087	0.0586	0.0917	0.0104	0.1136	0.071	0.0069	0.0976
CHST4	0.4139	0.0213	0.0515	0.2455	0.0253	0.103	0.2316	0.0219	0.0944
CISH	0.3447	0.0149	0.0434	0.237	0.0201	0.0846	0.2426	0.0218	0.0897
CLCN4	0.0094	0.0006	0.0617	0.0836	0.0115	0.1373	0.1037	0.0122	0.118
CLEC4E	0.4079	0.0118	0.029	0.3672	0.0421	0.1147	0.4574	0.0486	0.1063
CLK4	0.1139	0.0035	0.0308	0.1284	0.0044	0.0342	0.163	0.0062	0.0378
CMBL	0.1663	0.0053	0.0317	0.3686	0.0213	0.0579	0.2512	0.0196	0.0779
CNPY1	-1	0.0046	0	-1	0.0046	0	-1	0.0093	0
CNTFR	0.1283	0.0064	0.05	0.0747	0.0061	0.0817	0.1138	0.01	0.0882
CNTN6	0.2151	0.0076	0.0354	0.1269	0.009	0.0707	0.1593	0.0103	0.0648
COL20A1	0.2978	0.0218	0.0732						
COL5A2	0.0953	0.0036	0.0376	0.0684	0.0042	0.0613	0.1011	0.0052	0.0519
COPS4	0.0411	0.0011	0.0259	0.0949	0.005	0.0522	0.0187	0.0011	0.0567
COQ3	0.678	0.0206	0.0304	0.512	0.0311	0.0607	0.36	0.0249	0.069
CORO1C	0	0	0.0434	0.048	0.0023	0.0473	0	0	0.064
COX5B	0.1473	0.0107	0.0726	0.4146	0.0437	0.1055	0.7858	0.04	0.0509
CPA5	0.133	0.0101	0.0759	0.1138	0.0111	0.0977	0.1489	0.0162	0.1087
CPB2	0.3576	0.0166	0.0463	0.3525	0.0324	0.092	0.4442	0.0356	0.0802
CPT1B	0.0798	0.0046	0.058	0.1248	0.0114	0.0914	0.147	0.0133	0.0906
CWC22	0.2306	0.008	0.0348	0.175	0.0109	0.0621	0.2413	0.0132	0.0549
CXCR5	0.123	0.0073	0.059	0.1542	0.0133	0.0865	0.1232	0.0097	0.0786
CYLC1	0.6105	0.0336	0.055	0.569	0.0486	0.0854	0.7401	0.0577	0.0779
CYP3A5	0.3447	0.0131	0.0381	0.5481	0.0381	0.0696	0.4849	0.0377	0.0776
CYP4F11	0.1563	0.0131	0.0836	0.2432	0.0372	0.1532	0.2856	0.0417	0.146
CYTH1	0	0	0.0347	0	0	0.0991	0	0	0.1148
DACT2				0.2938	0.0382	0.1299			
DARC	0.3633	0.0126	0.0346	0.3373	0.0334	0.0989	0.4407	0.0369	0.0837
DBX1	0.4105	0.0162	0.0395	0.1913	0.0224	0.1172	0.2034	0.0208	0.1021
DCAF12L2	0.3902	0.0597	0.1529	0.3496	0.0595	0.1702	0.0184	0.0019	0.1058
DCAF4L1	0.2031	0.0101	0.0499	0.0736	0.0067	0.0915	0.1283	0.0113	0.0877
DCAF5	0.0631	0.0035	0.0561	0.0965	0.0076	0.0788	0.1149	0.007	0.0612
DCAF7	0	0	0.0477	0.0244	0.0013	0.0522	0.0225	0.0013	0.0567
DCTN6	0.1029	0.0025	0.0242	0.0331	0.0023	0.0699	0	0	0.084
DDB2	0.05	0.0031	0.0617	0.0997	0.0062	0.0619	0.0863	0.0072	0.0836
DDHD2	0.5421	0.008	0.0147	0.1899	0.0098	0.0516	0.2127	0.0086	0.0402
DDTL				1.1211	0.1238	0.1104			
DEF8	0.0857	0.0069	0.0804	0.0439	0.0048	0.1088	0.0303	0.0038	0.1263
DEFB103A	0	0	0.0205	0	0	0.1333	0	0	0.158
DEFB110	0.5065	0.0128	0.0253	1.0069	0.0257	0.0255	-1	0.0259	0
DENND4B	0.1996	0.0083	0.0415	0.1165	0.0075	0.0642	0.1589	0.0092	0.0581
DERL1	0.0778	0.0018	0.0226	0.1032	0.0035	0.0341	0.0304	0.0018	0.0577
DGAT1				0.2679	0.0216	0.0808			
DHRS7	0.1588	0.0053	0.0332	0.251	0.0159	0.0635	0.3459	0.0158	0.0458
DHTKD1	0.1372	0.0091	0.0665	0.1	0.0122	0.1216	0.1395	0.0161	0.1153
DIRC2	0.1559	0.0039	0.0247	0.0541	0.0029	0.0527	0.0905	0.0048	0.0534
DLEC1	0.3793	0.0168	0.0442	0.2386	0.0168	0.0705	0.3015	0.0237	0.0787
DLX6	0.3036	0.004	0.0131	0	0	0.0193	0.1446	0.0018	0.0123
DMGDH	0.2252	0.0094	0.042	0.1204	0.0087	0.0721	0.1548	0.0123	0.0793
DNAI2	0.2427	0.0184	0.0758	0.1378	0.0196	0.142	0.1684	0.0241	0.1429
DNAJC17	0.121	0.007	0.0579	0.1396	0.0146	0.1043	0.0783	0.0105	0.1344
DNAJC24	0.1788	0.0058	0.0324	0.1976	0.0204	0.1033	0.1771	0.0204	0.1153
DNAJC30	0.4778	0.0247	0.0516	0.4373	0.0438	0.1002	0.5884	0.0549	0.0933
DNAJC5G	0.5993	0.0497	0.0829	0.569	0.0327	0.0575	0.5711	0.0522	0.0914
DRAP1				0.1011	0.012	0.1189			
DSCR3	0.1042	0.0105	0.1006	0.0627	0.0105	0.1669	0.0432	0.006	0.1385
DUSP1	0	0	0.0449	0	0	0.0718	0	0	0.0787
EBI3	0.2103	0.0214	0.1016	0.1708	0.0327	0.1913	0.3173	0.0317	0.1
ECEL1	0.0846	0.0052	0.0617	0.043	0.0061	0.1422	0.0398	0.0055	0.1393
EFS	0.1653	0.0058	0.0351	0.2078	0.0184	0.0884	0.1793	0.0175	0.0978
EIF2C2	0.0704	0.0041	0.0576	0.0396	0.0033	0.0842	0.0054	0.0006	0.1028
EIF2C4	0	0	0.0319	0	0	0.0355	0	0	0.0477
ELF4	0.3394	0.0169	0.0497	0.1082	0.0061	0.0568	0.3497	0.0207	0.0592
ENOPH1	0	0	0.0277	0.109	0.0068	0.062	0.0994	0.0068	0.0679
EPB41L1	0.1423	0.0077	0.0543	0.0814	0.0047	0.0581	0.0777	0.0065	0.0838
EPB49	0.025	0.0011	0.0441	0.0134	0.0012	0.092	0.0134	0.0012	0.0922
EPHB3							0.0143	0.0014	0.0988
EPSTI1	0.4234	0.0166	0.0391	0.3636	0.03	0.0825	0.4674	0.0315	0.0675
EPT1	0.1564	0.0057	0.0367	0.1239	0.0069	0.0556	0.0957	0.0046	0.0479
ERC1	0.053	0.0024	0.045	0.0035	0.0004	0.1222	0.0163	0.0022	0.1365
ERCC3	0.1124	0.0067	0.0594	0.012	0.0011	0.0927	0.0668	0.0067	0.1001
EXD1	0.3932	0.0164	0.0418	0.2347	0.0193	0.0821	0.3664	0.0241	0.0659
EXPH5	0.6143	0.0277	0.0452	0.4855	0.0315	0.0649	0.4505	0.0376	0.0836
FAAH2	0.3914	0.0155	0.0395	0.1522	0.0125	0.0823	0.2414	0.0164	0.0681
FAM103A1	0	0	0.0718	0	0	0.0569	0	0	0.0423
FAM111A				0.8331	0.0495	0.0594			
FAM120A	0.3751	0.0204	0.0544	0.311	0.0214	0.0688	0.0314	0.0017	0.053
FAM126B	0.0321	0.0008	0.0261	0	0	0.0421	0.0198	0.0008	0.0421
FAM131A	0.1028	0.0048	0.0471	0.0592	0.0049	0.0831	0.1357	0.0099	0.0728
FAM165B	0.1406	0.0153	0.1092	0.0705	0.0076	0.1085	0.0692	0.0076	0.1101
FAM167A	0.2307	0.0168	0.0729						
FAM55B	0.2434	0.0125	0.0513	0.2198	0.0171	0.0779	0.2211	0.0173	0.0782
FAM64A	0.576	0.023	0.0399	0.4351	0.0374	0.0859	0.6546	0.0438	0.0669
FANCG	0.8996	0.0916	0.1018	0.3593	0.0199	0.0554	0.6225	0.0901	0.1448
FBL	0.1259	0.0103	0.082	0.0732	0.0071	0.097	0.1582	0.0185	0.1172
FBXL12	0.0173	0.0014	0.0811	0.0257	0.003	0.1188	0.0169	0.0015	0.0899
FBXO22	0.0773	0.0033	0.0425	0.1892	0.0105	0.0553	0.1445	0.0088	0.0609
FCRL2	0.5676	0.0228	0.0401	0.4991	0.0533	0.1069	0.6047	0.0583	0.0964
FGF2	0.17	0.0081	0.0475						
FGGY	0.1456	0.0054	0.037	0.1032	0.0088	0.0857	0.1348	0.0096	0.0715
FKRP	0.1504	0.0096	0.0638	0.0743	0.0113	0.1515	0.0655	0.0108	0.165
FLT3	0.1601	0.0072	0.045	0.2424	0.0158	0.0652	0.1743	0.0145	0.083
FMO6P	0.5962	0.0405	0.0679	0.5677	0.0655	0.1154	0.5539	0.0577	0.1042
FOLR2	0.0645	0.005	0.0778	0.1192	0.0152	0.1272	0.1276	0.0135	0.1055
FOSB	0	0	0.0267	0.0318	0.0013	0.0424	0.029	0.0013	0.0463
FTSJ2	0.1928	0.0165	0.0858	0.1591	0.0166	0.104	0.2005	0.0221	0.1104
FXYD3	0.3938	0.0264	0.067	0.0559	0.0064	0.1146	0.544	0.0371	0.0681
FZR1	0.0618	0.0059	0.0959	0.0488	0.0059	0.1215	0	0	0.1183
G6PC							0.128	0.0099	0.0776

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
GADD45A	0	0	0	0	0	0.0085	0	0	0.0529	0	0	0.0524
GAL3ST4	0.7101	0.0038	0.0053				0.4245	0.0113	0.0266	0.3252	0.0121	0.0373
GALNT12	0.098	0.0009	0.0095	0.7702	0.02	0.0259	0.1183	0.009	0.0762	0.0923	0.0058	0.0632
GCDH	0.4669	0.0108	0.0231	0.783	0.0152	0.0194	0.1388	0.0082	0.0593	0.1889	0.0082	0.0435
GCGR	0.1528	0.0043	0.0281	0.4499	0.0104	0.0231	0.2697	0.0216	0.08	0.1693	0.0139	0.0822
GCK	0.0768	0.0009	0.0123	0.4297	0.0184	0.0429	0.0141	0.0009	0.0669	0	0	0.0673
GCOM1	0.1432	0.0016	0.0109				0.3097	0.0371	0.1198	0.1401	0.0063	0.0448
GEMIN7	0.1801	0.0035	0.0195	0.3632	0.0035	0.0097	0.1808	0.0035	0.0194	0.3617	0.007	0.0194
GFOD2	0.0832	0.0023	0.028	0.0367	0.0012	0.0316	0.0161	0.0012	0.0721	0.0409	0.0036	0.0884
GFRAL	0.3582	0.0043	0.0121	0.6756	0.0054	0.008	0.436	0.0121	0.0278	0.3883	0.0195	0.0501
GIMAP2	0.1864	0.0051	0.0274	0.2014	0.0066	0.0326	0.5301	0.0194	0.0366	0.5254	0.0193	0.0368
GJA4	0.1371	0.0027	0.0198	0.0675	0.0027	0.0401	0.0553	0.0041	0.0736	0.037	0.0027	0.0734
GLYAT	0.0926	0.0015	0.0157	0.2352	0.0088	0.0372	0.1917	0.0102	0.0534	0.2738	0.0147	0.0536
GMNN	0.2891	0.0041	0.0144	0.2882	0.0062	0.0216	0.2844	0.0168	0.0589	0.1263	0.0104	0.0825
GNAO1	0	0	0.0042	0	0	0.0057	0.1383	0.04	0.2892	0.1196	0.0376	0.3143
GNAT2	0	0	0	0.1398	0.0012	0.0087	0.0208	0.0012	0.0582	0.0343	0.0012	0.0353
GNG5P2	0	0	0.0203	-1	0.0134	0	-1	0.0134	0	0.6591	0.0134	0.0203
GNPAT	0.1848	0.0032	0.0173	0.2685	0.0064	0.0238	0.169	0.007	0.0417	0.1114	0.0064	0.0575
GOLGA5	0.1454	0.003	0.0204	0.3891	0.0053	0.0136	0.2167	0.0071	0.0329	0.33	0.0102	0.0308
GOLGA6C	0.5956	0.0308	0.0518				0.4582	0.0542	0.1183	0.4038	0.0583	0.1444
GP1BA	0.2297	0.0049	0.0214	0.4677	0.0094	0.0201	0.5103	0.0333	0.0652	0.8032	0.0629	0.0784
GPHA2	0	0	0	0.3368	0.0035	0.0104	0.3352	0.007	0.0209	1.3511	0.0141	0.0104
GPR176	0.2903	0.007	0.024	0.0465	0.0009	0.0185	0.0496	0.0017	0.0348	0.0746	0.0026	0.0348
GPR179	0.4263	0.0064	0.015	0.5185	0.0062	0.012	0.4665	0.0211	0.0451	0.4447	0.0214	0.0481
GPR39	0.32	0.0039	0.0122	0.2659	0.0049	0.0184	0.2066	0.0138	0.0666	0.3671	0.0208	0.0566
GPR89A	0	0	0.013				0.1002	0.0013	0.013	0.0497	0.0013	0.0262
GPRASP2	2.0782	0.0036	0.0017	0.3274	0.0052	0.0158	0.2703	0.0062	0.023	0.3051	0.0114	0.0375
GPT2	0.2683	0.0043	0.0159	0	0	0.0185	0.0182	0.0009	0.0474	0.0247	0.0017	0.0685
GRIK3	0.0557	0.0019	0.0343	0.0412	0.0011	0.0259	0.0336	0.0019	0.0569	0.0126	0.001	0.0788
GSC	0.1727	0.0018	0.0102	0.0684	0.0018	0.0257	0.1709	0.0053	0.0309	0.1134	0.0035	0.031
GUCA1B	0	0	0.0156	0	0	0.0156	0	0	0.048	0	0	0.103
GUCY2F	0.4082	0.0033	0.0082	0.2451	0.0032	0.0129	0.1667	0.0063	0.038	0.2017	0.0072	0.0354
H2AFB3	1.1638	0.0123	0.0105				0.3177	0.0247	0.0777	0.5076	0.0332	0.0654
HAUS2	0	0	0	0.4256	0.0055	0.013	0	0	0.0297	0.7085	0.0092	0.013
HELB	0.1571	0.0024	0.0152	0.433	0.006	0.0138	0.3441	0.0136	0.0395	0.3665	0.0144	0.0393
HES5	0	0	0.0082	0	0	0.0163						
HEYL	0.4914	0.0056	0.0114	0.1361	0.0042	0.0309	0.1786	0.0098	0.055	0.2671	0.0234	0.0877
HIST1H2AJ	0	0	0.0194	0	0	0.0292	0	0	0.0597	0	0	0.1131
HIST1H2AL	0	0	0.0287	0.0202	0.0072	0.3546	0	0	0.0687	0	0	0.1331
HIST1H3F	0	0	0.0287	0.0045	0.0034	0.7391	0	0	0.0791	0	0	0.1003
HIST1H3G	0	0	0.0287				0	0	0.0894	0	0	0.0485
HLF	0	0	0.0097	0	0	0.0194	0.0491	0.0017	0.0344	0	0	0.0344
HM13	0	0	0	0	0	0.0137	0	0	0.0255	0.0326	0.001	0.0321
HMGCR	0.1034	0.001	0.0095	0.5264	0.0189	0.0359	0.1424	0.003	0.0208	0.0379	0.0015	0.039
HNRNPD	0	0	0.0042	0	0	0.0053	0	0	0.0126	0.2308	0.0049	0.0212
HNRPLL	0.0386	0.0008	0.021	0	0	0.0078	0.0441	0.0008	0.0183	0.0236	0.0008	0.0344
HRH3	0.4931	0.0175	0.0354	0.3622	0.0031	0.0085	0.5359	0.0099	0.0185	0.1094	0.0041	0.0376
HSD17B3	1.3096	0.0057	0.0044	0.2305	0.0072	0.0312	0.1592	0.0072	0.0452	0.2414	0.0086	0.0358
HSPB2							0.7274	0.0101	0.0139	0.0591	0.0025	0.0426
HSPBP1				0	0	0.0332						
ICT1	0.3036	0.0043	0.014	0.9356	0.0415	0.0444	0.2607	0.015	0.0576	0.5003	0.0117	0.0234
IDO2	0.665	0.0182	0.0274				0.5645	0.0143	0.0253	0.2826	0.0105	0.0373
IFI27L1	-1	0.0064	0				0.4105	0.0281	0.0685	0.4738	0.0412	0.0869
IFI44	0.4293	0.0099	0.023	0.3006	0.0069	0.0229	0.8675	0.0578	0.0667			
IFNA2	-1	0.0046	0	-1	0.0046	0	1.4452	0.0233	0.0161	0.5063	0.0269	0.0532
IL10RA	0.2585	0.0062	0.0238				0.4591	0.021	0.0458	0.4549	0.0257	0.0565
IL17RB	0.4891	0.007	0.0143	0.2167	0.0044	0.0201	0.299	0.0136	0.0454	0.3941	0.0149	0.0379
IL17REL				0.2435	0.0068	0.0278	0.3408	0.0135	0.0397	0.368	0.0181	0.0491
IL19	0.4666	0.0163	0.035	0.5126	0.0143	0.0278	0.5509	0.0269	0.0489	0.2882	0.0184	0.0639
ILKAP	0	0	0.0107	0.1027	0.0013	0.0128	0.0437	0.0022	0.0514	0.0434	0.0023	0.0538
INTS6	0.557	0.0032	0.0058	0.0995	0.001	0.01	0.299	0.0025	0.0083	0.4101	0.0165	0.0402
IRF8	0.0381	0.001	0.027	0.0874	0.0021	0.0235	0.1856	0.0083	0.0445	0.1228	0.0072	0.0588
IRX6	0.2917	0.0051	0.0175	0.5941	0.0116	0.0195	0.4226	0.0174	0.0413	0.3254	0.0216	0.0664
ISYNA1	0.2302	0.0016	0.007	0.0971	0.0032	0.0333	0.0944	0.0073	0.0778	0.0665	0.0049	0.073
ITGB3BP	0.5388	0.0048	0.009	1.1074	0.0113	0.0102	0.2655	0.0097	0.0365	0.4648	0.017	0.0366
ITGB8	0.0851	0.0017	0.0197	0.0255	0.0006	0.0254	0.0531	0.0022	0.0421	0.0972	0.0045	0.0461
JAG2	0.3614	0.0155	0.043	0.0412	0.0015	0.0356	0.1486	0.0153	0.1032	0.051	0.004	0.0779
JAM2	0.3214	0.0015	0.0046	0.749	0.0157	0.021	0.4038	0.0142	0.0353	0.9681	0.0158	0.0163
KANK3	0.2863	0.0056	0.0196	0.3195	0.0067	0.0211	0.5269	0.0288	0.0546	0.431	0.0164	0.0381
KCNB1	0	0	0.0118	0.0273	0.0007	0.0238	0.0118	0.0005	0.043	0.0227	0.001	0.0447
KCNG2	0.3016	0.0077	0.0256	0.099	0.005	0.0503						
KCNJ9	0.5164	0.0096	0.0185	0	0	0.0141	0	0	0.0276	0.3364	0.0032	0.0095
KDM5D	0.4915	0.0062	0.0126	0.197	0.0059	0.0299	0.2004	0.0124	0.0619			
KIAA0562	0.1386	0.0028	0.0204	0.2683	0.008	0.03	0.1668	0.01	0.0597	0.2655	0.0136	0.0511
KIAA0947	0.4057	0.0079	0.0195	0.3185	0.0075	0.0236	0.3014	0.013	0.0431	0.2533	0.014	0.0551
KIDINS220	0.1019	0.001	0.01	0.0802	0.0012	0.0154	0.084	0.0025	0.0294	0.0395	0.0018	0.0453
KLHDC4	0.3827	0.0085	0.0221	0.1405	0.0059	0.042	0.2142	0.0179	0.0834	0.2054	0.0178	0.0869
KLRG2	0.2201	0.0034	0.0153				0.1989	0.0113	0.0567	0.4504	0.0291	0.0646
KMO	0.4007	0.0062	0.0155	0.2041	0.0044	0.0218	0.4271	0.008	0.0188	0.2829	0.0098	0.0346
KPTN	0.4507	0.0113	0.0251	0.2262	0.0041	0.0183	0.2355	0.0125	0.053	0.5433	0.0374	0.0688
KRT36	0.5851	0.011	0.0189	0.573	0.0134	0.0234	0.166	0.0163	0.0985	0.2794	0.0203	0.0725
KRTAP4-7	0.8621	0.0085	0.0098				0.6885	0.025	0.0363	0.3428	0.0469	0.1368
L3MBTL1	0.1565	0.0016	0.01	0.3031	0.0029	0.0097	0.3066	0.0102	0.0334	0.2102	0.0079	0.0376
LAIR1	0.4549	0.0126	0.0278				0.8237	0.0616	0.0748			
LAMA4	0.2976	0.0037	0.0125	0.1102	0.0023	0.0206				0.1197	0.0059	0.049
LAMC2	0.4537	0.0044	0.0097	0.2823	0.0055	0.0194	0.3112	0.0103	0.0332	0.4437	0.014	0.0315
LAPTM4B	0.2045	0.0043	0.0209	0.4096	0.0124	0.0303	0.4094	0.0728	0.1778	0.7742	0.061	0.0788
LDB3	0.708	0.019	0.0268	0.1807	0.0037	0.0202	0.1512	0.0122	0.0808	0.0735	0.0062	0.0839
LEPREL4	0.2136	0.0061	0.0285	0.7332	0.0071	0.0096				0.1151	0.0061	0.0527
LETM2	0.9438	0.006	0.0063	-1	0.012	0	0.3438	0.0099	0.0289	0.5084	0.013	0.0255
LGALS7				0	0	0.039	0.1352	0.0067	0.0498	0.0855	0.0033	0.0391
LHFPL2	0	0	0.0184	0.1593	0.0019	0.0122	0.0813	0.0049	0.0598	0.0915	0.0064	0.0699
LHFPL5	0.157	0.0027	0.0175	0	0	0.0256						
LHX2	0	0	0.0075	0.1061	0.0022	0.0205	0	0	0.0205	0.0632	0.0022	0.0345
LIPH	0.2224	0.0029	0.013	0.4447	0.0062	0.0139	0.0978	0.004	0.0408	0.3626	0.0107	0.0294
LPAR3	0.1509	0.0025	0.0164	0.2319	0.0087	0.0375	0.1619	0.0074	0.046	0.2963	0.0125	0.0423
LRPPRC	0.1481	0.0022	0.0147	0.0782	0.0018	0.0225	0.454	0.019	0.0419	0.4256	0.0194	0.0456
LRRC2	0.8378	0.0035	0.0041	0.4656	0.0058	0.0124	0.2471	0.0116	0.047	0.2234	0.0104	0.0468
LRRC27	1.0017	0.0185	0.0185	0.5147	0.0152	0.0296	0.4293	0.0279	0.065	0.4097	0.0345	0.0842
LRRTM3	0	0	0.0074	0	0	0.014	0.1527	0.0023	0.0148	0	0	0.0173
LSM10	0	0	0.0112	0.3224	0.0073	0.0226	0.1064	0.0036	0.0341	0.0885	0.0073	0.0822
LSM7	0	0	0	0	0	0.0141	0.0735	0.0043	0.0582	0	0	0.0432
LTK	0.2559	0.0026	0.0103	0.3059	0.0041	0.0135	0.2702	0.0085	0.0313	0.3294	0.0146	0.0443
LYG1	0.2091	0.0046	0.0218	0.5696	0.0208	0.0365	1.9872	0.0361	0.0182	0.5055	0.0185	0.0365
MAGEA8	0.4726	0.0042	0.0088	0.1043	0.0014	0.0133	0.196	0.0098	0.0498	0.1809	0.0125	0.0693
MAGEB17	0.3425	0.0118	0.0345	0.6094	0.0212	0.0347	0.6639	0.0226	0.034	0.797	0.0346	0.0435
MAGEB3	-1	0.0113	0	3.4733	0.0151	0.0043	0.535	0.0189	0.0353	0.5101	0.0285	0.056

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
GADD45A	0.062	0.0027	0.0433	0	0	0.0085	0	0	0.0529	0	0	0.0524
GAL3ST4	0.2364	0.0189	0.0799				0.5298	0.0114	0.0215	0.4515	0.0132	0.0293
GALNT12	0.1269	0.0119	0.0937	0.1461	0.0019	0.0129	0.0428	0.0038	0.0884	0.0664	0.0049	0.0737
GCDH	0.0919	0.0082	0.0894	0.6536	0.0241	0.0368	0.219	0.017	0.0778	0.2761	0.017	0.0616
GCGR	0.2972	0.034	0.1144	0.6353	0.013	0.0205	0.3139	0.0242	0.0771	0.2219	0.0168	0.0759
GCK	0.2737	0.0263	0.0963	0.532	0.0194	0.0365	0.0313	0.0019	0.0602	0.0196	0.0012	0.059
GCOM1	0.0657	0.0063	0.0956				0.3462	0.0371	0.1072	0.1882	0.0063	0.0334
GEMIN7	0.296	0.0177	0.0598	0.7285	0.007	0.0097	0.179	0.007	0.0393	0.2685	0.0106	0.0394
GFOD2	0	0	0.1394	0.1108	0.0035	0.0315	0.0543	0.0035	0.0644	0.0756	0.006	0.08
GFRAL	1.143	0.0302	0.0264	0.1607	0.0032	0.0202	0.3007	0.0121	0.0403	0.2942	0.0173	0.0587
GIMAP2	0.6594	0.0366	0.0555	0.2024	0.0066	0.0325	0.5327	0.0194	0.0364	0.4679	0.0194	0.0414
GJA4	0.068	0.0068	0.0999	0.0995	0.0034	0.034	0.0521	0.0041	0.0781	0.0392	0.0027	0.0692
GLYAT	0.3771	0.0356	0.0944	0.3464	0.0073	0.021	0.2371	0.0088	0.037	0.3555	0.0132	0.0371
GMNN	0.3452	0.0231	0.0669	0.289	0.0021	0.0072	0.2852	0.0125	0.0439	0.0929	0.0062	0.067
GNAO1	0	0	0.0389	0	0	0.0057	0.1413	0.04	0.2831	0.1221	0.0376	0.3079
GNAT2	0.0168	0.0012	0.0722	0.1398	0.0012	0.0087	0.0208	0.0012	0.0582	0.0343	0.0012	0.0353
GNG5P2	0.4363	0.027	0.062	0.6614	0.0134	0.0202	0.6621	0.0134	0.0202	0.325	0.0134	0.0411
GNPAT	0.1803	0.0106	0.0588	0.2943	0.007	0.0239	0.1838	0.0077	0.0418	0.113	0.007	0.0623
GOLGA5	0.2181	0.0137	0.0629	0.2337	0.0026	0.0113	0.1119	0.0041	0.0371	0.1827	0.0072	0.0392
GOLGA6C	0.4848	0.1161	0.2395				0.6603	0.0669	0.1014	0.5357	0.0697	0.1302
GP1BA	0.6157	0.0692	0.1124	0.6338	0.0101	0.016	0.6038	0.0355	0.0588	0.8417	0.0649	0.0771
GPHA2	0.3302	0.0212	0.0643	0.3368	0.0035	0.0104	0.3352	0.007	0.0209	1.3511	0.0141	0.0104
GPR176	0.1118	0.0061	0.0542	0.2278	0.0061	0.0267	0.1609	0.007	0.0432	0.1442	0.0078	0.0544
GPR179	0.5374	0.0716	0.1333	0.6803	0.0098	0.0144	0.4901	0.0234	0.0477	0.4541	0.0234	0.0515
GPR39	0.3865	0.0298	0.077	0.4008	0.0049	0.0122	0.2175	0.0138	0.0633	0.415	0.0208	0.05
GPR89A	0.0363	0.0026	0.0718				0.0749	0.0013	0.0174	0.0425	0.0013	0.0306
GPRASP2	0.3063	0.0178	0.058	0.2213	0.0031	0.014	0.171	0.0036	0.0212	0.2184	0.0078	0.0356
GPT2	0.0185	0.0017	0.0916	0.2296	0.0043	0.0186	0.098	0.0052	0.0534	0.0834	0.006	0.0716
GRIK3	0.011	0.001	0.087	0.0533	0.0021	0.0401	0.0534	0.0029	0.0536	0.0252	0.002	0.0789
GSC	0.0336	0.0018	0.0523	0	0	0.0153	0.1726	0.0035	0.0204	0.0569	0.0018	0.0309
GUCA1B	0	0	0.1447	0	0	0	0	0	0.048	0	0	0.103
GUCY2F	0.1885	0.0115	0.0611	0.2439	0.0033	0.0137	0.1717	0.0067	0.0389	0.2169	0.0075	0.0348
H2AFB3	0.498	0.0656	0.1317				0.4369	0.0289	0.0661	0.6924	0.0375	0.0541
HAUS2	0.2446	0.0129	0.0529	0.4256	0.0055	0.013	0	0	0.0297	0.7085	0.0092	0.013
HELB	0.3654	0.0231	0.0633	0.5381	0.0052	0.0096	0.3641	0.0128	0.0351	0.3596	0.0136	0.0378
HES5	0.1076	0.0082	0.0757	0	0	0.0165						
HEYL	0.3586	0.0299	0.0835	0.0403	0.0014	0.0347	0.1189	0.007	0.059	0.2532	0.0234	0.0925
HIST1H2AJ	0	0	0.1586	0	0	0.0292	0	0	0.0598	0	0	0.1133
HIST1H2AL	0.0147	0.0036	0.2433	0.0178	0.0072	0.4014	0	0	0.079	0	0	0.1444
HIST1H3F	0	0	0.1562	0.0047	0.0034	0.7105	0	0	0.0483	0	0	0.0893
HIST1H3G	0	0	0.1225				0	0	0.0998	0	0	0.0585
HLF	0	0	0.0395	0	0	0.0097	0.0743	0.0017	0.0228	0	0	0.0244
HM13	0.016	0.001	0.0657	0	0	0.0137	0	0	0.0255	0.0326	0.001	0.0321
HMGCR	0.0893	0.0054	0.0609	0.4825	0.0189	0.0392	0.1234	0.003	0.024	0.035	0.0015	0.0423
HNRNPD	0	0	0.0169	0	0	0	0	0	0.0084	0.2894	0.0049	0.0169
HNRPLL	0.041	0.0024	0.0592	0.0342	0.0008	0.0237	0.0557	0.0016	0.029	0.0358	0.0016	0.0454
HRH3	0.0561	0.0072	0.1284	0.5763	0.0186	0.0323	0.6	0.0273	0.0455	0.3221	0.0197	0.0613
HSD17B3	0.219	0.0203	0.0929	0.2699	0.0072	0.0267	0.1776	0.0072	0.0405	0.2769	0.0086	0.0312
HSPB2	0	0	0.0354									
HSPBP1	0.0145	0.0013	0.087									
ICT1	0.3202	0.0259	0.0809	0.8803	0.0392	0.0446	0.1848	0.0107	0.0578	0.1767	0.007	0.0396
IDO2	0.3554	0.0283	0.0797				0.6103	0.0247	0.0405	0.4969	0.023	0.0462
IFI27L1	0.5891	0.063	0.107				0.2368	0.0196	0.0827	0.1318	0.0147	0.1117
IFI44				0.4535	0.0089	0.0196	1.0307	0.0579	0.0561			
IFNA2	0.5284	0.0352	0.0667	-1	0.0046	0	1.4452	0.0233	0.0161	0.5063	0.0269	0.0532
IL10RA	0.3156	0.0324	0.1027				0.4788	0.0195	0.0406	0.5388	0.0249	0.0463
IL17RB	0.26	0.0194	0.0745	0.2721	0.0079	0.0289	0.2979	0.0158	0.053	0.417	0.019	0.0455
IL17REL	0.4498	0.0385	0.0857									
IL19	0.6053	0.0408	0.0673	0.4075	0.0143	0.035	0.6446	0.0269	0.0418	0.2576	0.0184	0.0714
ILKAP	0.1099	0.0056	0.0513	0.0509	0.0013	0.0258	0.0357	0.0022	0.0629	0.0354	0.0023	0.0658
INTS6	0.0244	0.001	0.0408	0.2285	0.0032	0.0142	0.3341	0.0047	0.0142	0.3834	0.0178	0.0465
IRF8	0.0829	0.0052	0.0622	0.0275	0.001	0.0374	0.1229	0.0072	0.0587	0.0803	0.0062	0.077
IRX6	0.2606	0.0248	0.0951	0.2745	0.0081	0.0295	0.3064	0.0164	0.0536	0.2596	0.0206	0.0794
ISYNA1	0.0778	0.0108	0.1391	0.0621	0.0016	0.026	0.0798	0.0055	0.069	0.0496	0.0032	0.0653
ITGB3BP	0.5799	0.032	0.0552	0.5476	0.0113	0.0206	0.2103	0.0097	0.046	0.3681	0.017	0.0462
ITGB8	0.061	0.0045	0.0735	0.094	0.0019	0.0207	0.1032	0.0039	0.038	0.1333	0.005	0.0379
JAG2	0.0463	0.0064	0.1388	0.421	0.0151	0.0359	0.3116	0.0364	0.1168	0.2396	0.0195	0.0812
JAM2	0.2601	0.0166	0.064	0.6129	0.0158	0.0257	0.3563	0.0143	0.04	0.753	0.0158	0.0209
KANK3	0.2963	0.0299	0.1008	0.3479	0.0079	0.0226	0.5276	0.0308	0.0584	0.4104	0.0176	0.0428
KCNB1	0.0153	0.001	0.0663	0.025	0.0007	0.026	0.0113	0.0005	0.0447	0.0203	0.001	0.05
KCNG2				0.1806	0.0088	0.0488						
KCNJ9	0.0179	0.0011	0.0635	0.3013	0.0099	0.0328	0.2654	0.0096	0.036	0.1672	0.0032	0.019
KDM5D	0.2001	0.0321	0.1603	0.2986	0.0068	0.0226	0.2114	0.0127	0.0602			
KIAA0562	0.1505	0.0128	0.0851	0.2652	0.0071	0.0268	0.1509	0.009	0.0597	0.2395	0.0122	0.0508
KIAA0947	0.3178	0.0278	0.0874	0.4478	0.0098	0.0219	0.2718	0.0102	0.0376	0.2817	0.0149	0.0531
KIDINS220	0.0511	0.0041	0.0797	0.1244	0.0023	0.0185	0.1003	0.0036	0.0357	0.0575	0.0028	0.0488
KLHDC4	0.1467	0.0187	0.1275	0.2319	0.0084	0.0364	0.2634	0.0204	0.0776	0.2187	0.0204	0.0933
KLRG2	0.5027	0.0499	0.0993				0.2023	0.0101	0.0501	0.5104	0.028	0.0548
KMO	0.567	0.029	0.0511	0.2263	0.0071	0.0314	0.2549	0.0089	0.0349	0.244	0.0125	0.0511
KPTN	0.1983	0.0157	0.0789	0.4501	0.0113	0.0251	0.2261	0.0156	0.0689	0.6626	0.0544	0.082
KRT36	0.2021	0.0177	0.0874	0.4824	0.0091	0.0189	0.15	0.0139	0.093	0.214	0.0154	0.072
KRTAP4-7	0.515	0.1426	0.2769				0.7383	0.0329	0.0445	0.1898	0.0334	0.1761
L3MBTL1	0.3079	0.0097	0.0316	0.2018	0.0023	0.0116	0.3238	0.0108	0.0334	0.189	0.0084	0.0446
LAIR1	0.8493	0.0915	0.1077				1.0059	0.065	0.0647			
LAMA4	0.1267	0.0084	0.0664	0.2217	0.0043	0.0193				0.1652	0.0075	0.0455
LAMC2	0.2963	0.0166	0.056	0.25	0.0055	0.0219	0.3106	0.0103	0.0333	0.4094	0.014	0.0342
LAPTM4B	0.2752	0.0227	0.0825	0.3995	0.0142	0.0355	0.4052	0.0743	0.1834	0.6437	0.059	0.0917
LDB3	0.0696	0.0092	0.1324	0.6314	0.0266	0.0422	0.3629	0.0355	0.0978	0.2667	0.0256	0.0959
LEPREL4	0.085	0.0081	0.0951	0.2498	0.0061	0.0244				0.0858	0.0061	0.0711
LETM2	0.6031	0.0639	0.106	1.8989	0.012	0.0063	0.2805	0.01	0.0355	0.4055	0.013	0.032
LGALS7	0.1245	0.0101	0.0807									
LHFPL2	0.0923	0.0058	0.0632	0.1058	0.0019	0.0184	0.0732	0.0049	0.0664	0.0828	0.0064	0.0772
LHFPL5	0	0	0.0955	0.0776	0.0027	0.0354						
LHX2	0.0183	0.0011	0.0597	0.0794	0.0024	0.0304	0	0	0.0265	0	0	0.0421
LIPH	0.42	0.0234	0.0556	0.3434	0.0072	0.021	0.1251	0.006	0.0479	0.3214	0.0116	0.0362
LPAR3	0.1175	0.015	0.1276	0.2128	0.0062	0.0291	0.1319	0.005	0.0376	0.2355	0.01	0.0425
LRPPRC	0.602	0.0486	0.0808	0.3699	0.0044	0.0119	0.5676	0.0213	0.0375	0.5259	0.0216	0.0411
LRRC2	0.3698	0.0199	0.0539	0.2788	0.0023	0.0083	0.1899	0.0081	0.0427	0.1635	0.0069	0.0425
LRRC27				0.8671	0.0256	0.0295	0.5457	0.0385	0.0706	0.4731	0.0425	0.0899
LRRTM3	0	0	0.0248	0	0	0.014	0.1307	0.0023	0.0173	0	0	0.0198
LSM10	0.1901	0.011	0.0576	0.2127	0.0073	0.0342	0.079	0.0036	0.046	0.0766	0.0073	0.095
LSM7	0	0	0.1049	0	0	0.0141	0.0735	0.0043	0.0582	0	0	0.0432
LTK	0.2464	0.0187	0.076	0.4371	0.0059	0.0135	0.287	0.009	0.0313	0.3668	0.0151	0.0413
LYG1	0.9498	0.0349	0.0368	0.7202	0.0208	0.0289	1.0369	0.0302	0.0291	0.6392	0.0185	0.0289
MAGEA8				1.2638	0.0056	0.0044	0.3456	0.014	0.0404	0.2811	0.0168	0.0596
MAGEB17	0.5287	0.0347	0.0657	0.4523	0.0198	0.0438	0.462	0.0239	0.0517	0.5606	0.0346	0.0617
MAGEB3	0.5071	0.0344	0.0678	3.7937	0.0164	0.0043	0.5754	0.0202	0.0351	0.4599	0.0267	0.058

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
GADD45A	0.062	0.0027	0.0433	0	0	0.0619	0	0	0.0433	0.0515	0.0027	0.0521
GAL3ST4	0.2315	0.0181	0.0782									
GALNT12	0.0672	0.0065	0.0973	0.2521	0.0252	0.1001	0.0647	0.0044	0.0683	0.221	0.0235	0.1063
GCDH	0.1835	0.0165	0.0899	0.3043	0.0194	0.0637	0.476	0.022	0.0462	0.2282	0.0215	0.0941
GCGR	0.3294	0.0367	0.1114	0.4624	0.027	0.0584	0.2805	0.0178	0.0635	0.4234	0.0378	0.0892
GCK	0.3058	0.0273	0.0893	0.2252	0.0194	0.0862	0.0195	0.0012	0.0592	0.2381	0.0223	0.0936
GCOM1	0.0753	0.0063	0.0834									
GEMIN7	0.2636	0.0213	0.0808	0.2406	0.007	0.0293	0.361	0.0106	0.0293	0.3039	0.0213	0.0702
GFOD2	0.0168	0.0023	0.1389	0	0	0.0683	0.0286	0.0024	0.0843	0.0086	0.0012	0.1353
GFRAL	0.7748	0.0285	0.0368	0.3669	0.0132	0.036	0.2761	0.0162	0.0585	0.9107	0.0297	0.0326
GIMAP2	0.6626	0.0366	0.0553	0.6594	0.0213	0.0323	0.5701	0.0212	0.0373	0.7336	0.0377	0.0513
GJA4	0.0709	0.0068	0.0957	0.0445	0.0041	0.0913	0.033	0.0027	0.0822	0.0621	0.0068	0.1093
GLYAT	0.4435	0.0341	0.0768	0.5015	0.0132	0.0263	0.6683	0.0176	0.0264	0.5893	0.0386	0.0655
GMNN	0.3642	0.0188	0.0517	0.402	0.0146	0.0364	0.1403	0.0083	0.0593	0.4753	0.021	0.0441
GNAO1	0	0	0.0345	0.1228	0.0496	0.4041	0.1143	0.0496	0.4339	0	0	0.035
GNAT2	0.0168	0.0012	0.0722	0.0359	0.0024	0.0676	0.0547	0.0024	0.0443	0.0297	0.0024	0.0817
GNG5P2	0.3226	0.027	0.0838	-1	0.0271	0	1.341	0.027	0.0202	0.666	0.041	0.0616
GNPAT	0.1722	0.0116	0.0671	0.2108	0.0083	0.0395	0.1283	0.0077	0.06	0.1887	0.0122	0.0647
GOLGA5	0.1496	0.0107	0.0716	0.203	0.0046	0.0228	0.2908	0.0087	0.0298	0.147	0.0093	0.0632
GOLGA6C	0.5906	0.1316	0.2229									
GP1BA	0.6528	0.0717	0.1098	0.6961	0.0365	0.0524	0.9319	0.0633	0.0679	0.7312	0.0764	0.1045
GPHA2	0.3302	0.0212	0.0643	0.1106	0.0035	0.0316	0.5016	0.0105	0.021	0.2334	0.0176	0.0756
GPR176	0.1803	0.0113	0.0629	0.0229	0.0009	0.0376	0.0355	0.0017	0.0486	0.0909	0.0052	0.0571
GPR179	0.5517	0.0736	0.1333	0.555	0.023	0.0414	0.4827	0.0235	0.0487	0.5691	0.0747	0.1313
GPR39	0.4238	0.0298	0.0702	0.202	0.0128	0.0633	0.3952	0.0198	0.05	0.4096	0.0288	0.0702
GPR89A	0.0341	0.0026	0.0766									
GPRASP2	0.2511	0.0141	0.056	0.201	0.0057	0.0284	0.2544	0.0109	0.043	0.2713	0.0172	0.0635
GPT2	0.061	0.006	0.098	0.0172	0.0009	0.0503	0.0247	0.0017	0.0685	0.0191	0.0017	0.0887
GRIK3	0.0211	0.0019	0.0905	0.0326	0.0021	0.0655	0.0143	0.0011	0.0748	0.0107	0.0011	0.0996
GSC	0	0	0.0414	0.0976	0.0035	0.0361	0.0375	0.0018	0.0468	0	0	0.0575
GUCA1B	0	0	0.1447	0	0	0.048	0	0	0.103	0	0	0.1447
GUCY2F	0.2059	0.0121	0.059	0.1165	0.0047	0.0407	0.1617	0.006	0.0368	0.1614	0.0103	0.0639
H2AFB3	0.587	0.07	0.1193									
HAUS2	0.2446	0.0129	0.0529	0.1413	0.0063	0.0449	0.7568	0.0148	0.0195	0.2223	0.0148	0.0667
HELB	0.3758	0.0229	0.061	0.3913	0.0132	0.0337	0.3735	0.0136	0.0364	0.4121	0.0233	0.0566
HES5	0.0957	0.0082	0.0861							0.0867	0.0082	0.0945
HEYL	0.3091	0.0271	0.0875	0.1019	0.0056	0.055	0.2626	0.0217	0.0827	0.3069	0.0256	0.0834
HIST1H2AJ	0	0	0.1589	0	0	0.0701	0	0	0.1243	0	0	0.1705
HIST1H2AL	0.0139	0.0036	0.2565	0.0086	0.0036	0.4167	0	0	0.4679	0.0085	0.0036	0.4209
HIST1H3F	0	0	0.1442	0.0051	0.0034	0.6637	0.0052	0.0034	0.6413	0.0049	0.0034	0.688
HIST1H3G	0	0	0.1333									
HLF	0	0	0.0294	0.0491	0.0017	0.0344	0	0	0.0344	0	0	0.0344
HM13	0.016	0.001	0.0657	0	0	0.0279	0.047	0.0011	0.0242	0.0179	0.0011	0.0638
HMGCR	0.0847	0.0054	0.0643	0.5133	0.0209	0.0408	0.3259	0.0194	0.0595	0.2862	0.0235	0.082
HNRNPD	0	0	0.0126	0	0	0.0053	0	0	0.0106	0	0	0.0106
HNRPLL	0.0395	0.0032	0.082	0.0385	0.0008	0.021	0.0218	0.0008	0.0371	0.0359	0.0024	0.0676
HRH3	0.1526	0.0232	0.1518	0.572	0.0088	0.0154	0.0296	0.001	0.0347	0.0555	0.0065	0.1175
HSD17B3	0.2314	0.0203	0.0879	0.2138	0.0086	0.0404	0.2506	0.0101	0.0403	0.2236	0.0218	0.0976
HSPB2												
HSPBP1										0.0177	0.0016	0.093
ICT1	0.2647	0.0215	0.0812	0.5601	0.0507	0.0904	0.6762	0.0506	0.0748	0.5391	0.0621	0.1152
IDO2	0.4017	0.0373	0.093									
IFI27L1	0.592	0.0605	0.1021									
IFI44				0.782	0.0547	0.0699						
IFNA2	0.5284	0.0352	0.0667	1.4525	0.0233	0.0161	0.5089	0.027	0.053	0.5312	0.0353	0.0664
IL10RA	0.3452	0.0329	0.0952									
IL17RB	0.284	0.0234	0.0824	0.2323	0.0127	0.0546	0.2988	0.0141	0.047	0.2197	0.0185	0.0841
IL17REL				0.1817	0.0095	0.0523	0.2982	0.018	0.0605	0.3334	0.0331	0.0993
IL19	0.5441	0.0407	0.0749	0.7173	0.0248	0.0346	0.3891	0.0163	0.042	0.5732	0.0386	0.0674
ILKAP	0.0898	0.0056	0.0627	0.0689	0.0039	0.0572	0.0639	0.0039	0.0617	0.1648	0.0079	0.048
INTS6	0.0904	0.0042	0.0469	0.2135	0.0025	0.0117	0.3771	0.0165	0.0437	0.0225	0.001	0.0442
IRF8	0.0537	0.0041	0.0768	0.1499	0.0083	0.0551	0.0938	0.0072	0.077	0.0641	0.0052	0.0804
IRX6	0.1993	0.0216	0.1085	0.3511	0.0174	0.0497	0.271	0.0222	0.0818	0.1795	0.0199	0.1106
ISYNA1	0.069	0.0092	0.1333	0.0983	0.0074	0.0748	0.0666	0.0049	0.0729	0.0796	0.0108	0.1361
ITGB3BP	0.4921	0.032	0.0649	0.2701	0.0113	0.0417	0.3739	0.0198	0.053	0.6841	0.0432	0.0632
ITGB8	0.0777	0.005	0.0649	0.0654	0.0026	0.0397	0.1047	0.0039	0.0373	0.0662	0.0039	0.059
JAG2	0.1944	0.0246	0.1264	0.1538	0.0161	0.1044	0.0527	0.0041	0.0779	0.0524	0.0067	0.1275
JAM2	0.2393	0.0167	0.0696	0.0285	0.0015	0.0522	0.0907	0.003	0.0328	0.0206	0.0017	0.0843
KANK3	0.2971	0.0304	0.1025	0.5783	0.0315	0.0545	0.4547	0.0187	0.0412	0.3314	0.0322	0.0972
KCNB1	0.0145	0.001	0.0699	0.0256	0.0013	0.0508	0.0339	0.002	0.0576	0.0256	0.002	0.0762
KCNG2												
KCNJ9	0.1347	0.011	0.0817	0	0	0.0357	0.1333	0.0032	0.0239	0.0169	0.0012	0.0693
KDM5D	0.2152	0.0326	0.1516	0.1792	0.0121	0.0676				0.2132	0.0331	0.1553
KIAA0562	0.1394	0.0119	0.0851	0.1638	0.0095	0.0579	0.2963	0.0136	0.0458	0.1473	0.0116	0.0789
KIAA0947	0.2763	0.0231	0.0836	0.2874	0.0123	0.0428	0.2601	0.0143	0.0548	0.3057	0.0272	0.0889
KIDINS220	0.062	0.0052	0.0846	0.0933	0.0032	0.0344	0.0505	0.0026	0.0506	0.0566	0.0048	0.0851
KLHDC4	0.1681	0.0204	0.1215	0.2103	0.017	0.0808	0.1401	0.0135	0.0966	0.1496	0.0187	0.1249
KLRG2	0.5294	0.0487	0.0919									
KMO	0.4384	0.0299	0.0682	0.2044	0.0071	0.0348	0.1745	0.0089	0.051	0.4583	0.0281	0.0612
KPTN	0.2074	0.0228	0.1099	0.1886	0.0125	0.0661	0.4944	0.0374	0.0756	0.1691	0.0156	0.0925
KRT36	0.1797	0.0149	0.0831	0.1912	0.0163	0.0855	0.3564	0.0203	0.0568	0.2291	0.0173	0.0756
KRTAP4-7	0.5252	0.1768	0.3366									
L3MBTL1	0.3262	0.0103	0.0316	0.2953	0.0103	0.0348	0.2025	0.0088	0.0436	0.2967	0.0103	0.0347
LAIR1	1.094	0.095	0.0869									
LAMA4	0.1647	0.0107	0.0651				0.1252	0.006	0.0476	0.1384	0.0092	0.0668
LAMC2	0.2827	0.0166	0.0587	0.3235	0.0108	0.0332	0.3655	0.0144	0.0393	0.2829	0.0162	0.0573
LAPTM4B	0.2768	0.0242	0.0873	0.4636	0.0874	0.1884	0.7712	0.0873	0.1132	0.3731	0.0377	0.1011
LDB3	0.2093	0.0286	0.1367	0.2387	0.0106	0.0444	0.1019	0.0059	0.0579	0.0977	0.0118	0.1203
LEPREL4	0.0682	0.0073	0.1073				0.1435	0.0071	0.0493	0.0993	0.0091	0.0916
LETM2	0.565	0.064	0.1132	0.4488	0.013	0.0289	0.7195	0.016	0.0223	0.6352	0.0672	0.1059
LGALS7				0.1351	0.0067	0.0498	0.0854	0.0033	0.0391	0.0982	0.0101	0.1024
LHFPL2	0.0835	0.0058	0.0699	0.0308	0.0019	0.063	0.061	0.0043	0.0698	0.1234	0.0078	0.0632
LHFPL5	0.0208	0.0028	0.1358							0	0	0.1102
LHX2	0.0172	0.0012	0.0702	0.0631	0.0022	0.0345	0.0895	0.0044	0.0488	0.0419	0.0033	0.0782
LIPH	0.4019	0.0257	0.064	0.1571	0.0075	0.0475	0.4811	0.0135	0.028	0.4093	0.0265	0.0648
LPAR3	0.0973	0.0125	0.1281	0.1223	0.0062	0.0506	0.2017	0.0113	0.0558	0.0959	0.0137	0.1429
LRPPRC	0.6803	0.051	0.0749	0.5259	0.0205	0.0389	0.5195	0.0217	0.0417	0.7756	0.0558	0.072
LRRC2	0.3247	0.0159	0.0489	0.1907	0.0081	0.0425	0.1642	0.007	0.0423	0.3264	0.0159	0.0487
LRRC27				0.4188	0.03	0.0716	0.3794	0.0357	0.0942			
LRRTM3	0	0	0.0273	0.0673	0.0017	0.0254	0	0	0.0282	0	0	0.0311
LSM10	0.1567	0.0109	0.0699	0.1063	0.0036	0.0341	0.0884	0.0073	0.0823	0.1899	0.011	0.0577
LSM7	0	0	0.1049	0.099	0.0043	0.0432	0	0	0.0582	0	0	0.1212
LTK	0.2482	0.0194	0.0782	0.2765	0.0095	0.0342	0.332	0.0164	0.0492	0.2206	0.018	0.0815
LYG1	0.7051	0.0338	0.0479	0.9629	0.0422	0.0439	0.5536	0.022	0.0398	0.5129	0.0362	0.0707
MAGEA8				0.2471	0.0112	0.0451	0.216	0.0139	0.0645			
MAGEB17	0.4015	0.0367	0.0915	0.5115	0.0267	0.0521	0.6014	0.0374	0.0622	0.3963	0.0375	0.0946
MAGEB3	0.4916	0.0331	0.0674	0.5389	0.0215	0.0398	0.4715	0.0286	0.0606	0.5106	0.037	0.0725

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
GADD45A	0	0	0.0899	0.0334	0.0027	0.0803	0.0338	0.0027	0.0795
GAL3ST4	0.6535	0.017	0.0261	0.3471	0.0227	0.0655	0.2308	0.018	0.0781
GALNT12	0.0988	0.0066	0.0671	0.1289	0.0129	0.1001	0.0951	0.0095	0.0998
GCDH	0.1911	0.0113	0.0593	0.1032	0.0124	0.1199	0.0997	0.0103	0.1032
GCGR	0.2316	0.0202	0.0873	0.3599	0.0427	0.1185	0.2076	0.0242	0.1164
GCK	0.0131	0.0012	0.0883	0.2738	0.0273	0.0998	0	0	0.0884
GCOM1	0.404	0.0371	0.0918	0.2723	0.0367	0.1347	0.081	0.0063	0.0775
GEMIN7	0.0894	0.0035	0.0393	0.1756	0.0142	0.0806	0.2967	0.0177	0.0597
GFOD2	0.0428	0.0024	0.0563	0.0105	0.0012	0.1108	0.0269	0.0036	0.1345
GFRAL	0.354	0.0213	0.0602	0.8684	0.0302	0.0348	0.896	0.0374	0.0417
GIMAP2	0.4398	0.0181	0.0411	0.7771	0.0354	0.0455	0.5647	0.034	0.0601
GJA4	0.0555	0.0041	0.0734	0.0895	0.0082	0.0911	0.0739	0.0054	0.0735
GLYAT	0.4517	0.0191	0.0424	0.4885	0.0402	0.0823	0.4314	0.0356	0.0825
GMNN	0.0934	0.0062	0.0668	0.3905	0.0231	0.0592	0.2018	0.0167	0.0829
GNAO1	0.0567	0.0024	0.0432	0.1416	0.04	0.2826	0.1223	0.0376	0.3074
GNAT2	0.0452	0.0024	0.0536	0.0296	0.0024	0.0818	0.0453	0.0024	0.0535
GNG5P2	0.6652	0.0134	0.0201	0.4404	0.0271	0.0616	0.3241	0.0271	0.0835
GNPAT	0.0882	0.0045	0.0508	0.1619	0.009	0.0554	0.1507	0.0083	0.0553
GOLGA5	0.213	0.0066	0.0308	0.1503	0.0101	0.0673	0.1909	0.0108	0.0564
GOLGA6C	0.4576	0.0728	0.159	0.5315	0.1227	0.2309	0.4974	0.1107	0.2226
GP1BA	0.6557	0.0639	0.0975	0.6631	0.0752	0.1135	0.6206	0.0675	0.1087
GPHA2	0.4438	0.0141	0.0317	0.2439	0.0212	0.0871	0.3746	0.0284	0.0758
GPR176	0.0478	0.0026	0.0542	0.1061	0.0061	0.0571	0.07	0.0052	0.0741
GPR179	0.5135	0.0233	0.0453	0.5656	0.0765	0.1352	0.5636	0.0766	0.1359
GPR39	0.2723	0.0218	0.0799	0.2937	0.0308	0.1047	0.361	0.0278	0.0769
GPR89A	0	0	0.0218	0.0194	0.0013	0.0672	0.0182	0.0013	0.0718
GPRASP2	0.3071	0.0104	0.0339	0.2458	0.0156	0.0636	0.2485	0.0172	0.0693
GPT2	0.0325	0.0017	0.0532	0.0325	0.0026	0.0799	0.0346	0.0034	0.0978
GRIK3	0.0277	0.002	0.0717	0.02	0.0019	0.0956	0.0113	0.001	0.0877
GSC	0.5208	0.0053	0.0101	0.1726	0.0035	0.0204	0.0569	0.0018	0.0309
GUCA1B	0	0	0.0706	0	0	0.1262	0	0	0.1368
GUCY2F	0.2171	0.006	0.0275	0.2004	0.0103	0.0515	0.2269	0.011	0.0483
H2AFB3	0.3801	0.0123	0.0322	0.8014	0.0394	0.0492	0.5282	0.0438	0.083
HAUS2	0.1879	0.0085	0.0451	0.1621	0.0085	0.0524	0.2776	0.0186	0.0668
HELB	0.3955	0.0142	0.0359	0.3789	0.025	0.0659	0.3283	0.0201	0.0611
HES5									
HEYL	0.3665	0.0234	0.0638	0.4068	0.0256	0.0629	0.4719	0.0389	0.0825
HIST1H2AJ	0	0	0.1133	0	0	0.1357	0	0	0.22
HIST1H2AL	0	0	0.1217	0.0155	0.0036	0.2299	0.0139	0.0036	0.2561
HIST1H3F	0	0	0.0789	0	0	0.1329	0	0	0.1329
HIST1H3G	0	0	0.0686	0	0	0.1558	0	0	0.1114
HLF	0.0592	0.0017	0.0285	0.049	0.0017	0.0345	0	0	0.0344
HM13	0.04	0.0012	0.0292	0.0164	0.0012	0.0714	0.0319	0.0021	0.0657
HMGCR	0.1129	0.0035	0.0306	0.1422	0.0074	0.0523	0.0974	0.0059	0.061
HNRNPD	0.2894	0.0049	0.0169	0	0	0.0211	0.164	0.0049	0.0298
HNRPLL	0.0511	0.0016	0.0318	0.0522	0.0032	0.0621	0.0443	0.0032	0.0734
HRH3	0.1752	0.0077	0.0439	0.0786	0.0101	0.1282	0.0472	0.0052	0.109
HSD17B3	0.0792	0.0043	0.0544	0.1565	0.013	0.0831	0.1562	0.0145	0.0927
HSPB2	0.298	0.0127	0.0425	0.2863	0.0101	0.0353	0.0387	0.0025	0.0649
HSPBP1									
ICT1	0.0976	0.0047	0.0477	0.2386	0.0193	0.081	0.1927	0.014	0.0728
IDO2	0.3192	0.0139	0.0436	0.3468	0.0241	0.0694	0.3089	0.0271	0.0878
IFI27L1	0.2962	0.0255	0.0862	0.937	0.0446	0.0476	0.5856	0.0629	0.1074
IFI44									
IFNA2	0.5667	0.0281	0.0495	0.5212	0.0351	0.0674	0.3909	0.0401	0.1025
IL10RA	0.6662	0.0258	0.0387	0.3938	0.0325	0.0825	0.4389	0.0366	0.0834
IL17RB	0.4194	0.0154	0.0366	0.2584	0.0193	0.0749	0.4058	0.0234	0.0577
IL17REL	0.2487	0.0108	0.0434	0.3922	0.0301	0.0768	0.3059	0.0301	0.0983
IL19	0.2944	0.0165	0.056	0.77	0.0347	0.045	0.4041	0.0301	0.0745
ILKAP	0	0	0.0579	0.0571	0.0034	0.059	0.0651	0.0035	0.0538
INTS6	0.5445	0.017	0.0312	0.0776	0.0025	0.0321	0.2742	0.0165	0.0601
IRF8	0.1402	0.0093	0.0662	0.0895	0.0072	0.0807	0.0646	0.0062	0.0958
IRX6	0.342	0.0205	0.06	0.2638	0.0216	0.082	0.248	0.0237	0.0957
ISYNA1	0.1169	0.0073	0.0628	0.0919	0.0101	0.1101	0.0791	0.0092	0.1162
ITGB3BP	0.938	0.017	0.0181	0.7403	0.027	0.0364	1.9086	0.0344	0.018
ITGB8	0.2425	0.0067	0.0278	0.1338	0.0067	0.0503	0.1463	0.0067	0.046
JAG2	0.1295	0.0158	0.1222	0.0959	0.0163	0.1702	0.0426	0.006	0.1406
JAM2	0.0397	0.0015	0.0375	0	0	0.084	0.0316	0.0017	0.055
KANK3	0.4749	0.0323	0.068	0.3775	0.0479	0.127	0.3271	0.0346	0.1058
KCNB1	0.0274	0.0015	0.0555	0.0212	0.0015	0.0718	0.0263	0.002	0.0773
KCNG2									
KCNJ9	0.1333	0.0032	0.0239	0.0145	0.0011	0.0784	0.0231	0.0016	0.0689
KDM5D				0.1962	0.0343	0.1749			
KIAA0562	0.2637	0.0123	0.0468	0.1235	0.0102	0.0826	0.2013	0.0143	0.0711
KIAA0947	0.3143	0.0165	0.0525	0.3659	0.0306	0.0836	0.3561	0.0302	0.0848
KIDINS220	0.062	0.0028	0.0453	0.0645	0.0046	0.0709	0.0535	0.0045	0.0836
KLHDC4	0.1497	0.0135	0.09	0.1564	0.0195	0.1245	0.1515	0.0194	0.1283
KLRG2	0.4157	0.0262	0.063	0.5831	0.0505	0.0866	0.5019	0.0506	0.1008
KMO	0.186	0.0071	0.0382	0.4178	0.0244	0.0584	0.3488	0.0262	0.0751
KPTN	0.4518	0.0392	0.0868	0.1993	0.0178	0.0891	0.393	0.0429	0.1092
KRT36	0.2218	0.0154	0.0693	0.2164	0.0164	0.0756	0.3071	0.0203	0.066
KRTAP4-7	0.4568	0.0497	0.1088	0.5993	0.196	0.3269	0.5564	0.1377	0.2475
L3MBTL1	0.2569	0.0126	0.0489	0	0	0	0.2919	0.012	0.0412
LAIR1				0.9746	0.0957	0.0982			
LAMA4							0.1194	0.0085	0.0713
LAMC2	0.4155	0.0137	0.0329	0.2807	0.0162	0.0577	0.3243	0.0174	0.0538
LAPTM4B	0.4685	0.1077	0.2298	0.3324	0.0629	0.1892	0.7484	0.066	0.0882
LDB3	0.1651	0.0085	0.0516	0.1122	0.0152	0.1352	0.1077	0.0118	0.1092
LEPREL4							0.041	0.004	0.0984
LETM2	0.2859	0.013	0.0454	0.4833	0.0639	0.1322	0.4646	0.0602	0.1296
LGALS7	0.2026	0.0101	0.0499	0.1468	0.0169	0.1152	0.0825	0.0067	0.0809
LHFPL2	0.0915	0.0064	0.0699	0.2287	0.0107	0.0469	0.2313	0.0128	0.0555
LHFPL5									
LHX2	0.0524	0.0022	0.0416	0.0147	0.0011	0.0744	0.04	0.0033	0.0819
LIPH	0.1132	0.005	0.0441	0.3563	0.0198	0.0556	0.3534	0.021	0.0595
LPAR3	0.1795	0.01	0.0557	0.0807	0.0099	0.1233	0.1421	0.0151	0.106
LRPPRC	0.624	0.0268	0.043	0.7541	0.0582	0.0772	0.6811	0.0492	0.0722
LRRC2	0.1342	0.0081	0.0604	0.2934	0.0159	0.0541	0.2115	0.0152	0.0719
LRRC27	0.5017	0.0369	0.0735						
LRRTM3	0.0827	0.0023	0.0273	0.0646	0.0023	0.035	0	0	0.0324
LSM10	0.0519	0.0036	0.07	0.1591	0.0073	0.0458	0.1158	0.011	0.0946
LSM7	0.0582	0.0043	0.0734	0.031	0.0043	0.1378	0	0	0.1212
LTK	0.2727	0.0149	0.0545	0.2379	0.02	0.0842	0.2214	0.0184	0.0831
LYG1	1.2097	0.035	0.029	0.8228	0.0458	0.0556	0.4117	0.0291	0.0707
MAGEA8	0.2604	0.0168	0.0644						
MAGEB17	0.5445	0.0307	0.0563	0.4024	0.0335	0.0832	0.3251	0.0306	0.0941
MAGEB3	0.3726	0.026	0.0698	0.4469	0.0344	0.077	0.3805	0.0423	0.1111

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
MAP2	0.3075	0.0024	0.0078	0.2557	0.0036	0.0141	0.2139	0.0072	0.0339	0.2601	0.0086	0.0333
MAP3K7	0	0	0.0169	0	0	0.0169	0.0371	0.0007	0.0193	0.0246	0.0007	0.0292
MAP4K3	0.3646	0.0049	0.0134	0.1292	0.002	0.0153	0.1742	0.0031	0.0177	0.0769	0.0019	0.0251
MAP4K4	0.1017	0.002	0.0195	0	0	0.0075	0.0407	0.0007	0.0165	0.0201	0.0007	0.0334
MAP4K5	0.0841	0.001	0.0122	0.965	0.1236	0.128	0.0389	0.001	0.0263	0.0458	0.0015	0.0335
MARK2				0.0453	0.0006	0.0125	0.3572	0.0052	0.0147	0	0	0.0177
MARVELD3	0.3452	0.0047	0.0137	0.4693	0.0167	0.0355				0.3721	0.0231	0.062
MAT2A	0	0	0.0215	0	0	0.0288	0	0	0.0436	0.1042	0.0024	0.0229
MBD6	0.0808	0.0005	0.0058	0.2425	0.0014	0.0058	0.2164	0.0034	0.0156	0.2892	0.0057	0.0198
MBLAC2	0.2207	0.0032	0.0145				0.1083	0.0048	0.0444	0.0536	0.0032	0.0598
MBNL2	0	0	0.0037	0	0	0.0041	0.0524	0.0013	0.0251	0	0	0.0113
MBTPS2	0.0406	0.0009	0.0211	0.0645	0.0017	0.0266	0.0177	0.0009	0.0484	0.0244	0.0009	0.0362
MDM4	0.1134	0.0018	0.0155	0.1421	0.0018	0.0124	0.1073	0.0044	0.041	0.0624	0.0018	0.0281
ME2	0.1024	0.0015	0.0146	0.0383	0.0007	0.0196	0.0919	0.0032	0.0347	0.0404	0.0015	0.0371
MED19	0.1555	0.0018	0.0116	0	0	0.0414	0.0435	0.0018	0.0414	0.0335	0.0018	0.0537
MED7	0	0	0.0069	0	0	0	0	0	0.021	0	0	0.0281
MEGF10	0.1155	0.003	0.0263	0.0605	0.0017	0.0289	0.083	0.0046	0.0549	0.0691	0.0038	0.0549
METAP1D	0.0759	0.0013	0.0172	0.1516	0.0026	0.0172	0.3052	0.0066	0.0215	0.2267	0.0079	0.0347
METTL6	0.2783	0.003	0.0109	1.1235	0.0061	0.0054	0.2214	0.0061	0.0274	0.1124	0.0076	0.0677
MFSD6L	0.6967	0.0093	0.0133	0.5199	0.0093	0.0179	0.328	0.0203	0.0618	0.5357	0.0242	0.0453
MIER1	0	0	0.0141	0.1334	0.0022	0.0164	0.0893	0.0009	0.0106	0.0477	0.0019	0.0395
MLLT6	0.8958	0.0023	0.0025	0.2385	0.0017	0.0072	0.1236	0.0029	0.0238	0.1086	0.0035	0.0322
MLXIPL	0.174	0.0026	0.0148	0.2237	0.0088	0.0392						
MOAP1	0.2323	0.0038	0.0162	0.2322	0.0038	0.0162	0.4656	0.0075	0.0162	0.2048	0.005	0.0245
MOCS3	0.1858	0.002	0.0108	0.1485	0.002	0.0135	0.1472	0.004	0.0272	0.1819	0.007	0.0385
MPHOSPH9	1.04	0.0029	0.0028				0.2008	0.007	0.0348	0.2656	0.0087	0.0329
MPV17L	0.5735	0.0122	0.0212	0.3972	0.0171	0.043	0.7232	0.0352	0.0487	1.3626	0.0549	0.0403
MPZL2	0.1067	0.0021	0.0194				0.1899	0.0062	0.0328	0.0391	0.0021	0.0528
MRGPRD	1.8661	0.0156	0.0084	0.5049	0.0127	0.0251	0.3527	0.0231	0.0656	0.8569	0.0437	0.0509
MRGPRE	0.1064	0.003	0.0279	0.1003	0.0045	0.0444	0.1273	0.0089	0.0701	0.2014	0.015	0.0743
MRPL20	0	0	0.0092	0.4581	0.1	0.2182						
MRPL21	0.5295	0.0067	0.0126	1.4205	0.0089	0.0063	0.1875	0.0134	0.0716	0.3504	0.0089	0.0254
MRPL43	0.4396	0.0104	0.0236	0.7393	0.0502	0.0678	0.4552	0.0156	0.0342	0.1438	0.0058	0.0403
MRPL55	-1	0.0072	0	1.4604	0.0112	0.0077	0.3503	0.0144	0.041	0.4736	0.0226	0.0477
MS4A7	0.3328	0.0056	0.0169	1.6807	0.0094	0.0056	0.3717	0.017	0.0457	0.3266	0.0151	0.0462
MSL2	0	0	0.0099	0	0	0.0074	0.1989	0.002	0.0099	0.0216	0.0008	0.0351
MSRB2	0.505	0.0226	0.0447	0.1502	0.0031	0.0204	0.0487	0.003	0.0625	0.1906	0.0175	0.0919
MTG1	0.6705	0.0054	0.008				0.1782	0.0091	0.0508	0.2794	0.0162	0.058
MTIF3	-1	0.0016	0	0.2862	0.0047	0.0163	0.5279	0.0237	0.0448	0.4659	0.0255	0.0548
MYL6B	0.1569	0.0021	0.0135	0.1701	0.0663	0.3896	0.0617	0.0021	0.0344	0.076	0.0042	0.0559
NCKAP1L	0.0763	0.0012	0.0153	0.0956	0.0023	0.0243	0.0882	0.0027	0.0308	0.163	0.0075	0.046
NCOR2	0.0917	0.0022	0.0241	0.1142	0.0035	0.0305	0.1163	0.008	0.0689	0.0922	0.0062	0.0676
NDP	0.1049	0.0033	0.0319	0	0	0.0211	0	0	0.0429	0	0	0.0411
NDUFA6	0	0	0.023	0.453	0.0086	0.0189	0.1473	0.0086	0.0582	0.0595	0.0029	0.0479
NLGN3	0.1657	0.0005	0.0033	0.1312	0.0011	0.0082	0.0653	0.0011	0.0164	0.0232	0.0005	0.0231
NPFF	-1	0.008	0	-1	0.0226	0	1.3795	0.0327	0.0237	1.3804	0.0327	0.0237
NPFFR1	0.4182	0.0063	0.0152	0.23	0.0063	0.0275	0.2812	0.0095	0.0338	0.2997	0.0149	0.0496
NPY1R	0.0469	0.0011	0.0239	0.0401	0.0011	0.028	0.031	0.0011	0.0362	0.07	0.0022	0.0321
NPY5R	0	0	0.0033	0	0	0.0066	0.0981	0.001	0.0099	0.0789	0.0029	0.0371
NR1D2	0.1551	0.0029	0.019	0.1088	0.0015	0.0135	0.1688	0.0037	0.022	0.0535	0.0022	0.0416
NR1I3	0	0	0.008	1.2844	0.005	0.0039	0.0939	0.0037	0.0396	0.1355	0.0037	0.0275
NR2C2	0.0519	0.0007	0.0138	0	0	0.0179	0	0	0.0301	0.0708	0.0022	0.0313
NSUN3	0.3065	0.0039	0.0126	0.2431	0.0052	0.0212	0.2685	0.0104	0.0386	0.2278	0.0078	0.0341
NT5M	0.6613	0.0039	0.0059	0.2217	0.0138	0.0621						
NUDCD1	0.1908	0.0015	0.0077	0.4849	0.004	0.0082	0.2845	0.0059	0.0208	0.1394	0.0059	0.0424
NUP88	0.2188	0.003	0.0135	0.2607	0.0032	0.0125	0.288	0.0116	0.0402	0.4247	0.0169	0.0397
NXT1	0	0	0.0324	0	0	0.0435	0	0	0.0548	0	0	0.0328
OAS1	-1	0.0165	0	0.5275	0.0077	0.0145	1.3352	0.0243	0.0182	1.3419	0.0345	0.0257
OAZ2	0	0	0.0152	0	0	0.0156	0	0	0.0229	0.3076	0.0023	0.0076
OLA1	0	0	0	0.0688	0.0011	0.0157	0.0915	0.0022	0.0236	0.034	0.0011	0.0317
OR10G3	0.4639	0.0058	0.0125	0.9603	0.016	0.0167	0.2166	0.0102	0.0469	0.6032	0.0309	0.0512
OR13J1	1.0662	0.0088	0.0082	2.4899	0.0102	0.0041	0.6703	0.0403	0.0602	0.6703	0.0403	0.0602
OR14A2	0.4365	0.0115	0.0263	0.746	0.0129	0.0173	0.4668	0.0143	0.0306			
OR1A2	0.61	0.0086	0.014	0.8191	0.0114	0.0139	0.4436	0.032	0.0721			
OR1N1	1.2786	0.0057	0.0045	1.4337	0.0129	0.009	0.4703	0.0172	0.0366			
OR1N2	0.2729	0.0068	0.0248	0.5146	0.015	0.0291	0.1828	0.0109	0.0596	0.3739	0.0192	0.0513
OR2J3	0.6621	0.0086	0.0131	2.3433	0.0203	0.0087	0.3031	0.0277	0.0915			
OR51F2	1.4389	0.0117	0.0081	1.4412	0.0117	0.0081	0.7731	0.0223	0.0288			
OR5AS1	0.3073	0.0068	0.0221	0	0	0.0266				0.2061	0.015	0.073
OR5H6	0.445	0.0162	0.0365	0.3705	0.0197	0.053	0.4551	0.0493	0.1084			
OR6M1	0.3286	0.0057	0.0173	0.5461	0.0071	0.013	0.35	0.0172	0.0492	1.043	0.0231	0.0221
OR6X1	0.6008	0.013	0.0216	1.3495	0.0174	0.0129	0.9719	0.0337	0.0347			
ORC2	0.4722	0.0037	0.0079	0.2819	0.0028	0.0098	0.1055	0.0022	0.0212	0.0623	0.0015	0.0239
OVOL2	0.129	0.0048	0.0371	0.0497	0.0018	0.0362	0.0895	0.0048	0.0535	0.0412	0.0022	0.0526
PADI1	0.3606	0.0051	0.0142	0.2396	0.0046	0.0193	0.2063	0.0133	0.0645	0.2213	0.0147	0.0663
PAFAH1B1	0.4414	0.0032	0.0072	0.0973	0.0014	0.0141	0.1751	0.0032	0.0181	0.408	0.0074	0.0182
PAX9	0.1156	0.0013	0.0115	0	0	0.0102	0.0428	0.0013	0.0309	0.042	0.0027	0.0631
PCDH7				0.0266	0.0004	0.0138	0.0758	0.0019	0.0245	0.0321	0.0012	0.0368
PCDHA1	0.5691	0.0052	0.0091				0.2467	0.0181	0.0733	0.279	0.0178	0.0639
PCDHA3	0.1703	0.0033	0.0195	0.1951	0.003	0.0151	0.363	0.0125	0.0345	0.155	0.0085	0.055
PCDHB5	0.2369	0.0079	0.0335	0.3632	0.0223	0.0615	0.2128	0.0119	0.0561	0.1824	0.0151	0.0825
PDK3	0	0	0.0104	0.075	0.0014	0.0193	0	0	0.0246	0.0331	0.0011	0.0317
PDZD7	0.1314	0.0027	0.0203	0.0694	0.0018	0.0257	0.3236	0.0153	0.0472	0.13	0.0088	0.0675
PER3	0.3615	0.0081	0.0224				0.2892	0.0144	0.0498	0.3582	0.0281	0.0786
PFDN6	0	0	0.0105	0	0	0.0105	0.1088	0.0035	0.032	0	0	0.065
PGAM1	0	0	0.0226				-1	0.0017	0	0.0508	0.0017	0.0341
PIAS1	0	0	0.0086	0.0389	0.0007	0.018	0	0	0.035	0	0	0.0305
PIGA	0.158	0.0009	0.0058	0.252	0.0036	0.0145	0.3929	0.0091	0.0233	0.3521	0.0082	0.0233
PINX1	0.2817	0.008	0.0282				0.213	0.0133	0.0625	0.2802	0.0133	0.0474
PIP4K2C	0.1519	0.0023	0.0154	0.0504	0.0012	0.0233	0.1636	0.0071	0.0432	0.0307	0.0013	0.0417
PITPNM1	0.2128	0.0036	0.017	0.1128	0.0029	0.0256	0.0867	0.0047	0.0543	0.1004	0.0076	0.0755
PLAU	0.3016	0.0061	0.0202	0.1795	0.0061	0.0339	0.2449	0.0092	0.0374	0.2697	0.0136	0.0504
PLB1	0.1801	0.0033	0.0184	0.2436	0.0077	0.0317	0.2292	0.0127	0.0556	0.4131	0.0186	0.0451
PLCB1	0.0189	0.0004	0.0189	0.0947	0.0011	0.012	0.0129	0.0004	0.0275	0.0434	0.0014	0.0326
PLCH2	0.1829	0.0047	0.0258	0.1828	0.006	0.0329	0.1703	0.0136	0.0801	0.1829	0.0151	0.0824
PLEKHA5	0.3636	0.002	0.0056				0.2069	0.005	0.0241	0.2244	0.0058	0.0259
PLEKHB2	0.1034	0.002	0.0192	0.1524	0.0025	0.0162	0.1142	0.006	0.0523	0.1096	0.008	0.0728
PLK2	0.0483	0.0006	0.013	0	0	0.013	0.0536	0.0019	0.0353	0.0839	0.0032	0.0376
PLP1	0	0	0.0147	0	0	0.0049	0	0	0.0097	0	0	0.0097
PLS3	0.1122	0.0014	0.0126	0.0466	0.0007	0.0146	0	0	0.0147	0	0	0.0245
PLXDC2	0.1528	0.0025	0.0162	0.4625	0.005	0.0108	0.188	0.0083	0.0442	0.121	0.0062	0.0514
PM20D2	0.0823	0.001	0.0124				0.1752	0.0113	0.0646	0.2095	0.0082	0.0391
PMFBP1	0.3142	0.0055	0.0174	0.438	0.008	0.0183	0.2616	0.0145	0.0554	0.5953	0.0265	0.0446
PNKP	0.2609	0.0085	0.0325	0.1609	0.0063	0.0392	0.1488	0.0087	0.0587	0.1636	0.0182	0.1112
PNLIPRP3	0.3625	0.0046	0.0128	0.2305	0.0042	0.0181	0.3393	0.0121	0.0357	0.5093	0.0131	0.0257
PNMA1	0	0	0.004	0	0	0.004	0	0	0.016	0.2345	0.0082	0.0348
PNPLA7	0.5128	0.0201	0.0391	0.3037	0.0099	0.0326	0.372	0.022	0.0592	0.2511	0.0197	0.0783

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
MAP2	0.183	0.0103	0.0565	0.2915	0.0046	0.0156	0.2499	0.0082	0.033	0.2619	0.0091	0.0349
MAP3K7	0	0	0.0223	0	0	0.0144	0.0425	0.0007	0.0169	0.0268	0.0007	0.0267
MAP4K3	0.0622	0.0024	0.0389	0.1785	0.004	0.0224	0.2068	0.0052	0.0251	0.1093	0.0039	0.0357
MAP4K4	0.0831	0.0045	0.0539	0.141	0.0023	0.0163	0.1285	0.0027	0.0209	0.067	0.0027	0.0402
MAP4K5	0.0519	0.0031	0.0592	0.9588	0.1248	0.1301	0.0834	0.002	0.0246	0.0807	0.0026	0.0317
MARK2	0.0343	0.0017	0.0495									
MARVELD3				0.4705	0.013	0.0277				0.3467	0.0215	0.0619
MAT2A	0.0505	0.0033	0.0663	0	0	0.0143	0	0	0.0288	0.2101	0.0024	0.0114
MBD6	0.1569	0.0055	0.0353	0.2021	0.0009	0.0046	0.2009	0.0029	0.0144	0.26	0.0052	0.0198
MBLAC2	0.0596	0.0048	0.0808				0.0548	0.0016	0.0293	0	0	0.0443
MBNL2	0.0543	0.0014	0.0266	0	0	0.0083	0.0448	0.0013	0.0294	0	0	0.015
MBTPS2	0.0411	0.0027	0.0649	0.108	0.0026	0.0238	0.0648	0.0017	0.0264	0.0579	0.0018	0.0304
MDM4				0.1898	0.0018	0.0092	0.1165	0.0044	0.0377	0.0704	0.0018	0.0249
ME2	0.0668	0.0031	0.0462	0.0383	0.0007	0.0196	0.0995	0.0032	0.032	0.0554	0.0015	0.0271
MED19	0.0229	0.0018	0.0789	0.0615	0.0018	0.0293	0.123	0.0036	0.0293	0.087	0.0036	0.0415
MED7	0	0	0.0556	0	0	0.0069	0	0	0.0281	0	0	0.0352
MEGF10	0.0434	0.0038	0.0877	0.0719	0.0017	0.0243	0.0975	0.0046	0.0467	0.0657	0.0038	0.0578
METAP1D	0.1676	0.0066	0.0391	0.1522	0.0013	0.0086	0.4085	0.0052	0.0128	0.2528	0.0066	0.0259
METTL6	0.4894	0.0245	0.0501	1.1259	0.0061	0.0054	0.2219	0.0061	0.0273	0.1126	0.0076	0.0676
MFSD6L	0.5383	0.0407	0.0756	0.5531	0.0124	0.0225	0.353	0.0218	0.0619	0.5165	0.0258	0.05
MIER1	0.0176	0.0011	0.0637	0.1334	0.0022	0.0164	0.0534	0.0009	0.0177	0.0477	0.0019	0.0395
MLLT6	0.0895	0.0037	0.0418	0.1801	0.0005	0.0026	0.0709	0.0014	0.0191	0.0847	0.0024	0.0282
MLXIPL				0.2589	0.0078	0.03						
MOAP1	0.1608	0.0101	0.0626	0	0	0.0326	0.1925	0.0063	0.0326	0.0914	0.0038	0.0411
MOCS3	0.2854	0.0233	0.0817	0.2973	0.004	0.0135	0.2211	0.006	0.0272	0.2341	0.009	0.0385
MPHOSPH9	0.3099	0.0138	0.0444				0.2658	0.0093	0.0348	0.3322	0.0109	0.0329
MPV17L	0.5865	0.0546	0.0931	0.2726	0.0097	0.0356	0.4485	0.0295	0.0657	0.7018	0.046	0.0656
MPZL2	0.1348	0.0062	0.0461				0.1563	0.0083	0.0532	0.0562	0.0041	0.0736
MRGPRD	0.4808	0.0664	0.138	1.019	0.017	0.0167	0.3255	0.0173	0.0531	0.9203	0.0421	0.0458
MRGPRE	0.2197	0.0241	0.1096	0.3124	0.0075	0.0239	0.2089	0.0119	0.0571	0.258	0.018	0.0698
MRPL20	0.1368	0.012	0.0879	0.4346	0.1	0.2301						
MRPL21	0.3202	0.034	0.1063	0.3532	0.0067	0.0189	0.1314	0.0112	0.0851	0.1742	0.0067	0.0383
MRPL43	0.1767	0.0136	0.0768	0.7069	0.0528	0.0747	0.5488	0.0245	0.0447	0.2826	0.0127	0.045
MRPL55	0.4831	0.047	0.0973	-1	0.0072	0	0.3503	0.0144	0.041	0.4718	0.0144	0.0305
MS4A7	0.5255	0.0304	0.0578	0.5018	0.0113	0.0225	0.2384	0.0151	0.0633	0.2659	0.017	0.064
MSL2	0	0	0.0174	0	0	0.0124	0.1189	0.002	0.0166	0.0233	0.0008	0.0326
MSRB2	0.0235	0.0031	0.1308	0.301	0.0061	0.0204	0.0977	0.0061	0.0625	0.3223	0.0406	0.1259
MTG1	0.441	0.037	0.084				0.1086	0.006	0.0555	0.2332	0.0135	0.0579
MTIF3	1.0951	0.0613	0.056	0.1909	0.0031	0.0163	0.4929	0.0221	0.0448	0.4351	0.0238	0.0547
MYL6B				0.1572	0.0644	0.4096	0	0	0.0343	0.038	0.0021	0.0558
NCKAP1L	0.0802	0.0053	0.0656	0.0798	0.0019	0.0243	0.0827	0.0023	0.0282	0.1696	0.0071	0.0419
NCOR2	0.0659	0.0073	0.1109	0.1269	0.0044	0.0347	0.128	0.0095	0.0741	0.0944	0.0074	0.0778
NDP	0	0	0.0887	0.3191	0.0033	0.0105	0.1048	0.0033	0.0319	0.1584	0.0043	0.0271
NDUFA6	0.382	0.026	0.0682	0.072	0.0034	0.047	0.142	0.0102	0.0718	0.0475	0.0034	0.0713
NLGN3	0	0	0.0421	0.0471	0.0005	0.0117	0.0273	0.0005	0.0201	0	0	0.0269
NPFF	1.3799	0.0495	0.0359	-1	0.0113	0	1.0389	0.0244	0.0235	1.0396	0.0244	0.0235
NPFFR1	0.2136	0.0191	0.0896	0.0864	0.0021	0.0244	0.2412	0.0074	0.0307	0.2748	0.0127	0.0463
NPY1R	0.0367	0.0022	0.0612	0	0	0.028	0	0	0.0362	0.0401	0.0011	0.028
NPY5R	0.0503	0.0029	0.0581	0	0	0.0033	0.1475	0.001	0.0066	0.087	0.0029	0.0336
NR1D2	0.0459	0.0029	0.0642	0.0904	0.0015	0.0163	0.1345	0.0037	0.0276	0.047	0.0022	0.0473
NR1I3	0.2374	0.0126	0.053	0.4214	0.0051	0.0121	0.0512	0.0025	0.0495	0.0893	0.0025	0.0284
NR2C2	0	0	0.0691	0.0342	0.0009	0.0269	0.0237	0.0007	0.0301	0.0612	0.0022	0.0362
NSUN3	0.1375	0.0091	0.0663	0.4576	0.0039	0.0084	0.3539	0.009	0.0256	0.305	0.0065	0.0212
NT5M				0.2466	0.0138	0.0558						
NUDCD1	0.2388	0.008	0.0334	0.3623	0.004	0.011	0.252	0.0059	0.0235	0.1307	0.0059	0.0452
NUP88	0.1719	0.0149	0.0867	0.4901	0.0049	0.01	0.3559	0.0122	0.0342	0.5214	0.0175	0.0335
NXT1	0	0	0.1138	0	0	0.0324	0	0	0.0435	0	0	0.0217
OAS1	0.7999	0.049	0.0613	1.2048	0.0176	0.0146	1.9191	0.0317	0.0165	1.4639	0.0379	0.0259
OAZ2	0	0	0	0	0	0.0315	0	0	0.0385	0.1015	0.0023	0.0229
OLA1	0	0	0.0317	0.0688	0.0011	0.0157	0.0915	0.0022	0.0236	0.034	0.0011	0.0317
OR10G3	0.1933	0.0211	0.1094	1.0508	0.0131	0.0125	0.1902	0.0072	0.0381	0.6589	0.0279	0.0424
OR13J1	0.3879	0.0566	0.1459	1.3085	0.0162	0.0123	0.6747	0.0435	0.0644	0.6747	0.0435	0.0644
OR14A2	0.477	0.0275	0.0576	0.6032	0.0159	0.0263	0.7873	0.0173	0.022			
OR1A2				1.8479	0.0172	0.0093	0.5633	0.038	0.0675			
OR1N1				0.951	0.0129	0.0135	0.4159	0.0172	0.0413			
OR1N2				0.5261	0.0109	0.0207	0.1339	0.0068	0.0507	0.4672	0.0178	0.0381
OR2J3	0.1625	0.0174	0.1069	1.3312	0.0174	0.0131	0.2566	0.0248	0.0965			
OR51F2				0.2368	0.0039	0.0164	0.3835	0.0143	0.0373			
OR5AS1	0.3288	0.0297	0.0905	0.5154	0.0068	0.0132				0.3736	0.022	0.0588
OR5H6				0.448	0.0196	0.0438	0.4232	0.0508	0.12			
OR6M1	0.2648	0.0304	0.1149	0.3273	0.0071	0.0217	0.2958	0.0172	0.0583	0.7441	0.0231	0.0311
OR6X1	0.3075	0.0345	0.1121	0.3888	0.0101	0.026	0.5463	0.0263	0.0481			
ORC2	0.1308	0.0067	0.0514	0.7059	0.0046	0.0066	0.2261	0.003	0.0132	0.1407	0.0022	0.0159
OVOL2	0.0446	0.0054	0.1217	0.085	0.0036	0.0424	0.2004	0.0096	0.048	0.1167	0.0043	0.0372
PADI1	0.1738	0.0221	0.1271	0.3096	0.0044	0.0141	0.2386	0.0139	0.0584	0.2357	0.0155	0.0656
PAFAH1B1	0.0534	0.0032	0.0595	0.1942	0.0027	0.0141	0.2331	0.0042	0.0182	0.4656	0.0085	0.0182
PAX9	0.09	0.0053	0.059	0	0	0.0206	0.0758	0.0027	0.0351	0.0591	0.004	0.0675
PCDH7	0.028	0.002	0.0724									
PCDHA1	0.1869	0.0177	0.0946				0.2541	0.0167	0.0658	0.2732	0.015	0.0549
PCDHA3	0.147	0.016	0.1089	0.1846	0.0053	0.0288	0.3084	0.0148	0.0481	0.153	0.0108	0.0707
PCDHB5	0.1979	0.0212	0.1071	0.4135	0.0253	0.0613	0.2703	0.0142	0.0527	0.2352	0.0186	0.0789
PDK3	0	0	0.0458	0.075	0.0014	0.0193	0	0	0.021	0.0297	0.0011	0.0354
PDZD7	0.1687	0.0188	0.1114	0.1161	0.0036	0.0312	0.2702	0.0173	0.0641	0.1371	0.0116	0.0846
PER3	0.3176	0.0328	0.1033				0.3331	0.0143	0.043	0.402	0.0273	0.0679
PFDN6	0	0	0.0539	0	0	0	0.1643	0.0035	0.0212	0	0	0.0538
PGAM1	0	0	0.0458				0.0768	0.0017	0.0225	0.0334	0.0017	0.0517
PIAS1	0	0	0.0508	0.0783	0.0007	0.009	0	0	0.0261	0	0	0.0217
PIGA	0.6272	0.0203	0.0323	0.1889	0.0027	0.0145	0.2816	0.0082	0.0292	0.2492	0.0073	0.0293
PINX1	0.2438	0.024	0.0985				0.1829	0.0133	0.0727	0.3258	0.0188	0.0576
PIP4K2C	0.1106	0.0071	0.0638	0.076	0.0012	0.0154	0.201	0.0071	0.0351	0.0386	0.0013	0.0332
PITPNM1	0.0703	0.0085	0.1216	0.1847	0.0043	0.0235	0.1268	0.0069	0.0544	0.1343	0.01	0.0743
PLAU	0.4586	0.0327	0.0712	0.1984	0.0081	0.041	0.2519	0.0112	0.0445	0.2149	0.0125	0.0581
PLB1	0.2388	0.024	0.1006	0.281	0.008	0.0286	0.2543	0.0133	0.0525	0.4013	0.0189	0.0472
PLCB1	0.0678	0.0035	0.0522	0.0774	0.0011	0.0147	0.0194	0.0007	0.0369	0.0484	0.0018	0.0369
PLCH2	0.1844	0.0222	0.1204	0.1772	0.006	0.034	0.1778	0.0138	0.0776	0.1827	0.0146	0.0797
PLEKHA5							0.1398	0.0039	0.0277	0.1572	0.0047	0.0298
PLEKHB2	0.1197	0.012	0.1004	0.3041	0.0049	0.0162	0.1748	0.008	0.0456	0.1514	0.01	0.0659
PLK2	0.0536	0.0019	0.0353	0.0727	0.0006	0.0087	0.082	0.0025	0.0308	0.1009	0.0038	0.0376
PLP1	0.1653	0.0016	0.0097	0	0	0.0097	0	0	0.0147	0	0	0.0147
PLS3	0	0	0.0345	0.0929	0.0021	0.0229	0.0618	0.0014	0.0231	0.0505	0.0014	0.0281
PLXDC2	0.0884	0.0091	0.1034	0.1538	0.0025	0.0162	0.1238	0.0058	0.0469	0.0727	0.0037	0.0513
PM20D2	0.2024	0.0144	0.0712				0.1592	0.0103	0.0648	0.1744	0.0068	0.0393
PMFBP1	0.2865	0.0252	0.088	0.5708	0.0076	0.0132	0.3275	0.0132	0.0403	0.6863	0.0256	0.0372
PNKP	0.1492	0.0149	0.0998	0.4538	0.0127	0.028	0.2495	0.0151	0.0606	0.2098	0.0213	0.1015
PNLIPRP3	1.0255	0.0276	0.0269	0	0	0.0254	0.2196	0.0093	0.0423	0.3184	0.0102	0.0322
PNMA1	0.0234	0.0012	0.0533	0	0	0	0	0	0.012	0.2665	0.0082	0.0306
PNPLA7				0.4186	0.0191	0.0455	0.5033	0.0352	0.0699	0.34	0.0318	0.0936

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
MAP2	0.1904	0.0111	0.0582	0.2294	0.0086	0.0376	0.2399	0.0091	0.0381	0.1819	0.011	0.0602
MAP3K7	0	0	0.0273	0.0425	0.0007	0.0169	0.0329	0.0007	0.0218	0	0	0.0248
MAP4K3	0.0883	0.0044	0.0497	0.1054	0.0021	0.0199	0.0319	0.001	0.031	0.0357	0.0015	0.0416
MAP4K4	0.0619	0.0025	0.0401	0.0612	0.0008	0.0127	0.0338	0.0008	0.0226	0.1023	0.0052	0.0505
MAP4K5	0.0681	0.0038	0.0564	0.8619	0.1247	0.1447	0.8376	0.1256	0.15	0.7028	0.125	0.1779
MARK2				0.2185	0.0053	0.0243	0.0209	0.0006	0.027	0.0425	0.0023	0.0534
MARVELD3							0.2615	0.0243	0.0931			
MAT2A	0.0656	0.0033	0.051	0	0	0.0362	0.1252	0.0024	0.0191	0.0571	0.0033	0.0586
MBD6	0.181	0.0055	0.0306	0.2009	0.0029	0.0144	0.2599	0.0052	0.0198	0.1568	0.0055	0.0354
MBLAC2	0.0247	0.0016	0.0648									
MBNL2	0.0464	0.0014	0.0311	0.0631	0.0013	0.0209	0	0	0.0083	0.0643	0.0016	0.025
MBTPS2	0.0605	0.0036	0.0587	0.0502	0.0026	0.0511	0.0677	0.0026	0.0391	0.0719	0.0044	0.0617
MDM4				0.1073	0.0044	0.041	0.0624	0.0018	0.0281			
ME2	0.0666	0.0031	0.0463	0.0595	0.0024	0.0402	0.0202	0.0007	0.0371	0.0531	0.0023	0.0436
MED19	0.0545	0.0036	0.0662	0.038	0.0018	0.0475	0.0301	0.0018	0.0599	0.0212	0.0018	0.0852
MED7	0	0	0.0639	0	0	0.021	0	0	0.0281	0	0	0.0556
MEGF10	0.0377	0.0034	0.0908	0.0517	0.0031	0.0591	0.028	0.0017	0.0624	0.0229	0.0022	0.0958
METAP1D	0.1731	0.0052	0.0303	0.5097	0.0066	0.0129	0.3029	0.0079	0.026	0.2159	0.0066	0.0303
METTL6	0.4905	0.0245	0.05	0.42	0.0091	0.0217	0.1737	0.0107	0.0615	0.6888	0.0285	0.0413
MFSD6L	0.5248	0.0423	0.0806	0.339	0.0223	0.0658	0.5	0.0275	0.055	0.5116	0.044	0.086
MIER1	0.0204	0.0011	0.0549	0.0666	0.0011	0.0164	0.0523	0.0022	0.0418	0.0201	0.0013	0.0626
MLLT6	0.0564	0.0023	0.04	0.0592	0.0013	0.022	0.0568	0.0018	0.0319	0.0531	0.0021	0.0405
MLXIPL												
MOAP1	0.1102	0.0088	0.0799	0.258	0.0063	0.0243	0.1149	0.0038	0.0327	0.1238	0.0088	0.0711
MOCS3	0.3106	0.0254	0.0817	0.2008	0.006	0.0299	0.2183	0.009	0.0413	0.3109	0.0254	0.0816
MPHOSPH9	0.3386	0.015	0.0444									
MPV17L	0.4471	0.0472	0.1055	0.4703	0.0345	0.0734	0.7657	0.0535	0.0698	0.4605	0.0523	0.1136
MPZL2	0.1243	0.0083	0.0667									
MRGPRD	0.5012	0.066	0.1317	0.3239	0.0232	0.0715	0.6428	0.0399	0.062	0.4305	0.0634	0.1473
MRGPRE	0.2945	0.0256	0.0871	0.1401	0.0104	0.0744	0.2233	0.0195	0.0873	0.2567	0.0264	0.1028
MRPL20	0.1226	0.012	0.0981							0.4084	0.1124	0.2751
MRPL21	0.264	0.0318	0.1203	0.172	0.0134	0.0782	0.2805	0.0089	0.0318	0.3218	0.0341	0.1059
MRPL43	0.2994	0.0245	0.0817	0.7389	0.0618	0.0836	0.5244	0.0524	0.0998	0.4585	0.062	0.1352
MRPL55	0.5553	0.0548	0.0987	0.3503	0.0144	0.041	0.5714	0.0226	0.0396	0.5602	0.0545	0.0973
MS4A7	0.376	0.0285	0.0758	0.3806	0.0151	0.0396	0.2541	0.0132	0.052	0.4946	0.0285	0.0576
MSL2	0	0	0.0174	0.1188	0.002	0.0166	0.0201	0.0008	0.0377	0	0	0.0199
MSRB2	0.0471	0.0062	0.1308	0.0973	0.0061	0.0632	0.0701	0.0092	0.1317	0.0471	0.0062	0.1308
MTG1	0.4091	0.0343	0.0837									
MTIF3	0.9661	0.0596	0.0617	0.3545	0.0221	0.0622	0.3336	0.0204	0.061	0.7084	0.0563	0.0795
MYL6B				0.1612	0.0644	0.3992	0.1618	0.0666	0.4117			
NCKAP1L	0.0757	0.0049	0.0641	0.0739	0.0029	0.0394	0.1348	0.0075	0.0556	0.0801	0.0061	0.0757
NCOR2	0.0642	0.0081	0.126	0.149	0.0104	0.0696	0.1155	0.0084	0.0731	0.0737	0.0084	0.1139
NDP	0.0434	0.0033	0.0769	0	0	0.0211	0	0	0.0134	0	0	0.0655
NDUFA6	0.1415	0.0137	0.0965	0.2174	0.0172	0.0792	0.1673	0.0115	0.0684	0.3236	0.0289	0.0894
NLGN3	0	0	0.0458	0.0593	0.0011	0.0181	0.0216	0.0005	0.0248	0.014	0.0006	0.0403
NPFF	1.3934	0.0496	0.0356	0.6458	0.0227	0.0352	0.3234	0.0113	0.0349	0.995	0.0345	0.0347
NPFFR1	0.21	0.0181	0.0861	0.2408	0.0074	0.0307	0.2743	0.0127	0.0464	0.2181	0.0181	0.0828
NPY1R	0.0161	0.0011	0.0697	0	0	0.0403	0.031	0.0011	0.0362	0.0152	0.0011	0.074
NPY5R	0.0536	0.0029	0.0546	0.0981	0.001	0.0099	0.0789	0.0029	0.037	0.0503	0.0029	0.0581
NR1D2	0.0459	0.0029	0.0642	0.1011	0.0022	0.022	0.0206	0.0007	0.0359	0.024	0.0015	0.0613
NR1I3	0.2035	0.0127	0.0626	0.198	0.0087	0.0439	0.2751	0.0087	0.0316	0.2626	0.0151	0.0575
NR2C2	0.0097	0.0007	0.0741	0	0	0.0423	0	0	0.0411	0	0	0.0775
NSUN3	0.148	0.0078	0.0528	0.3019	0.0077	0.0256	0.2428	0.0052	0.0212	0.1227	0.0065	0.0529
NT5M												
NUDCD1	0.2197	0.008	0.0363	0.3713	0.0072	0.0194	0.182	0.0072	0.0395	0.2194	0.008	0.0365
NUP88	0.1779	0.0143	0.0804	0.2788	0.0106	0.0381	0.5512	0.0205	0.0373	0.1679	0.0152	0.0903
NXT1	0	0	0.0778	0	0	0.0548	0	0	0.0328	0	0	0.0896
OAS1	0.7938	0.0491	0.0618	0.8649	0.0271	0.0313	0.8139	0.0333	0.0409	0.6686	0.049	0.0732
OAZ2	0	0	0.0152	0	0	0.0396	0.3092	0.0024	0.0078	0	0	0.0156
OLA1	0	0	0.0317	0.2073	0.0032	0.0157	0.0913	0.0022	0.0236	0.0456	0.0011	0.0237
OR10G3	0.1947	0.0189	0.0973	0.3738	0.0175	0.0468	0.7521	0.0385	0.0512	0.2747	0.0293	0.1068
OR13J1	0.3953	0.0614	0.1553	0.6978	0.0388	0.0556	0.6978	0.0388	0.0556	0.4246	0.0598	0.1408
OR14A2	0.6256	0.0306	0.0489	0.705	0.0216	0.0306				0.5709	0.0341	0.0598
OR1A2				0.6111	0.0409	0.067						
OR1N1				0.4409	0.0193	0.0439						
OR1N2				0.3972	0.015	0.0378	0.7906	0.0234	0.0295			
OR2J3	0.1703	0.0174	0.102	0.3681	0.0337	0.0915				0.257	0.0262	0.1019
OR51F2				0.3841	0.0143	0.0373						
OR5AS1	0.4299	0.0368	0.0857				0.2783	0.015	0.054	0.3288	0.0297	0.0905
OR5H6				0.4323	0.0531	0.1229						
OR6M1	0.2093	0.026	0.1244	0.4658	0.0187	0.0401	1.3879	0.0245	0.0177	0.2896	0.0319	0.1101
OR6X1	0.2215	0.027	0.1219	0.7875	0.0308	0.0391				0.2698	0.0315	0.1167
ORC2	0.1734	0.0075	0.0431	0.187	0.0037	0.0198	0.1045	0.0028	0.0266	0.1372	0.0074	0.0541
OVOL2	0.0281	0.0036	0.1287	0.1182	0.0072	0.0612	0.0701	0.0052	0.0735	0.067	0.0073	0.1082
PADI1	0.1902	0.0236	0.1243	0.2434	0.014	0.0574	0.2363	0.014	0.0593	0.1993	0.0228	0.1144
PAFAH1B1	0.071	0.0042	0.0596	0.1156	0.0027	0.0237	0.2877	0.0082	0.0287	0.0402	0.0027	0.0682
PAX9	0.105	0.0067	0.0634	0	0	0.0257	0	0	0.063	0.0674	0.0035	0.0522
PCDH7				0.0606	0.0015	0.0245	0.031	0.0012	0.0381	0.0331	0.0024	0.0724
PCDHA1	0.254	0.0256	0.101									
PCDHA3	0.1524	0.0182	0.1193	0.2258	0.0101	0.0446	0.0983	0.0065	0.0662	0.1233	0.0158	0.1282
PCDHB5	0.2255	0.0244	0.1082	0.3984	0.0252	0.0634	0.3172	0.028	0.0883	0.2665	0.0311	0.1168
PDK3	0	0	0.0497	0.0497	0.0014	0.0291	0.1197	0.0029	0.0242	0.0334	0.0016	0.0487
PDZD7	0.1759	0.0218	0.1241	0.2403	0.0153	0.0636	0.0929	0.0072	0.0771	0.1495	0.0189	0.1266
PER3	0.3445	0.0327	0.095									
PFDN6	0	0	0.0428	0.1643	0.0035	0.0212	0	0	0.0538	0	0	0.0428
PGAM1	0	0	0.0698									
PIAS1	0	0	0.0417	0.0238	0.0007	0.0295	0.031	0.0007	0.0226	0.0192	0.0007	0.0365
PIGA	0.5043	0.0193	0.0383	0.2842	0.0091	0.0322	0.3117	0.0101	0.0323	0.4902	0.0203	0.0413
PINX1	0.2574	0.0255	0.0992									
PIP4K2C	0.1106	0.0071	0.0638	0.2165	0.0059	0.0272	0	0	0.0374	0.0922	0.0059	0.0637
PITPNM1	0.0834	0.0108	0.1293	0.1183	0.0062	0.0522	0.1214	0.0092	0.0756	0.0816	0.01	0.123
PLAU	0.4162	0.0358	0.0861	0.2175	0.0112	0.0515	0.186	0.0141	0.0759	0.3834	0.0358	0.0935
PLB1	0.2393	0.0243	0.1017	0.2568	0.0149	0.0581	0.3974	0.0221	0.0557	0.2621	0.0273	0.1043
PLCB1	0.0661	0.0039	0.0596	0.0512	0.0015	0.0296	0.0702	0.0023	0.0323	0.0852	0.0045	0.0534
PLCH2	0.1762	0.0219	0.1241	0.2023	0.014	0.0693	0.2113	0.0162	0.0765	0.1976	0.0227	0.1147
PLEKHA5												
PLEKHB2	0.1503	0.014	0.0934	0.0993	0.0049	0.0497	0.0995	0.0049	0.0497	0.112	0.0124	0.1111
PLK2	0.082	0.0025	0.0308	0.0614	0.0019	0.0308	0.0839	0.0032	0.0376	0.0614	0.0019	0.0308
PLP1	0.1098	0.0016	0.0147	0	0	0.0049	0	0	0.0049	0.3317	0.0016	0.0049
PLS3	0.0323	0.0014	0.0439	0.0277	0.0007	0.0247	0.0197	0.0007	0.0345	0.0152	0.0007	0.0447
PLXDC2	0.0644	0.0066	0.1031	0.2172	0.0083	0.0383	0.1372	0.0062	0.0454	0.0947	0.0092	0.0967
PM20D2	0.1879	0.0134	0.0713									
PMFBP1	0.3157	0.0239	0.0757	0.2735	0.013	0.0475	0.5808	0.025	0.043	0.3061	0.024	0.0786
PNKP	0.1892	0.0199	0.1052	0.2121	0.0117	0.0554	0.1642	0.0147	0.0894	0.1874	0.0172	0.0919
PNLIPRP3	0.6605	0.0246	0.0372	0.1816	0.0073	0.0403	0.2528	0.0073	0.029	0.6312	0.0265	0.042
PNMA1	0.0254	0.0012	0.0491	0	0	0.012	0.2665	0.0082	0.0306	0.0254	0.0012	0.0491
PNPLA7				0.3702	0.02	0.0541	0.2498	0.0191	0.0766			

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
MAP2	0.2351	0.0098	0.0415	0.1871	0.012	0.0644	0.213	0.0113	0.0532
MAP3K7	0.0537	0.0014	0.0267	0.0245	0.0007	0.0298	0.0195	0.0007	0.0375
MAP4K3	0.0384	0.001	0.0267	0.0389	0.0015	0.0395	0.0105	0.0005	0.0459
MAP4K4	0.0417	0.0014	0.0327	0.0955	0.0052	0.0546	0.0759	0.0052	0.0688
MAP4K5	0.0625	0.0015	0.0246	0.0572	0.0031	0.0537	0.0717	0.0036	0.05
MARK2	0.237	0.0052	0.0221	0.1278	0.0071	0.0555	0.0343	0.0017	0.0495
MARVELD3									
MAT2A	0.0891	0.0024	0.0268	0.0505	0.0033	0.0662	0.1555	0.006	0.0385
MBD6	0.1691	0.0048	0.0281	0.1596	0.0064	0.0401	0.2317	0.0097	0.0419
MBLAC2	0.0362	0.0016	0.0443	0.0495	0.0032	0.0648	0.0199	0.0016	0.0806
MBNL2	0.1058	0.0013	0.0125	0.0914	0.0032	0.0351	0.0819	0.0014	0.0176
MBTPS2	0	0	0.0418	0.0288	0.0018	0.0616	0.033	0.0018	0.0555
MDM4	0.1055	0.0026	0.025						
ME2	0.0348	0.0016	0.0457	0.0506	0.0033	0.0648	0.0259	0.0015	0.0596
MED19	0	0	0.0476	0	0	0.0725	0	0	0.0855
MED7	0	0	0.0353	0	0	0.0556	0	0	0.0723
MEGF10	0.0573	0.0038	0.0662	0.0472	0.0046	0.0967	0.0315	0.003	0.0967
METAP1D	0.5122	0.0066	0.0128	0.461	0.0079	0.0171	0.3043	0.0092	0.0302
METTL6	0.0913	0.0046	0.05	0.6522	0.0214	0.0329	0.3694	0.0239	0.0646
MFSD6L	0.3646	0.0242	0.0665	0.3886	0.0346	0.0891	0.4407	0.0371	0.0841
MIER1	0.033	0.0009	0.0285	0	0	0.0505	0.0203	0.0011	0.055
MLLT6	0.0655	0.0022	0.0338	0.0521	0.0025	0.0483	0.046	0.0022	0.0476
MLXIPL									
MOAP1	0.2304	0.0075	0.0327	0.2021	0.0126	0.0624	0.1412	0.0101	0.0713
MOCS3	0.2342	0.009	0.0385	0.4137	0.0259	0.0626	0.2363	0.0222	0.0941
MPHOSPH9	0.2495	0.0113	0.0453	0.2434	0.0152	0.0624	0.2878	0.0171	0.0595
MPV17L	1.0673	0.043	0.0403	0.5783	0.0497	0.0859	0.766	0.0639	0.0834
MPZL2	0.0894	0.0041	0.0464	0.2097	0.0083	0.0397	0.0691	0.0041	0.0598
MRGPRD	0.8118	0.0334	0.0412	0.4795	0.0483	0.1007	0.6728	0.0796	0.1182
MRGPRE	0.1701	0.0164	0.0966	0.1818	0.0225	0.1239	0.1915	0.021	0.1098
MRPL20									
MRPL21	0.0901	0.0089	0.0991	0.1854	0.0318	0.1717	0.233	0.0306	0.1313
MRPL43	0.6131	0.0176	0.0287	0.3938	0.0255	0.0647	0.2654	0.0155	0.0584
MRPL55	0.7048	0.0216	0.0307	0.3821	0.0472	0.1235	0.4972	0.0544	0.1094
MS4A7	0.1608	0.0132	0.0822	0.3247	0.0285	0.0878	0.2796	0.0266	0.0952
MSL2	0.0582	0.003	0.0509	0.1188	0.002	0.0166	0.0201	0.0008	0.0377
MSRB2	0.1138	0.0122	0.1076	0.0572	0.0062	0.1076	0.0597	0.0093	0.155
MTG1	0.2449	0.0136	0.0556	0.3248	0.0275	0.0847	0.4561	0.0342	0.0751
MTIF3	0.3354	0.0273	0.0814	0.9224	0.0631	0.0684	0.6765	0.0591	0.0874
MYL6B	0.0511	0.0021	0.0415						
NCKAP1L	0.2392	0.0089	0.0372	0.111	0.0065	0.0584	0.1278	0.009	0.0707
NCOR2	0.1134	0.0098	0.0866	0.1017	0.0119	0.1172	0.0793	0.0088	0.111
NDP	0	0	0.0271	0	0	0.0656	0	0	0.0701
NDUFA6	0.0834	0.0057	0.0684	0.2614	0.0289	0.1107	0.2601	0.0231	0.0889
NLGN3	0.018	0.0005	0.0298	0.0114	0.0006	0.0494	0	0	0.0421
NPFF	0.3427	0.0162	0.0474	0.8312	0.0498	0.0599	0.8318	0.0498	0.0599
NPFFR1	0.2374	0.0095	0.0401	0.1865	0.0148	0.0796	0.2316	0.0192	0.0827
NPY1R	0.0469	0.0011	0.0239	0.0197	0.0011	0.057	0.0395	0.0022	0.057
NPY5R	0.1132	0.0044	0.0388	0.0733	0.0044	0.0599	0.0468	0.0039	0.0834
NR1D2	0.0411	0.0015	0.036	0.0396	0.0022	0.0561	0.0105	0.0007	0.0706
NR1I3	0.0359	0.0025	0.0689	0.1585	0.0126	0.0792	0.1747	0.01	0.0574
NR2C2	0.0538	0.0022	0.0411	0	0	0.0666	0.0334	0.0022	0.0666
NSUN3	0.3656	0.0078	0.0212	0.1785	0.0078	0.0437	0.1619	0.0078	0.0482
NT5M									
NUDCD1	0.1708	0.007	0.0411	0.2277	0.0096	0.042	0.1874	0.0096	0.051
NUP88	0.4102	0.0184	0.0449	0.1986	0.017	0.0856	0.2432	0.0197	0.081
NXT1	0	0	0.044	0	0	0.1262	0	0	0.0787
OAS1	1.1218	0.0396	0.0353	0.5592	0.0455	0.0813	0.601	0.0466	0.0775
OAZ2	0.0757	0.0023	0.0307	0	0	0.0229	0.3076	0.0023	0.0076
OLA1	0.1025	0.0032	0.0316	0.0683	0.0022	0.0317	0.0456	0.0011	0.0237
OR10G3	0.5739	0.0294	0.0512	0.1983	0.0209	0.1054	0.3593	0.0384	0.1068
OR13J1	0	0	0	0.4358	0.0662	0.1519	0.4358	0.0662	0.1519
OR14A2				0.6197	0.0245	0.0395			
OR1A2									
OR1N1									
OR1N2	0.5676	0.0192	0.0338						
OR2J3				0.2125	0.0337	0.1584			
OR51F2									
OR5AS1							0.2827	0.0283	0.1003
OR5H6									
OR6M1	0.5755	0.0261	0.0453	0.2327	0.0305	0.131	0.3266	0.0365	0.1117
OR6X1				0.2942	0.0271	0.092			
ORC2	0.0254	0.0007	0.0293	0.0872	0.0045	0.0513	0.1016	0.0052	0.0514
OVOL2	0.0411	0.0022	0.0527	0.0298	0.0036	0.1214	0	0	0.1551
PADI1	0.2395	0.0187	0.0782	0.1709	0.0224	0.1312	0.1858	0.0235	0.1264
PAFAH1B1	0.2885	0.0085	0.0294	0.0593	0.0042	0.0714	0.1331	0.0085	0.0637
PAX9	0.0241	0.0013	0.055	0.0673	0.004	0.0591	0.0286	0.0027	0.0926
PCDH7	0.0502	0.002	0.0397	0.0433	0.0032	0.0728	0.0336	0.0026	0.0763
PCDHA1	0.2553	0.0175	0.0685	0.2363	0.0304	0.1286	0.2718	0.0305	0.1123
PCDHA3	0.1981	0.0111	0.056	0.1766	0.0207	0.117	0.1185	0.0166	0.14
PCDHB5	0.2408	0.015	0.0625	0.2183	0.0218	0.0997	0.2358	0.0239	0.1013
PDK3	0.05	0.0011	0.021	0	0	0.0341	0.0433	0.0011	0.0264
PDZD7	0.2759	0.0153	0.0554	0.2776	0.0271	0.0978	0.1831	0.0188	0.1027
PER3	0.3396	0.0233	0.0686	0.316	0.0269	0.0852	0.4265	0.0358	0.0839
PFDN6	0.0645	0.0035	0.054	0.0809	0.0035	0.043	0	0	0.0538
PGAM1	0.1018	0.0035	0.034	0.0379	0.0017	0.0457	0.0211	0.0017	0.082
PIAS1	0	0	0.035	0	0	0.0531	0	0	0.0485
PIGA	0.3374	0.0119	0.0353	0.4987	0.0221	0.0444	0.6541	0.0212	0.0324
PINX1	0.4091	0.0215	0.0525	0.2718	0.0269	0.099	0.3002	0.0296	0.0985
PIP4K2C	0.1543	0.0064	0.0416	0.1639	0.0118	0.072	0.0946	0.0071	0.0747
PITPNM1	0.082	0.006	0.0728	0.0792	0.0089	0.1127	0.0768	0.0092	0.1201
PLAU	0.2717	0.0163	0.0601	0.382	0.0321	0.0841	0.3744	0.0291	0.0777
PLB1	0.3461	0.0171	0.0493	0.232	0.0217	0.0937	0.251	0.025	0.0997
PLCB1	0.0281	0.0011	0.0378	0.0747	0.0039	0.0522	0.0747	0.0039	0.0522
PLCH2	0.1468	0.0127	0.0866	0.1431	0.0179	0.1248	0.156	0.0198	0.1268
PLEKHA5	0.2143	0.006	0.0281						
PLEKHB2	0.0821	0.006	0.0728	0.0996	0.01	0.1004	0.1119	0.012	0.1074
PLK2	0.0811	0.0038	0.0467	0	0	0	0.0811	0.0038	0.0467
PLP1	0	0	0.0097	0.1653	0.0016	0.0097	0.1653	0.0016	0.0097
PLS3	0	0	0.0348	0	0	0.0399	0	0	0.0447
PLXDC2	0.0725	0.0046	0.0629	0.075	0.0091	0.1219	0.0635	0.0071	0.111
PM20D2	0.1815	0.0096	0.0529	0.1899	0.0176	0.0924	0.1149	0.0082	0.0713
PMFBP1	0.3776	0.0189	0.0502	0.2044	0.0184	0.0899	0.381	0.0296	0.0777
PNKP	0.1463	0.0182	0.1244	0.1452	0.0149	0.1025	0.1287	0.0182	0.1413
PNLIPRP3	0.395	0.014	0.0355	0.6618	0.0246	0.0371	1.0979	0.0256	0.0233
PNMA1	0.3083	0.0082	0.0265	0.0278	0.0012	0.0449	0.182	0.0094	0.0518
PNPLA7	0.3398	0.0264	0.0777						

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
PNPT1	0.0917	0.0011	0.0123	0.1612	0.0018	0.0112	0.2171	0.0074	0.034	0.1449	0.0069	0.0475
POFUT2	0.312	0.002	0.0066	0.0254	0.001	0.0403	0.1185	0.0103	0.0868	0.0914	0.0085	0.0927
POGK	0.0489	0.0007	0.0145	0.2951	0.0021	0.0072	0.0575	0.0022	0.0382	0.1021	0.0043	0.0419
POLR2F	0	0	0.0115	0.6095	0.0072	0.0119	0	0	0.0232	0	0	0.0351
POU2F2	0	0	0.0029	0.112	0.001	0.0087	0.149	0.004	0.0267	0.1804	0.0088	0.0488
PPIG	0.0858	0.0006	0.0065	0.7367	0.0231	0.0313	0.153	0.0033	0.0219	0.1367	0.0039	0.0286
PPM1E	0.0997	0.0006	0.0061	0	0	0.0025	0.2898	0.0036	0.0124	0.2566	0.007	0.0271
PPM1K	0	0	0.0077	0	0	0.0116	0.062	0.0013	0.0217	0.121	0.0024	0.0194
PPP1R12A	1.0501	0.0056	0.0053	0.0612	0.0004	0.0072	0.0355	0.0009	0.0242	0.0547	0.0017	0.031
PPP2R2C	-1	0.001	0	0.0465	0.0019	0.0414	0	0	0.0474	0.0162	0.001	0.0595
PRKCD	0.1065	0.0021	0.0202	0.0213	0.0006	0.0297	0.0281	0.0019	0.0678	0.0404	0.0025	0.0629
PRKRIP1	0.5908	0.0047	0.008	0.1935	0.0047	0.0244	0	0	0.0411	0.0576	0.0029	0.0501
PRMT6	0	0	0.0176				0.0336	0.0012	0.0358	0.0221	0.0012	0.0542
PRPF4B	0.0571	0.0004	0.0075	0.0283	0.0004	0.0155	0.043	0.0017	0.0397	0.0518	0.0021	0.0413
PRRC1	0.2163	0.0031	0.0142	0.2158	0.0031	0.0142	0.0969	0.0032	0.0326	0.177	0.0082	0.0465
PRRG1	0.1635	0.005	0.0306	0.0987	0.002	0.0203	0.0587	0.002	0.0341	0	0	0.0203
PRSS55	0.3556	0.0114	0.032	0.2121	0.0139	0.0656	0.3684	0.0242	0.0656	0.4319	0.032	0.0741
PSMD4	0	0	0.0151	0	0	0.0113	0.0619	0.0012	0.0192	0	0	0.0304
PSMD9	-1	0.0059	0				0.148	0.0079	0.0532	0.4711	0.0108	0.023
PTPRCAP	0.1281	0.0023	0.0176	0.2867	0.0068	0.0237	0.4109	0.0276	0.0671	0.1878	0.0137	0.0729
PTTG2	0.321	0.0094	0.0292				0.3828	0.026	0.0678	0.4246	0.0455	0.1073
PYGO2	0.1741	0.0011	0.0064	0.1159	0.0011	0.0096	0.0785	0.0033	0.0425	0.0844	0.0038	0.0453
RAB17	0.2365	0.0063	0.0266	0.5336	0.0227	0.0425	0.2768	0.019	0.0686	0.3349	0.0276	0.0825
RABEP1	0.1048	0.0015	0.0142	0.175	0.0025	0.0142	0.0919	0.0035	0.0379	0.0592	0.0035	0.0593
RABGGTA	0.0982	0.0016	0.0162	0.1717	0.0032	0.0185	0.2111	0.0064	0.0302	0.1387	0.0044	0.0315
RAD21L1	0.8197	0.0046	0.0056	0.3615	0.0061	0.017	1.2083	0.017	0.0141	0.7392	0.0136	0.0184
RAE1	0.0347	0.0012	0.0336	0.0399	0.0012	0.0293	0	0	0.0554	0.0549	0.0028	0.0517
RALGDS	0.0542	0.0016	0.0287	0.0433	0.0017	0.0387	0.0714	0.0055	0.0765	0.1565	0.0122	0.0782
RAP1GAP2	0.0765	0.0027	0.0354	0.0834	0.0021	0.0251	0.0413	0.0024	0.0582	0.1656	0.0111	0.0673
RBBP6	0.0848	0.0015	0.0172	0.1565	0.0024	0.0155	0.1239	0.0046	0.0372	0.1213	0.0042	0.0348
RBBP7	0.4963	0.0047	0.0095				0.0713	0.0021	0.0288	0	0	0.025
RBCK1	0.0788	0.0009	0.011				0	0	0.0308	0.1796	0.0035	0.0193
RBM7	0.1413	0.0016	0.0114				0.2439	0.0114	0.0466	0.1193	0.0048	0.0406
RBP7	0	0	0.0123				0.2539	0.0095	0.0375	0.4238	0.0159	0.0376
RC3H1	0.0539	0.0004	0.0072	0.1097	0.0009	0.0078	0.0802	0.0024	0.0303	0.1247	0.0027	0.0219
RCN2	0.1734	0.0025	0.0146	0.2629	0.0013	0.0048	0	0	0.0308	0.2168	0.0063	0.0292
RD3	0.0933	0.0046	0.0494	0.0403	0.0023	0.0569	0.253	0.0162	0.0642	0.1431	0.0092	0.0645
RESP18	3.4947	0.0215	0.0062	-1	0.0176	0	0.8047	0.0359	0.0446			
RFX7	0.1111	0.0012	0.0108	0.2534	0.0033	0.0131	0.1795	0.003	0.0167	0.1553	0.0052	0.0335
RGS18	0.2683	0.0036	0.0135	0.0883	0.0018	0.0205	0.2672	0.0054	0.0204	0.3577	0.0073	0.0203
RGS8	0.1471	0.0022	0.0149	0.0976	0.0022	0.0225	0.0481	0.0022	0.0457			
RHOB	0	0	0.0217	0	0	0.017	0.0526	0.005	0.095	0	0	0.0517
RNF11	0	0	0	0	0	0.0093	0	0	0.0282	0	0	0.0128
RNF208	0	0	0.0276	0	0	0.0245	0.0247	0.0017	0.0709			
RNF216	0.0701	0.0009	0.0132				0.0731	0.0023	0.0318	0.1086	0.006	0.0549
RNF34	0.6038	0.0024	0.0039	0.0497	0.0012	0.0235	0.0732	0.0035	0.0481	0.1314	0.0047	0.0357
ROBO4	0.394	0.0052	0.0131	0.3579	0.0068	0.019	0.331	0.013	0.0392	0.2915	0.0181	0.0621
ROR2	0.1048	0.0024	0.0231	0.1047	0.0029	0.0277	0.0862	0.0042	0.0491	0.0957	0.0081	0.0848
RPL23A	0	0	0	0.5058	0.0815	0.1611	0	0	0.0461	0	0	0.0651
RPL26	0	0	0.0206	0.4065	0.0106	0.026	0.3605	0.0151	0.042	0.0476	0.003	0.0632
RPS12	0	0	0.0226				0	0	0.0822	0.2858	0.02	0.0701
RPS23	0	0	0.0293	0	0	0	0	0	0.0495	0	0	0.0702
RTN4RL2	0.7241	0.0142	0.0196	0.0537	0.0011	0.0205	0.2697	0.0056	0.0207	0.263	0.0128	0.0487
S100A4	0	0	0.0162	0	0	0.0162	0	0	0.0671	0	0	0.0328
S1PR3	0.1599	0.0012	0.0073	0.1056	0.0023	0.0222	0.1039	0.0047	0.0451	0.2198	0.0082	0.0374
SCG3	0.09	0.0009	0.0101	0	0	0.0191	0.0406	0.0018	0.0448	0.0461	0.0027	0.0591
SCN1B	0	0	0.0338	0.1345	0.0065	0.0483	0	0	0.0621	0	0	0.0615
SCT	0.4046	0.0079	0.0196	0.7307	0.018	0.0246						
SDAD1	0	0	0.0137	0.0732	0.0019	0.0254	0.0889	0.0031	0.0348	0.3115	0.0375	0.1203
SDC2	0.6525	0.0044	0.0068	0.6525	0.0044	0.0068	0.7177	0.0123	0.0171	0.1607	0.0044	0.0276
SDHA	0.1589	0.005	0.0318				0.0238	0.0013	0.0564	0.4122	0.0318	0.077
SDSL	0.2107	0.0041	0.0197	0.1996	0.0055	0.0277	0.2711	0.0153	0.0564	0.3234	0.0202	0.0626
SEC13	0.3997	0.0047	0.0119	0.2993	0.0036	0.0119	0.1471	0.0059	0.0403	0.1348	0.0071	0.0528
SEC14L5	0.1998	0.0036	0.0179	0.3158	0.0046	0.0145	0.1184	0.0057	0.0485	0.0874	0.007	0.0805
SECTM1	0.4542	0.018	0.0396	0.516	0.0165	0.0321				0.45	0.0431	0.0958
SEMA4B	0.2638	0.0083	0.0316	0.1536	0.0051	0.0332	0.1632	0.0103	0.0629	0.1713	0.0135	0.0786
SEMA6B	0.2274	0.0034	0.0148				0.1019	0.0051	0.0498	0.079	0.0048	0.0609
SFRP1	0.0707	0.0028	0.0389	0.1426	0.0041	0.029	0.2465	0.0134	0.0544	0.0485	0.0041	0.0853
SH3D21	0.5622	0.0079	0.014	0.3292	0.0097	0.0295	0.3678	0.0168	0.0457	0.7215	0.0262	0.0363
SHMT2	0.2584	0.0027	0.0104	0.1376	0.0018	0.013	0.217	0.0063	0.0289	0.0965	0.0036	0.0372
SHPRH	0.1355	0.0018	0.0132	0.2557	0.0061	0.0239	0.0854	0.0028	0.033	0.0755	0.0033	0.0441
SIPA1	0	0	0.0166	0.1332	0.0036	0.027	0.1142	0.0052	0.0453	0.0686	0.0037	0.0536
SIX6	0	0	0.0108							0.0546	0.0037	0.067
SLC16A8	0.2625	0.0037	0.0141				0.1471	0.0066	0.0448	0.1753	0.0093	0.0531
SLC22A17	0.0937	0.0009	0.0091	0.3767	0.0009	0.0023	0.0676	0.0017	0.0253	0.0245	0.0009	0.0348
SLC24A4	0.1047	0.0024	0.0226	0.0344	0.0016	0.0459	0.0294	0.0016	0.0538	0.0927	0.0047	0.0512
SLC25A23	0.0959	0.0019	0.0203	0.056	0.001	0.0171	0.0192	0.0011	0.0573			
SLC31A1	0	0	0.0079	0	0	0	0.0711	0.0023	0.032	0.1138	0.0046	0.0402
SLC35C1	0.1747	0.0037	0.0214	0.1738	0.005	0.0287	0.0918	0.0075	0.0816	0.1322	0.0087	0.0662
SLC45A2	0.3254	0.005	0.0155	0.4196	0.0076	0.018	0.12	0.005	0.042	0.2576	0.0144	0.0557
SLC4A4	0.0332	0.0004	0.012	0	0	0.0205	0.1378	0.0024	0.0177	0.0403	0.0012	0.0301
SLC5A3	0.1038	0.0012	0.0118	0.0812	0.0009	0.0109				0.2016	0.006	0.0299
SLC6A4	0.1268	0.0028	0.0221	0.0783	0.0016	0.0205	0.0891	0.0042	0.0473	0.0707	0.0051	0.0722
SLC7A14	0.1227	0.0017	0.0141	0.0813	0.0017	0.0213	0.068	0.0023	0.0339	0.0314	0.0014	0.0459
SLIT1	0.0668	0.0012	0.0174	0.1197	0.0033	0.0272	0.0645	0.0032	0.0494	0.0664	0.0035	0.052
SMC2	0.0936	0.0011	0.0115	0.1399	0.0021	0.0154	0.0553	0.0014	0.0262	0.0381	0.0014	0.0376
SMC5	0.3324	0.0023	0.007	0.1102	0.0016	0.0141	0.3323	0.0088	0.0265	0.2512	0.0085	0.0338
SMPD3	0.0659	0.0014	0.0207				0.0806	0.0042	0.0527	0.0399	0.0027	0.0682
SMR3B	2.8286	0.0212	0.0075	0	0	0.0201	0.4901	0.0305	0.0623	0.4727	0.0369	0.0781
SNRPA1	0	0	0.0107	0	0	0.0121	0	0	0.027	0	0	0.0269
SOAT2	0.1917	0.0034	0.0179	0.0843	0.0009	0.0102	0.1643	0.0093	0.0567	0.2135	0.013	0.0607
SOCS4	0.1386	0.001	0.007	0.0458	0.001	0.0212				0.1004	0.0034	0.0339
SPIB	0.085	0.0018	0.0215	0.1131	0.0018	0.0156	0.0994	0.0051	0.0517			
SPTB	0.1392	0.0024	0.0175	0.0993	0.0026	0.0264	0.0501	0.0028	0.056	0.1761	0.012	0.0683
SQSTM1	0.0316	0.001	0.0318	0.0786	0.003	0.0384	0.3172	0.0319	0.1007	0.0705	0.0082	0.117
SREK1	0.2015	0.0014	0.0069	0.3024	0.0007	0.0023				0.0598	0.0014	0.0233
STAT5B	0.0373	0.0006	0.0148	0.0164	0.0006	0.0337	0.0561	0.0028	0.0493	0.0457	0.002	0.0441
STH	0.4922	0.0106	0.0214	0.6622	0.007	0.0106	0.6648	0.029	0.0437			
STUB1	0	0	0.0097	0	0	0.0397	0	0	0.0765	0	0	0.0816
STX2	0.1404	0.0015	0.0106	0.0385	0.0015	0.0398	0.0844	0.0049	0.0586	0.0685	0.003	0.0437
SULF2	0.1611	0.0037	0.023	0.1093	0.003	0.0274	0.123	0.0068	0.0555	0.0367	0.003	0.0816
SUMF1	0.1622	0.0048	0.0294	0.233	0.0071	0.0303	0.16	0.0084	0.0523	0.1766	0.0156	0.0883
SUSD3	0.1362	0.0035	0.026	0.2261	0.0071	0.0314	0.2587	0.008	0.031	0.3005	0.0143	0.0475
SUV39H1	0	0	0.0134	0	0	0.01	0	0	0.0374	0	0	0.0339
SV2B	0.1435	0.0019	0.0132	0.0571	0.0013	0.0221	0.0255	0.0013	0.0495	0.0206	0.0013	0.0613
SYNJ2BP	0.3266	0.0031	0.0094	0	0	0				0.3259	0.0031	0.0094

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
PNPT1	0.1407	0.0091	0.0646	0.0807	0.0006	0.0074	0.1938	0.0062	0.0322	0.1255	0.0057	0.0457
POFUT2	0.0523	0.0057	0.1083	0.0255	0.001	0.0402	0.1189	0.0103	0.0866	0.0917	0.0085	0.0925
POGK	0.0663	0.005	0.0754	0.1178	0.0014	0.0121	0.0337	0.0015	0.0434	0.0759	0.0036	0.0469
POLR2F	0	0	0.0594	0.3023	0.0072	0.0239	0	0	0.0351	0	0	0.0471
POU2F2	0.0656	0.003	0.0455	0.1695	0.0009	0.0056	0.1691	0.0039	0.0228	0.1996	0.0085	0.0424
PPIG	0.0828	0.005	0.0607	0.8264	0.0237	0.0287	0.199	0.0039	0.0197	0.1698	0.0045	0.0263
PPM1E	0.1448	0.0042	0.0287	0.291	0.0007	0.0025	0.3476	0.0043	0.0124	0.2077	0.0043	0.0206
PPM1K	0.1	0.0035	0.0353	0	0	0.0194	0.0441	0.0013	0.0305	0.086	0.0024	0.0273
PPP1R12A	0.0479	0.0017	0.0354	0.771	0.0054	0.007	0.1822	0.0044	0.024	0.2089	0.0064	0.0308
PPP2R2C	0.0089	0.001	0.1082	0.0697	0.0029	0.0414	0.0212	0.001	0.0475	0.0323	0.0019	0.0595
PRKCD	0.035	0.0034	0.0962	0.0374	0.0014	0.0383	0.0366	0.0029	0.0785	0.0474	0.0036	0.0757
PRKRIP1	0.063	0.0095	0.1506	0.5873	0.0095	0.0162	0.1454	0.0047	0.0326	0.1743	0.0087	0.05
PRMT6	0.0155	0.0012	0.0771				0.0483	0.0012	0.0249	0.0278	0.0012	0.043
PRPF4B	0.0828	0.0051	0.062	0	0	0.0108	0.0366	0.0013	0.035	0.0467	0.0017	0.0366
PRRC1	0.1387	0.0085	0.0614	0.3602	0.0041	0.0114	0.1788	0.0042	0.0236	0.2465	0.0093	0.0376
PRRG1	0.0415	0.002	0.0481	0.1268	0.003	0.0237	0.0799	0.003	0.0375	0.2112	0.005	0.0237
PRSS55	0.2677	0.0307	0.1146	0.4209	0.0204	0.0484	0.4953	0.0281	0.0568	0.4709	0.0347	0.0737
PSMD4	0.0176	0.0012	0.0661	0	0	0.0187	0.034	0.0012	0.035	0	0	0.0457
PSMD9	0.1248	0.0138	0.1109				0.1104	0.0059	0.0534	0.3834	0.0088	0.0231
PTPRCAP	0.0951	0.0114	0.1196	0.2555	0.0045	0.0177	0.4154	0.0252	0.0607	0.1712	0.0114	0.0665
PTTG2	0.6433	0.0494	0.0768				0.5886	0.0308	0.0523	0.4998	0.0455	0.0911
PYGO2				0	0	0.0032	0.062	0.0022	0.0359	0.0677	0.0026	0.0377
RAB17	0.3183	0.0384	0.1207	0.94	0.0143	0.0152	0.2666	0.0126	0.0473	0.418	0.0255	0.0609
RABEP1	0.0484	0.0047	0.0974	0.1866	0.002	0.0106	0.0871	0.003	0.0343	0.0541	0.003	0.0556
RABGGTA	0.1341	0.008	0.06	0.0763	0.0016	0.0208	0.1469	0.0048	0.0326	0.0679	0.0024	0.0351
RAD21L1	0.5018	0.0202	0.0402	0.5463	0.0061	0.0113	1.2127	0.017	0.0141	0.7419	0.0136	0.0183
RAE1	0	0	0.1054	0.0798	0.0023	0.0293	0.0229	0.0012	0.051	0.0824	0.0043	0.0517
RALGDS	0.0893	0.0085	0.0954	0.0578	0.0022	0.0387	0.0879	0.007	0.08	0.1498	0.0128	0.0852
RAP1GAP2	0.0775	0.0077	0.0998	0.1094	0.004	0.0368	0.0755	0.0041	0.0538	0.1871	0.0133	0.071
RBBP6	0.1049	0.0053	0.051	0.2193	0.0034	0.0155	0.1573	0.0056	0.0356	0.1602	0.0053	0.033
RBBP7	0.0679	0.0028	0.041				0.0817	0.0021	0.0252	0.1633	0.0047	0.029
RBCK1	0.0363	0.0017	0.0477				0.0284	0.0009	0.0308	0.2247	0.0043	0.0193
RBM7	0.1258	0.013	0.1032				0.2094	0.0097	0.0465	0.0797	0.0032	0.0405
RBP7	0.3515	0.0277	0.0789				0.3841	0.0095	0.0248	0.6411	0.0159	0.0248
RC3H1	0.1025	0.0047	0.0458	0.0823	0.0004	0.0052	0.073	0.002	0.0277	0.0959	0.0023	0.0244
RCN2	0.0743	0.0027	0.036	0.3917	0.0038	0.0097	0.0369	0.0013	0.0361	0.2583	0.0089	0.0343
RD3	0.225	0.0179	0.0796	0.0467	0.0023	0.0493	0.1816	0.0116	0.0638	0.1872	0.0092	0.0494
RESP18	0.9088	0.0613	0.0674	2.5343	0.0156	0.0062	0.6654	0.0339	0.051			
RFX7	0.0892	0.0042	0.0471	0.1735	0.0026	0.0153	0.1355	0.0024	0.0177	0.1329	0.0046	0.0346
RGS18	0.2118	0.0073	0.0343	0.266	0.0054	0.0205	0.4474	0.0091	0.0203	0.5392	0.0109	0.0203
RGS8	0.1225	0.0066	0.0539	0	0	0.0074	0	0	0.0302			
RHOB	0	0	0.1152	0	0	0.0084	0.0737	0.005	0.0678	0	0	0.0291
RNF11	0	0	0.0187	0	0	0.0093	0	0	0.0282	0	0	0.0128
RNF208	0.0572	0.0053	0.092	0	0	0.022	0.0293	0.002	0.0683			
RNF216	0.1143	0.0091	0.08				0.1146	0.0033	0.0284	0.1373	0.0067	0.0486
RNF34	0.0431	0.0035	0.082	0.4521	0.0035	0.0078	0.1337	0.0059	0.044	0.2556	0.0071	0.0277
ROBO4	0.2806	0.0238	0.0849	0.3104	0.0036	0.0117	0.4009	0.0128	0.0318	0.3102	0.0171	0.055
ROR2	0.0512	0.0063	0.1231	0.0554	0.0014	0.0262	0.0599	0.0029	0.0484	0.073	0.0059	0.0807
RPL23A	0	0	0.0949	0.5058	0.0815	0.1611	0	0	0.0461	0	0	0.0651
RPL26	0	0	0.0634	0.4065	0.0106	0.026	0.3605	0.0151	0.042	0.0476	0.003	0.0632
RPS12	0	0	0.1074				0	0	0.0578	0.4356	0.02	0.046
RPS23	0	0	0.1021	0	0	0.0293	0	0	0.0598	0	0	0.0808
RTN4RL2	0.0909	0.006	0.0661	0.3737	0.013	0.0349	0.4403	0.0155	0.0353	0.397	0.0233	0.0588
S100A4	0	0	0.0853	0	0	0	0	0	0.0498	0	0	0.0162
S1PR3	0.0953	0.0086	0.0901	0.0528	0.0012	0.0221	0.0779	0.0035	0.045	0.1563	0.007	0.045
SCG3	0.1138	0.0101	0.0884	0.0662	0.001	0.0152	0.066	0.0027	0.0413	0.0654	0.0036	0.0556
SCN1B	0.0663	0.006	0.091	0.1584	0.0065	0.041	0	0	0.0549	0	0	0.0434
SCT				0.1606	0.0076	0.0475						
SDAD1	0.1082	0.0065	0.0603	0.0732	0.0019	0.0254	0.0955	0.0031	0.0324	0.3264	0.0375	0.1148
SDC2	0.1583	0.0089	0.0562	0	0	0.0137	0.3226	0.0078	0.0241	0	0	0.0347
SDHA	0.0462	0.005	0.1092				0.0879	0.0064	0.0728	0.4365	0.0371	0.0849
SDSL	0.171	0.0212	0.1239	0.0347	0.0014	0.0397	0.1797	0.0139	0.0774	0.2135	0.016	0.0751
SEC13	0.0806	0.0065	0.0809	0.4501	0.0036	0.0079	0.1333	0.0059	0.0445	0.1248	0.0071	0.0571
SEC14L5	0.0955	0.0122	0.1275	0.2226	0.0044	0.0197	0.1284	0.0065	0.0502	0.077	0.0065	0.084
SECTM1				0.6083	0.0158	0.0259				0.4638	0.0411	0.0886
SEMA4B				0.1176	0.003	0.0258	0.1603	0.0087	0.0541	0.1636	0.0115	0.0703
SEMA6B	0.0707	0.0064	0.0904				0.127	0.0068	0.0534	0.0982	0.0064	0.0651
SFRP1	0.0428	0.0055	0.129	0.0716	0.0014	0.0192	0.1496	0.01	0.067	0.0184	0.0014	0.0747
SH3D21	0.4922	0.0401	0.0814	0.4743	0.0069	0.0145	0.4569	0.0159	0.0347	0.8281	0.0249	0.0301
SHMT2	0.0736	0.0054	0.073	0.147	0.0027	0.0182	0.2093	0.0072	0.0343	0.1053	0.0045	0.0427
SHPRH	0.1227	0.009	0.0733	0.3056	0.0053	0.0174	0.0901	0.0026	0.0284	0.0712	0.0031	0.0432
SIPA1	0.0659	0.0072	0.1089	0.1333	0.0036	0.0271	0.1142	0.0052	0.0453	0.0654	0.0037	0.0563
SIX6	0.0645	0.0055	0.0851							0.066	0.0037	0.0554
SLC16A8	0.1975	0.0145	0.0735				0.0866	0.0044	0.0506	0.1673	0.0093	0.0557
SLC22A17	0.0249	0.0017	0.0688	0	0	0.0068	0.0285	0.0009	0.03	0	0	0.0396
SLC24A4	0.0515	0.0047	0.0922	0.0718	0.0024	0.033	0.0581	0.0024	0.0408	0.1136	0.0055	0.0488
SLC25A23	0.01	0.001	0.0959	0.1441	0.0029	0.0203	0.0615	0.0034	0.0548			
SLC31A1	0.2859	0.0069	0.024	0	0	0.0079	0.0566	0.0023	0.0403	0.0943	0.0046	0.0485
SLC35C1	0.2196	0.0163	0.0743	0.2177	0.0062	0.0287	0.1073	0.0088	0.0816	0.1514	0.01	0.0661
SLC45A2	0.1778	0.0177	0.0998	0.5466	0.0042	0.0077	0.1073	0.0034	0.0313	0.2825	0.0126	0.0448
SLC4A4	0.069	0.0033	0.0473	0.0333	0.0006	0.0168	0.1244	0.002	0.0164	0.0564	0.0016	0.0287
SLC5A3	0.0729	0.0037	0.0514	0	0	0.0109				0.1927	0.0053	0.0274
SLC6A4	0.0623	0.0056	0.0902	0.0522	0.0008	0.0153	0.0593	0.0028	0.0473	0.0541	0.0036	0.0673
SLC7A14	0.0674	0.0052	0.0771	0.05	0.0012	0.0231	0.046	0.0017	0.0376	0.0123	0.0006	0.0468
SLIT1	0.0467	0.0052	0.111	0.1336	0.004	0.0297	0.0496	0.0024	0.0489	0.0748	0.0041	0.0546
SMC2	0.0665	0.0043	0.0647	0.1507	0.0025	0.0166	0.0881	0.0025	0.0288	0.0645	0.0025	0.0389
SMC5	0.1237	0.0069	0.0556	0.05	0.0008	0.0155	0.2845	0.008	0.0281	0.2174	0.0077	0.0353
SMPD3	0.0401	0.0044	0.1106				0.0638	0.0042	0.0665	0.0374	0.0027	0.0728
SMR3B	0.2926	0.0432	0.1476	0	0	0.0201	1.061	0.0494	0.0465	0.7962	0.0495	0.0622
SNRPA1	0	0	0.0325	0	0	0.0121	0	0	0.027	0	0	0.038
SOAT2	0.2198	0.0164	0.0747	0.1437	0.0026	0.0178	0.1704	0.0111	0.0651	0.2218	0.0146	0.0657
SOCS4	0.0842	0.0058	0.0694	0	0	0.0212				0.0912	0.0024	0.0266
SPIB				0	0	0.0161	0.096	0.0037	0.0382			
SPTB	0.0731	0.0074	0.1015	0.1336	0.0032	0.0238	0.0631	0.0033	0.0519	0.2022	0.0127	0.0626
SQSTM1	0.0584	0.0091	0.1558	0.0792	0.002	0.0254	0.3593	0.0308	0.0858	0.0759	0.0072	0.095
SREK1	0.0779	0.0035	0.045	0.4531	0.0021	0.0046				0.0543	0.0014	0.0256
STAT5B	0.017	0.0017	0.0976	0	0	0.0376	0.0448	0.0022	0.0493	0.0262	0.0013	0.0513
STH	0.9085	0.0734	0.0808	0.1094	0.0035	0.0321	0.384	0.0254	0.0662			
STUB1	0	0	0.1318	0	0	0.0397	0	0	0.0765	0	0	0.0816
STX2	0.0893	0.0049	0.0552	0.1088	0.0031	0.0282	0.142	0.0066	0.0465	0.1382	0.0045	0.0325
SULF2	0.0483	0.0045	0.0932	0.2072	0.0043	0.0209	0.0976	0.0043	0.0445	0.0647	0.0043	0.0669
SUMF1				0.2788	0.0085	0.0304	0.3236	0.0108	0.0333	0.2796	0.018	0.0644
SUSD3	0.2495	0.0249	0.0996	0.1929	0.0071	0.0368	0.2144	0.008	0.0374	0.2691	0.0143	0.053
SUV39H1	0	0	0.0479	0	0	0.0033	0	0	0.0305	0	0	0.027
SV2B	0.0083	0.0006	0.0756	0.1074	0.0019	0.0176	0.0422	0.0019	0.0449	0.0334	0.0019	0.0567
SYNJ2BP	0.1927	0.0093	0.0482	0.3266	0.0031	0.0094				0.3245	0.0062	0.019

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
PNPT1	0.1373	0.0082	0.0593	0.3205	0.0072	0.0226	0.1835	0.0067	0.0365	0.1421	0.0077	0.0544
POFUT2	0.0524	0.0057	0.108	0.1116	0.0093	0.083	0.0835	0.0074	0.0887	0.0436	0.0045	0.1037
POGK	0.0498	0.0043	0.0859	0.0823	0.0029	0.0356	0.1269	0.005	0.0394	0.0733	0.0057	0.078
POLR2F	0	0	0.0719	0.1999	0.0072	0.0362	0.1487	0.0072	0.0486	0.0975	0.0072	0.0741
POU2F2	0.071	0.0029	0.0407	0.1685	0.0049	0.0288	0.1919	0.0098	0.051	0.0825	0.0039	0.0471
PPIG	0.0959	0.0056	0.0583	0.6763	0.0264	0.039	0.6181	0.0257	0.0416	0.5063	0.0237	0.0468
PPM1E	0.1689	0.0049	0.0288	0.3629	0.0036	0.0099	0.2409	0.0036	0.0149	0.1568	0.0043	0.0276
PPM1K	0.0814	0.0035	0.0434	0.0778	0.0013	0.0173	0.1517	0.0024	0.0155	0.0897	0.0035	0.0393
PPP1R12A	0.1829	0.0064	0.0353	0.0189	0.0004	0.0237	0.0431	0.0013	0.0308	0.041	0.0013	0.0324
PPP2R2C	0.0178	0.0019	0.1083	0	0	0.0861	0.0199	0.0019	0.0967	0.0207	0.0029	0.1397
PRKCD	0.0401	0.0046	0.1146	0.0228	0.0013	0.0557	0.0374	0.0019	0.0509	0.0315	0.0027	0.0855
PRKRIP1	0.1141	0.0155	0.1357	0.0952	0.0047	0.0497	0.143	0.0087	0.0608	0.1167	0.0143	0.1221
PRMT6	0.0173	0.0012	0.0694									
PRPF4B	0.0823	0.0047	0.0572	0.0364	0.0013	0.0361	0.0465	0.0018	0.0377	0.0797	0.0048	0.0606
PRRC1	0.1848	0.0096	0.0519	0.1421	0.0042	0.0297	0.2122	0.0093	0.0436	0.1642	0.0096	0.0583
PRRG1	0.0581	0.003	0.0517	0	0	0.0134	-1	0.002	0	0	0	0.0271
PRSS55	0.3614	0.0346	0.0959	0.3795	0.0281	0.074	0.4263	0.0333	0.0782	0.2509	0.0333	0.1327
PSMD4	0.0141	0.0012	0.0826	0.0515	0.0012	0.0231	0	0	0.034	0.0166	0.0012	0.0702
PSMD9	0.1064	0.0118	0.1112									
PTPRCAP	0.0805	0.0091	0.1128	0.4615	0.0252	0.0546	0.1883	0.0114	0.0604	0.0853	0.0091	0.1064
PTTG2	0.7917	0.0545	0.0689									
PYGO2				0.0568	0.0022	0.0392	0.0615	0.0025	0.0414			
RAB17	0.3705	0.0363	0.0978	0.3741	0.0251	0.0671	0.5254	0.035	0.0665	0.454	0.0452	0.0995
RABEP1	0.0449	0.0042	0.0933	0.0872	0.003	0.0342	0.0542	0.003	0.0555	0.0416	0.0039	0.0943
RABGGTA	0.112	0.0064	0.0575	0.2114	0.0064	0.0302	0.1216	0.004	0.0327	0.1464	0.008	0.055
RAD21L1	0.5036	0.0202	0.0401	0.8618	0.017	0.0198	0.5671	0.012	0.0212	0.4384	0.0202	0.046
RAE1	0.0098	0.0012	0.1198	0.023	0.0012	0.0509	0.0827	0.0043	0.0516	0.0111	0.0012	0.1052
RALGDS	0.0914	0.0091	0.0991	0.0937	0.0067	0.0718	0.1348	0.0112	0.0834	0.0969	0.009	0.093
RAP1GAP2	0.1084	0.0103	0.0949	0.0249	0.0014	0.0561	0.1462	0.0107	0.0729	0.0604	0.0065	0.1085
RBBP6	0.1355	0.0063	0.0467	0.1764	0.0066	0.0372	0.1747	0.0061	0.0348	0.1509	0.0073	0.0483
RBBP7	0.1594	0.0057	0.0356									
RBCK1	0.0437	0.0026	0.0593									
RBM7	0.1102	0.0114	0.103									
RBP7	0.4441	0.0277	0.0624									
RC3H1	0.0939	0.0043	0.0458	0.0927	0.0026	0.0276	0.1028	0.0026	0.0249	0.0851	0.0038	0.0452
RCN2	0.097	0.004	0.0414	0	0	0.0256	0.3134	0.0076	0.0243	0.087	0.0027	0.0308
RD3	0.2869	0.0179	0.0626	0.2453	0.0139	0.0567	0.1214	0.0069	0.0569	0.244	0.0153	0.0629
RESP18	0.8833	0.0593	0.0671	0.4877	0.0217	0.0446				0.7555	0.0509	0.0674
RFX7	0.0748	0.0036	0.0481	0.2172	0.0033	0.0152	0.1924	0.0065	0.0336	0.1105	0.0055	0.0496
RGS18	0.3193	0.0109	0.0342	0.2649	0.0073	0.0274	0.3325	0.0091	0.0274	0.1579	0.0054	0.0345
RGS8	0.115	0.0044	0.0382	0	0	0.0379				0.0954	0.0044	0.0461
RHOB	0	0	0.0906	0.0642	0.006	0.094	0	0	0.0345	0	0	0.0986
RNF11	0	0	0.0187	0	0	0.0378	0	0	0.0128	0	0	0.0282
RNF208	0.0577	0.006	0.1045	0.0317	0.0017	0.0551				0.054	0.0053	0.0975
RNF216	0.1467	0.0101	0.0689									
RNF34	0.076	0.0059	0.0777	0.1069	0.0047	0.044	0.2126	0.0059	0.0276	0.0608	0.0047	0.0777
ROBO4	0.2542	0.0201	0.0792	0.3032	0.0107	0.0352	0.2786	0.0158	0.0566	0.2518	0.0214	0.0848
ROR2	0.0417	0.0048	0.1161	0.0484	0.0024	0.05	0.0606	0.0054	0.0892	0.0349	0.0044	0.1249
RPL23A	0	0	0.0949	0.4947	0.083	0.1678	0.5046	0.0815	0.1614	0.5044	0.0815	0.1615
RPL26	0	0	0.0634	0.9893	0.0258	0.0261	0.3882	0.0121	0.0311	0.2891	0.009	0.0313
RPS12	0	0	0.0821									
RPS23	0	0	0.1132	0	0	0.0495	0	0	0.0702	0	0	0.1021
RTN4RL2	0.0845	0.0062	0.0731	0.1505	0.0045	0.0297	0.2193	0.0115	0.0522	0.0911	0.006	0.066
S100A4	0	0	0.0675	0	0	0.0498	0	0	0.0162	0	0	0.0675
S1PR3	0.0904	0.0073	0.0813	0.1575	0.0047	0.0297	0.2764	0.0082	0.0297	0.1113	0.0086	0.0771
SCG3	0.1189	0.011	0.0923	0.058	0.002	0.0348	0.0648	0.003	0.0468	0.1216	0.0102	0.0835
SCN1B	0.0722	0.006	0.0836	0.1241	0.0061	0.0495	0	0	0.0524	0.1365	0.0127	0.0931
SCT												
SDAD1	0.1179	0.0065	0.0553	0.153	0.005	0.0324	0.3358	0.0395	0.1175	0.1339	0.0084	0.0627
SDC2	0.0696	0.0044	0.0637	0.3226	0.0078	0.0241	0	0	0.0347	0.0696	0.0044	0.0637
SDHA	0.0718	0.0088	0.122									
SDSL	0.1544	0.0198	0.1281	0.2222	0.0153	0.0689	0.2616	0.0174	0.0666	0.1654	0.0212	0.1282
SEC13	0.0765	0.0065	0.0853	0.0532	0.0024	0.0445	0.0622	0.0036	0.0571	0.0346	0.003	0.0854
SEC14L5	0.0778	0.0101	0.1294	0.1098	0.0046	0.0416	0.0735	0.0061	0.083	0.0861	0.0107	0.1243
SECTM1							0.4742	0.0451	0.0952			
SEMA4B				0.1126	0.0068	0.0605	0.1496	0.0091	0.0607			
SEMA6B	0.0838	0.0081	0.0967									
SFRP1	0.0351	0.0041	0.1178	0.2796	0.0117	0.0419	0.051	0.0028	0.054	0.0517	0.0055	0.1067
SH3D21	0.5428	0.0383	0.0706	0.3549	0.0167	0.0471	0.5449	0.022	0.0403	0.4753	0.0383	0.0805
SHMT2	0.0797	0.0063	0.0787	0.1988	0.0063	0.0316	0.0781	0.0027	0.0344	0.0767	0.0054	0.0701
SHPRH	0.1163	0.0084	0.0718	0.1735	0.0069	0.0399	0.1393	0.0075	0.0535	0.1396	0.0117	0.0842
SIPA1	0.0659	0.0072	0.109	0.1218	0.0063	0.0519	0.0747	0.0042	0.0566	0.0726	0.0073	0.1009
SIX6	0.075	0.0055	0.0732									
SLC16A8	0.1904	0.0145	0.0762									
SLC22A17	0.0116	0.0009	0.0737	0.0372	0.0009	0.023	0	0	0.0324	0.0129	0.0009	0.0663
SLC24A4	0.0658	0.0055	0.0841	0.0293	0.0016	0.0539	0.0838	0.0047	0.0567	0.0565	0.0047	0.084
SLC25A23	0.031	0.0029	0.0944	0	0	0.0502				0.023	0.0019	0.0832
SLC31A1	0.2133	0.0069	0.0321	0.0711	0.0023	0.032	0.1138	0.0046	0.0402	0.2859	0.0069	0.024
SLC35C1	0.2198	0.0163	0.0742	0.0837	0.0075	0.0895	0.1184	0.0087	0.0739	0.2196	0.0163	0.0742
SLC45A2	0.1759	0.016	0.0907	0.1739	0.0059	0.0338	0.3212	0.0152	0.0474	0.19	0.0178	0.0935
SLC4A4	0.0642	0.0029	0.0444	0.1634	0.0035	0.0212	0.033	0.0011	0.034	0.086	0.004	0.0471
SLC5A3	0.0485	0.0025	0.0514				0.1191	0.0036	0.0305	0.0199	0.0009	0.0456
SLC6A4	0.0493	0.0042	0.0854	0.0776	0.0024	0.0309	0.0571	0.0033	0.0585	0.054	0.004	0.0742
SLC7A14	0.0544	0.0046	0.0849	0.0419	0.0017	0.0413	0.0162	0.0009	0.0534	0.0543	0.0046	0.085
SLIT1	0.0535	0.0058	0.1092	0.1171	0.0055	0.0473	0.115	0.0059	0.051	0.0735	0.0075	0.1021
SMC2	0.0783	0.0054	0.0688	0.1034	0.0033	0.0315	0.092	0.0036	0.0389	0.0901	0.0065	0.0717
SMC5	0.1047	0.0057	0.0541	0.2551	0.0072	0.0281	0.1722	0.0069	0.0399	0.0894	0.0053	0.0588
SMPD3	0.0354	0.0044	0.125									
SMR3B	0.4775	0.0623	0.1305	0.5134	0.0322	0.0626	0.4812	0.0405	0.0842	0.2105	0.0323	0.1534
SNRPA1	0	0	0.0325	0	0	0.0243	0	0	0.0367	0	0	0.0305
SOAT2	0.2097	0.0176	0.084	0.1559	0.0083	0.0533	0.2189	0.012	0.0548	0.2219	0.0167	0.0755
SOCS4	0.0701	0.0049	0.0694				0.059	0.0024	0.0412	0.0574	0.0049	0.0848
SPIB				0.0737	0.0035	0.0479						
SPTB	0.0835	0.008	0.0958	0.0501	0.0028	0.056	0.1809	0.0122	0.0676	0.0827	0.0078	0.0943
SQSTM1	0.0644	0.0081	0.1257	0.3057	0.0308	0.1008	0.0845	0.0093	0.1097	0.0575	0.0081	0.1408
SREK1	0.0779	0.0035	0.0449				0.0996	0.0021	0.021	0.0987	0.0042	0.0425
STAT5B	0.0108	0.0011	0.1018	0.0415	0.0022	0.0532	0.0274	0.0013	0.0489	0.0108	0.0011	0.1018
STH	0.7512	0.0695	0.0925	0.3988	0.0217	0.0545				0.7109	0.0656	0.0922
STUB1	0	0	0.1318	0	0	0.0872	0	0	0.0814	0	0	0.1316
STX2	0.1546	0.0066	0.0425	0.0417	0.0034	0.0814	0.024	0.0015	0.0639	0.0884	0.0066	0.0744
SULF2	0.0732	0.0056	0.0763	0.1525	0.0075	0.0489	0.0375	0.003	0.0799	0.0616	0.0055	0.0896
SUMF1				0.2139	0.0113	0.0529	0.2484	0.0213	0.0858			
SUSD3	0.1887	0.0203	0.1074	0.6506	0.012	0.0185	0.4855	0.0178	0.0368	0.3203	0.0271	0.0847
SUV39H1	0	0	0.0409	0	0	0.027	0	0	0.0236	0	0	0.0444
SV2B	0.0178	0.0013	0.0709	0.0268	0.0013	0.0471	0.0214	0.0013	0.0589	0.0086	0.0006	0.0731
SYNJ2BP	0.2132	0.0124	0.0582				0.3259	0.0031	0.0094	0.1927	0.0093	0.0482

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
PNPT1	0.2611	0.008	0.0308	0.242	0.0113	0.0468	0.2186	0.0108	0.0495
POFUT2	0.0994	0.0085	0.0852	0.0342	0.0034	0.0993	0.0411	0.0035	0.0852
POGK	0.0428	0.0022	0.0513	0.051	0.0044	0.0864	0.0503	0.005	0.0994
POLR2F	0	0	0.0594	0	0	0.0594	0	0	0.0719
POU2F2	0.2423	0.0126	0.0519	0.1369	0.0069	0.0507	0.1547	0.0097	0.0626
PPIG	0.2552	0.0062	0.0241	0.1299	0.0073	0.056	0.0766	0.0045	0.0583
PPM1E	0.2884	0.0058	0.02	0.1985	0.0065	0.0327	0.173	0.0063	0.0362
PPM1K	0.1243	0.0027	0.0217	0.1113	0.0054	0.0485	0.1243	0.0059	0.0474
PPP1R12A	0.0521	0.0017	0.0329	0.0426	0.0017	0.0404	0.054	0.0025	0.0471
PPP2R2C	0	0	0.0589	0	0	0.1062	0.0171	0.0019	0.1122
PRKCD	0.0315	0.0019	0.0604	0.0223	0.002	0.0906	0.0144	0.0013	0.0933
PRKRIP1	0.0311	0.0029	0.0927	0.0525	0.0095	0.1806	0.1558	0.0145	0.0933
PRMT6	0.0513	0.0024	0.0469	0.0311	0.0024	0.0774	0.0248	0.0024	0.0967
PRPF4B	0.0396	0.0021	0.0539	0.0799	0.006	0.0751	0.0917	0.0064	0.0702
PRRC1	0.4102	0.0085	0.0206	0.2096	0.0099	0.047	0.2717	0.015	0.0551
PRRG1	0.1487	0.002	0.0134	0	0	0.041	0.0737	0.002	0.0271
PRSS55	0.4931	0.0386	0.0783	0.2792	0.0294	0.1052	0.3365	0.0428	0.1271
PSMD4	0.0341	0.0012	0.0349	0.0333	0.0024	0.0715	0.0166	0.0012	0.0701
PSMD9	0.1686	0.0108	0.0642	0.1096	0.0138	0.1261	0.1132	0.0118	0.1044
PTPRCAP	0.3193	0.0264	0.0828	0.1768	0.0194	0.1098	0.115	0.0137	0.119
PTTG2	0.6651	0.0504	0.0757	0.7465	0.0518	0.0694	1.0286	0.0545	0.053
PYGO2	0.0417	0.0025	0.0611						
RAB17	0.4155	0.0254	0.0612	0.3239	0.0318	0.0983	0.2834	0.0341	0.1203
RABEP1	0.0705	0.0035	0.0498	0.0633	0.0052	0.0828	0.0501	0.0053	0.1055
RABGGTA	0.2189	0.0056	0.0255	0.2042	0.0097	0.0474	0.1315	0.0072	0.055
RAD21L1	0.8297	0.014	0.0169	0.6645	0.0198	0.0298	0.3734	0.0172	0.0459
RAE1	0.0613	0.0028	0.0463	0	0	0.1149	0.0298	0.0028	0.0955
RALGDS	0.1791	0.012	0.0671	0.0889	0.008	0.0899	0.1424	0.0133	0.0937
RAP1GAP2	0.1561	0.0105	0.0674	0.0677	0.0064	0.0952	0.1055	0.0117	0.1114
RBBP6	0.1637	0.0055	0.0339	0.1162	0.0063	0.0544	0.115	0.0058	0.0505
RBBP7	0.0956	0.0021	0.0215	0.0713	0.0021	0.0288	0.0806	0.0028	0.0346
RBCK1	0.1042	0.0035	0.0337	0.0234	0.0018	0.0748	0.1029	0.0052	0.0506
RBM7	0.1602	0.0065	0.0404	0.1629	0.0146	0.0899	0.1139	0.0081	0.0711
RBP7	0.7714	0.0192	0.0248	0.5093	0.0318	0.0624	0.6379	0.0399	0.0626
RC3H1	0.1071	0.0028	0.0265	0.0894	0.0045	0.0499	0.1175	0.0051	0.0433
RCN2	0	0	0.0361	0.0647	0.0027	0.0413	0.087	0.0027	0.0308
RD3	0.385	0.0162	0.0422	0.3264	0.0231	0.0709	0.1789	0.0127	0.0712
RESP18				0.6679	0.0452	0.0677			
RFX7	0.1796	0.0049	0.0273	0.0913	0.0042	0.046	0.1009	0.0058	0.0577
RGS18	0.9482	0.0128	0.0135	0.468	0.0128	0.0273	0.4019	0.0109	0.0272
RGS8				0.1152	0.0044	0.0381			
RHOB	0.0649	0.005	0.077	0.0328	0.005	0.1523	0	0	0.0909
RNF11	0	0	0.0128	0	0	0.0187	0	0	0
RNF208				0.0255	0.0035	0.1372			
RNF216	0.1041	0.0052	0.0504	0.1368	0.0087	0.0633	0.1343	0.0123	0.0919
RNF34	0.0884	0.0035	0.0399	0.0575	0.0047	0.0821	0.0805	0.0059	0.0734
ROBO4	0.2829	0.0151	0.0533	0.287	0.0218	0.0761	0.2712	0.024	0.0886
ROR2	0.1088	0.0076	0.0703	0.0394	0.0048	0.1231	0.0495	0.0059	0.1192
RPL23A	0	0	0.0557	0	0	0.0852	0	0	0.085
RPL26	0.2864	0.0182	0.0636	0.2369	0.0151	0.0638	0.0476	0.003	0.0632
RPS12	0.243	0.02	0.0825	0	0	0.1203	0.2432	0.02	0.0824
RPS23	0	0	0.0194	0	0	0.0493	0	0	0.07
RTN4RL2	0.2982	0.0158	0.0529	0.1204	0.0091	0.0752	0.1574	0.019	0.1207
S100A4	0	0	0.0671	0	0	0.1224	0	0	0.0853
S1PR3	0.1297	0.0059	0.0451	0.0855	0.0073	0.0859	0.143	0.011	0.0772
SCG3	0.1666	0.0045	0.0273	0.1699	0.0119	0.07	0.1567	0.011	0.07
SCN1B	0	0	0.0524	0.0662	0.006	0.0911	0.103	0.0073	0.0705
SCT									
SDAD1	0.3759	0.0381	0.1014	0.135	0.0071	0.0529	0.3396	0.0373	0.11
SDC2	0.1711	0.0078	0.0454	0.2044	0.0123	0.06	0.0622	0.0044	0.0712
SDHA	0.3247	0.0317	0.0978	0.0359	0.005	0.1403	0.3105	0.0361	0.1162
SDSL	0.3059	0.0217	0.0709	0.1655	0.0212	0.1282	0.2258	0.0263	0.1163
SEC13	0.0967	0.0059	0.0614	0.0594	0.0053	0.0898	0.1025	0.0065	0.0636
SEC14L5	0.0463	0.0038	0.0826	0.0939	0.0112	0.1193	0.094	0.0125	0.1333
SECTM1									
SEMA4B	0.13	0.0076	0.0581						
SEMA6B	0.1049	0.0069	0.0655	0.0746	0.0076	0.1014	0.0615	0.0066	0.1073
SFRP1	0.1595	0.0117	0.0734	0.1121	0.0134	0.1196	0.0447	0.0055	0.1234
SH3D21	0.5715	0.0254	0.0444	0.3903	0.0388	0.0994	0.6038	0.0449	0.0744
SHMT2	0.2165	0.0063	0.0291	0.1325	0.0076	0.0575	0.0636	0.0036	0.0565
SHPRH	0.0973	0.0041	0.0422	0.1237	0.0089	0.0717	0.1248	0.0095	0.0763
SIPA1	0.1233	0.0052	0.042	0.08	0.0075	0.0935	0.0516	0.0055	0.107
SIX6							0.0694	0.0055	0.0791
SLC16A8	0.1046	0.0044	0.0419	0.1235	0.0103	0.0835	0.163	0.0155	0.095
SLC22A17	0.0264	0.0009	0.0324	0.0279	0.0017	0.0613	0.012	0.0009	0.0713
SLC24A4	0.0976	0.0047	0.0486	0.0566	0.0047	0.0839	0.0707	0.0063	0.0896
SLC25A23				0.0228	0.0022	0.0966			
SLC31A1	0.289	0.0069	0.0238	0.3832	0.0092	0.0239	0.3591	0.0115	0.032
SLC35C1	0.0667	0.0062	0.0935	0.0985	0.0113	0.1142	0.1831	0.015	0.0821
SLC45A2	0.2448	0.011	0.0447	0.1563	0.0142	0.0906	0.2497	0.0204	0.0818
SLC4A4	0.0825	0.0021	0.0251	0.1015	0.0041	0.0402	0.0826	0.0037	0.0452
SLC5A3							0.047	0.0023	0.0492
SLC6A4	0.0682	0.0051	0.0748	0.0547	0.0056	0.1027	0.0551	0.0066	0.1192
SLC7A14	0.0212	0.0012	0.0543	0.0465	0.004	0.0869	0.0418	0.004	0.0967
SLIT1	0.0874	0.0052	0.059	0.0687	0.0068	0.0996	0.0681	0.0072	0.1059
SMC2	0.059	0.0022	0.0368	0.0529	0.0036	0.0686	0.0689	0.005	0.0729
SMC5	0.3148	0.0122	0.0387	0.1864	0.0101	0.054	0.1316	0.0089	0.0673
SMPD3	0.0638	0.0042	0.0665	0.0425	0.0046	0.1081	0.0369	0.0044	0.1202
SMR3B	0.7119	0.0559	0.0786	0.3351	0.0623	0.186	0.4171	0.0691	0.1656
SNRPA1	0	0	0.0436	0	0	0.0325	0	0	0.0492
SOAT2	0.1908	0.0176	0.0924	0.2426	0.0228	0.094	0.2049	0.0219	0.1071
SOCS4							0.1082	0.0073	0.0676
SPIB									
SPTB	0.1215	0.0089	0.0732	0.0636	0.0069	0.1084	0.1116	0.012	0.1079
SQSTM1	0.3656	0.0349	0.0956	0.294	0.0354	0.1203	0.1058	0.0124	0.1174
SREK1							0.0324	0.0021	0.0646
STAT5B	0.066	0.004	0.0611	0.0313	0.0033	0.1061	0.0242	0.002	0.0833
STH				1.6692	0.0752	0.0451			
STUB1	0	0	0.0981	0	0	0.1615	0	0	0.1089
STX2	0.0843	0.0049	0.0587	0.1238	0.0085	0.0687	0.1633	0.0049	0.0302
SULF2	0.0961	0.0062	0.0647	0.0852	0.0075	0.0879	0.0507	0.0055	0.1088
SUMF1	0.2454	0.0168	0.0684						
SUSD3	1.1445	0.0141	0.0123	0.3177	0.0252	0.0792	0.3432	0.0317	0.0925
SUV39H1	0	0	0.0515	0	0	0.0732	0	0	0.0695
SV2B	0.0223	0.0013	0.0565	0.0084	0.0006	0.0755	0.0068	0.0006	0.0927
SYNJ2BP							0.2127	0.0124	0.0583

Gene	HCng_w	HC_dN	HC_dS	HGng_w	HG_dN	HG_dS	HOng_w	HO_dN	HO_dS	HSng_w	HS_dN	HS_dS
SYNPO2L	0.0945	0.0009	0.01	0.1714	0.0024	0.0138	0.5085	0.0159	0.0313	0.1604	0.0097	0.0602
TAC4	1.3689	0.0161	0.0118	0.338	0.0141	0.0418	1.208	0.0285	0.0236	0.9434	0.0458	0.0485
TACR2	0.3212	0.0078	0.0244	0.3218	0.0079	0.0244	0.2231	0.0135	0.0604	0.311	0.0169	0.0544
TAGLN	0	0	0.015	0	0	0.0075	0	0	0.0303	0	0	0.038
TBC1D17	0.1185	0.0035	0.0291	0.1401	0.0044	0.0316	0.0391	0.0028	0.0706	0.0732	0.0048	0.0662
TBC1D9	0	0	0.0161	0	0	0.0182	0.0089	0.0003	0.0389	0.0252	0.001	0.0409
TBCB	0	0	0.0114	0.0615	0.0021	0.0345	0.0385	0.0018	0.047	0.1185	0.0057	0.0484
TBR1	0	0	0.0081	0	0	0.0103	0	0	0.0224	0	0	0.0299
TBRG1	0.4769	0.0032	0.0068	0.4232	0.0043	0.0102	0.1577	0.0032	0.0204	0.4225	0.0043	0.0102
TBXA2R	0.0557	0.0014	0.0244	0.3863	0.0137	0.0354	0.0296	0.0014	0.0461	0.0673	0.0041	0.0608
TEKT5	0.2523	0.0099	0.0394	0.2223	0.0101	0.0454	0.0859	0.0081	0.0945	0.3272	0.0255	0.0781
TFEC	0.3005	0.0025	0.0084	0.4572	0.0048	0.0105	0.0424	0.0013	0.0296	0.1699	0.005	0.0296
TGM1	0.1414	0.0016	0.0116	0.1383	0.0029	0.0208	0.0636	0.0044	0.0686	0.0933	0.0069	0.0738
THY1	0	0	0.0164	0	0	0.0164	0.0959	0.0056	0.0588	0.1353	0.0056	0.0416
TIAF1	-1	0.0039	0				0.518	0.0119	0.023	-1	0.0325	0
TJP2	0.1648	0.003	0.0179	0.1097	0.002	0.0185	0.1669	0.0097	0.0578	0.174	0.0094	0.0542
TMC8	0.5722	0.007	0.0122	0.3301	0.0063	0.0191	0.4231	0.0172	0.0405	0.3139	0.0195	0.062
TMCC3	0.0426	0.0009	0.0214	0.0424	0.0012	0.0272	0.1362	0.0055	0.0403	0.0739	0.0027	0.0371
TMED4	0.317	0.0019	0.0061	0	0	0.0312	0.0679	0.0039	0.0573	0	0	0.051
TMEM105	0.7536	0.0072	0.0096	1.7003	0.0329	0.0194				2.2637	0.0445	0.0196
TMEM106B	0	0	0	0	0	0	0.1478	0.0032	0.0215	0.1971	0.0032	0.0161
TMEM121				0.123	0.0014	0.0117	0.1111	0.0058	0.0522	0.0718	0.0043	0.0605
TMEM139	1.0562	0.0063	0.006	1.4068	0.0084	0.006	0.564	0.017	0.0302	0.4715	0.0109	0.0231
TMEM178				1.1528	0.0185	0.0161	0.1134	0.003	0.0268			
TMEM179	-1	0.0023	0	0	0	0	0.2785	0.0299	0.1074	0	0	0.0499
TMEM18	0	0	0.0105	0.2863	0.0036	0.0124	0.07	0.0036	0.0508	0.1268	0.0126	0.0993
TMEM194A	0.6207	0.002	0.0032				0.3504	0.0079	0.0226	0.4831	0.0109	0.0226
TMEM208	0	0	0.0079	0.3232	0.0026	0.008	0	0	0.024	0	0	0.024
TMEM232	0.587	0.0068	0.0116	0.3934	0.0051	0.0129	0.3536	0.0118	0.0334	0.2055	0.0097	0.0474
TMEM38B	-1	0.003	0	0	0	0.0147	0.4359	0.0106	0.0244	0.1909	0.0076	0.0397
TMEM42	0	0	0.0083	0	0.0033	0	0.0473	0.0028	0.06			
TMEM43	0.1649	0.0033	0.0203	0.1779	0.0067	0.0377	0.0844	0.0056	0.0663	0.0496	0.0039	0.079
TMEM61	0.2725	0.0076	0.0279	0.3557	0.0111	0.0313	0.1485	0.0132	0.0887	0.716	0.022	0.0307
TMEM92	0.5508	0.0158	0.0287	0.3343	0.0114	0.0341	0.5303	0.0229	0.0432	1.5272	0.0258	0.0169
TNFAIP8L3	0.1519	0.003	0.0198	0.1506	0.003	0.0199	0.0656	0.0041	0.0623	0.0373	0.0015	0.0403
TNFSF9				0.0651	0.0024	0.0374						
TNIP3	0.1301	0.0024	0.0182	0.3956	0.0137	0.0347	0.3618	0.0204	0.0563	0.4427	0.0204	0.0461
TNS3	0.0907	0.0015	0.0169	0.1274	0.0028	0.0217	0.1758	0.0114	0.0651	0.1555	0.0106	0.068
TOP3A	0.2319	0.0039	0.017	0.3331	0.0063	0.0188	0.4547	0.0153	0.0336	0.244	0.0124	0.0506
TRAIP	0.4092	0.0037	0.0091	1.081	0.0066	0.0061	0.4039	0.0195	0.0482	0.3041	0.0094	0.0308
TRIM39	0.3218	0.0009	0.0027	0.0456	0.0009	0.0187	0.1415	0.0036	0.0257	0.115	0.0034	0.0297
TSPAN15	0	0	0.0143	0	0	0.024	0.0386	0.0015	0.0388	0.0565	0.0039	0.0699
TSPAN8	0.4452	0.0111	0.0249	0.4452	0.0111	0.0249	0.8534	0.0377	0.0441	1.7708	0.0723	0.0408
TSSK2	-1	0.0061	0	1.2155	0.0049	0.004	0.1052	0.0061	0.0581	0.3635	0.0143	0.0394
TSSK4	0.3013	0.0053	0.0177	0.151	0.0027	0.0176	0.5978	0.0189	0.0316	0.4015	0.0258	0.0642
TTC29	0.2802	0.0045	0.0161	0.2799	0.0029	0.0104	0.6736	0.0109	0.0162	0.3083	0.0091	0.0294
TTF1	0.1652	0.0052	0.0312	0.422	0.0086	0.0203	0.4156	0.0204	0.049	0.3604	0.0187	0.052
TTLL9	0.1642	0.0039	0.024	0.4981	0.0273	0.0549	0.1315	0.0069	0.0525	0.2571	0.024	0.0934
TTYH1	0.2071	0.0041	0.0196	0.3009	0.0053	0.0176	0.1973	0.0068	0.0342	0.1898	0.0095	0.0498
TUBB	0	0	0.0066	0	0	0.0098	0.4343	0.0244	0.0563	0	0	0.0265
TXNDC11	0.6043	0.0038	0.0063	0.3796	0.0056	0.0148	0.2836	0.0137	0.0482	0.2605	0.0116	0.0445
UBLCP1	0	0	0.0145	0	0	0.0194	0.1114	0.0027	0.0243	0	0	0.0194
UGT1A3	0.2506	0.0074	0.0296				0.2436	0.0133	0.0544			
UNC13C	0.1825	0.0021	0.0117				0.16	0.0062	0.0385	0.1133	0.0059	0.0523
UPF2	0.0671	0.0007	0.0099	0.1238	0.0019	0.015	0.0559	0.0014	0.0249	0.0635	0.002	0.0315
USP1	0.1654	0.0016	0.0099				0.1559	0.0044	0.0279	0.208	0.0071	0.0341
USP18	0.1593	0.0046	0.029				0.4264	0.0234	0.0549	0.415	0.021	0.0507
USP26	0.9795	0.0184	0.0188	0.5518	0.0075	0.0136	0.7075	0.0194	0.0274	0.6004	0.0283	0.0471
USP7	0.0379	0.0004	0.0101	0.0204	0.0004	0.0192	0.0242	0.0004	0.0167	0.0138	0.0004	0.0278
VCX2	1.6507	0.0669	0.0405				0.8352	0.1019	0.122			
VPREB1	0.3105	0.0092	0.0296	0.1548	0.0062	0.0398	0.3905	0.0156	0.04	0.4465	0.0294	0.0659
VPS13D	0.1183	0.0015	0.0126				0.0983	0.0035	0.0355	0.1527	0.0053	0.035
VPS52	0	0	0.0056	0.0408	0.0006	0.0151	0.0535	0.0021	0.0391	0.0381	0.0012	0.0323
VSIG1	1.272	0.0042	0.0033	0.4731	0.0063	0.0132	0.8412	0.0084	0.0099	0.431	0.0117	0.0272
WDFY2	0.2948	0.0022	0.0074	0.4436	0.0033	0.0073	0.066	0.0033	0.0493	0.1091	0.0033	0.0298
WDR33	0.0527	0.0003	0.0062	0.0631	0.0007	0.0104	0.0738	0.0013	0.0178	0.0311	0.001	0.0318
WDR5B	0.3037	0.0013	0.0044	0.1808	0.004	0.022	0.0676	0.004	0.0588	0.2003	0.0053	0.0265
WDR63	0.211	0.0033	0.0159	0.096	0.0024	0.0254	0.183	0.0072	0.0393	0.1629	0.0068	0.0419
WDR74	2.0648	0.0084	0.0041	0.2087	0.0058	0.028	0.1329	0.0047	0.0351	0.4024	0.0135	0.0335
WFDC11	0.4825	0.0097	0.0201	0.1202	0.0048	0.0403	0.4816	0.0195	0.0406	0.4786	0.0195	0.0408
WFDC6	0.5723	0.0102	0.0178				1.0183	0.0363	0.0356	0.5334	0.0337	0.0632
WISP3	0.1228	0.0035	0.0284	0.0721	0.0012	0.0161	0.2402	0.0058	0.0243	0.1032	0.0047	0.0451
WSB2	0	0	0.0105	0.1539	0.0015	0.0095	0.0347	0.0011	0.0314	0.181	0.006	0.0333
YLPM1	0.1206	0.001	0.0085	0.1288	0.0014	0.0112	0.1979	0.003	0.0153	0.1063	0.0031	0.0292
YTHDC1	0.097	0.0012	0.0123	0	0	0.0143	0.0239	0.0006	0.0254	0.0206	0.0006	0.0289
ZBP1	0.4775	0.0093	0.0195	0.4547	0.0104	0.0228	0.3904	0.0262	0.067	0.5044	0.04	0.0794
ZBTB38	0.1645	0.0025	0.0153	0.0703	0.0014	0.0204	0.1572	0.0052	0.0329	0.0923	0.0043	0.0468
ZC3H12D	0.3472	0.0088	0.0253	0.2446	0.006	0.0246	0.2366	0.0141	0.0596	0.1827	0.0141	0.077
ZC3H13	0.0592	0.0005	0.0088	0.1562	0.0023	0.015	0.1005	0.0032	0.0315	0.0858	0.0028	0.0324
ZC4H2	0	0	0.0206	0	0	0.0217	0	0	0.0206	0	0	0.0347
ZCCHC17	0	0	0.0195	0	0	0.0293				0	0	0.0843
ZFP37	2.9411	0.0074	0.0025	2.67	0.0067	0.0025	0.6633	0.0135	0.0204	0.7673	0.0187	0.0243
ZFP57	2.0257	0.0056	0.0028	0.5263	0.0089	0.0169	0.8185	0.015	0.0183	0.4338	0.0142	0.0327
ZFP64	0.1714	0.0026	0.0149	0.1195	0.0026	0.0214	0.1646	0.0064	0.039	0.1376	0.0065	0.047
ZFYVE20	0.3022	0.0033	0.011	0.3018	0.0045	0.0148	0.2014	0.0084	0.0415	0.2352	0.0084	0.0356
ZMYND17	0.2766	0.0049	0.0176	0.1892	0.0039	0.0205	0.3799	0.0078	0.0205	0.2526	0.0098	0.0386
ZNF117	1.0698	0.0516	0.0482	0.6354	0.0299	0.0471	0.5493	0.015	0.0274	0.5129	0.097	0.189
ZNF157	0.2769	0.0027	0.0096	0.1119	0.0017	0.0151	0.1671	0.0052	0.0313	0.3581	0.0077	0.0214
ZNF192	1.7782	0.0045	0.0025	0.4451	0.0024	0.0054	0.3601	0.0121	0.0336	0.5307	0.0136	0.0256
ZNF20	-1	0.0032	0				0.5183	0.0112	0.0216	0.3819	0.0125	0.0326
ZNF235	0.1632	0.0047	0.0286	0.2566	0.0069	0.0268	0.1733	0.0087	0.0499			
ZNF275	0.1468	0.002	0.0138	0.1053	0.0041	0.0393	0.0512	0.004	0.0791	0.0855	0.0071	0.083
ZNF30	0.5017	0.0134	0.0267	0.4267	0.0144	0.0336	0.3972	0.0167	0.042	0.2778	0.0152	0.0546
ZNF302	0.4487	0.0074	0.0166	0.6573	0.0122	0.0185	0.4302	0.065	0.1511	0.1926	0.0143	0.0745
ZNF324B	0.2451	0.008	0.0326	0.162	0.0049	0.0303	0.1712	0.0115	0.0673	0.2582	0.0275	0.1066
ZNF335	0.1731	0.0037	0.0215	0.1647	0.003	0.0181	0.1267	0.0067	0.0525	0.1164	0.007	0.0604
ZNF528	0.1592	0.0041	0.0255				0.2617	0.0115	0.0441	0.3664	0.0171	0.0466
ZNF540	0.9239	0.0045	0.0049				0.4028	0.0109	0.0272	0.3239	0.0129	0.0398
ZNF561	0.5107	0.008	0.0156	0.3974	0.0759	0.191	0.8322	0.079	0.095	0.2561	0.0188	0.0733
ZNF569	0	0	0.0073	0.2497	0.0043	0.0171	0.0618	0.0018	0.0296	0.1447	0.0052	0.0359
ZNF570	0	0	0.015	0.0743	0.0017	0.023	0.0999	0.004	0.0396			
ZNF574	0.2633	0.0015	0.0057	0.099	0.0018	0.0185	0.0214	0.001	0.0468			
ZNF575	1.7849	0.0066	0.0037	2.8762	0.0116	0.004	0.274	0.01	0.0367	0.3096	0.0117	0.0378
ZNF592	0.0621	0.0007	0.0111	0.0487	0.001	0.0213	0.1541	0.0032	0.0205	0.0715	0.0024	0.0339
ZNF625				0.1355	0.0042	0.0309	0.1209	0.007	0.0577	0.1097	0.0112	0.1021
ZNF652	0.1839	0.0014	0.0077	0.0689	0.0007	0.0102	0.4344	0.013	0.03	0	0	0.0199
ZNRD1	0	0	0	0	0	0.012	0.1454	0.0105	0.0722	0.3007	0.007	0.0232

Gene	HMng_w	HM_dN	HM_dS	CGng_w	CG_dN	CG_dS	COng_w	CO_dN	CO_dS	CSng_w	CS_dN	CS_dS
SYNPO2L	0.1992	0.0136	0.0682	0.2399	0.0033	0.0138	0.546	0.0171	0.0313	0.1762	0.0106	0.0602
TAC4				0.412	0.0223	0.0542	1.0329	0.0369	0.0357	0.8896	0.0544	0.0611
TACR2	0.2581	0.0214	0.0831	0.3237	0.0045	0.0138	0.2044	0.0101	0.0494	0.3847	0.0133	0.0345
TAGLN	0.0349	0.0022	0.0617	0	0	0.0226	0	0	0.0458	0	0	0.0537
TBC1D17	0.0605	0.0069	0.1145	0.0934	0.0029	0.0316	0.0284	0.0021	0.0728	0.0608	0.0042	0.0684
TBC1D9	0	0	0.0732	0	0	0.0206	0.0124	0.0005	0.042	0.0238	0.001	0.0433
TBCB	0.0232	0.0018	0.0779	0.0616	0.0021	0.0344	0.0385	0.0018	0.047	0.1187	0.0057	0.0483
TBR1	0.0183	0.0007	0.0387	0	0	0.0103	0	0	0.0224	0	0	0.0299
TBRG1	0.2652	0.0119	0.0449	0.3166	0.0032	0.0102	0.1049	0.0021	0.0205	0.3162	0.0032	0.0102
TBXA2R	0.1336	0.0137	0.1028	0.3873	0.0123	0.0318	0	0	0.0424	0.0511	0.0027	0.0534
TEKT5	0.1453	0.0182	0.1251	0.2218	0.0108	0.0489	0.0926	0.009	0.0976	0.3144	0.026	0.0828
TFEC	0.267	0.0114	0.0426	0.5055	0.008	0.0159	0.1271	0.0038	0.0297	0.2546	0.0076	0.0297
TGM1	0.0933	0.0093	0.0998	0.1668	0.0023	0.0138	0.064	0.0038	0.0597	0.0978	0.0063	0.0647
THY1	0.0413	0.0029	0.0693	0	0	0	0.0958	0.0056	0.0588	0.1353	0.0056	0.0416
TIAF1	1.1232	0.06	0.0534				0.3435	0.0079	0.0231	-1	0.0283	0
TJP2	0.1119	0.0092	0.0819	0.1339	0.0028	0.0212	0.1557	0.01	0.0645	0.151	0.0094	0.0625
TMC8	0.2496	0.0156	0.0627	0.2534	0.0044	0.0175	0.3584	0.0153	0.0427	0.3118	0.0189	0.0606
TMCC3	0.0315	0.0023	0.0741	0	0	0.0233	0.1231	0.0046	0.0371	0.0538	0.0018	0.0339
TMED4	0.1015	0.0078	0.077	0.0782	0.0019	0.0249	0.1153	0.0058	0.0507	0	0	0.0423
TMEM105	0.8223	0.0405	0.0492	0.8696	0.0255	0.0293				1.2401	0.0369	0.0297
TMEM106B	0.0715	0.0048	0.0667	0	0	0	0.1478	0.0032	0.0215	0.1971	0.0032	0.0161
TMEM121	0.053	0.0043	0.0818									
TMEM139	1.1906	0.0368	0.0309	-1	0.0105	0	0.5266	0.0192	0.0364	0.7096	0.0164	0.0231
TMEM178	0	0	0.0641									
TMEM179				-1	0.0025	0	0.3002	0.0323	0.1076	0.0507	0.0025	0.05
TMEM18				0.142	0.0036	0.0251	0.0555	0.0036	0.0641	0.1132	0.0126	0.1112
TMEM194A	0.2299	0.0129	0.0562				0.3054	0.0079	0.0259	0.4211	0.0109	0.0259
TMEM208	0.0447	0.0026	0.0576	-1	0.0026	0	0	0	0.0159	0	0	0.0159
TMEM232	0.3776	0.0219	0.0579	0.4313	0.0068	0.0157	0.339	0.0111	0.0327	0.2246	0.0086	0.0381
TMEM38B	0.1193	0.0091	0.0763	0.2061	0.003	0.0147	0.5623	0.0137	0.0244	0.2681	0.0106	0.0397
TMEM42				0.3357	0.0033	0.0098	0.0555	0.0028	0.0512			
TMEM43	0.0967	0.0146	0.1512	0.2074	0.0078	0.0378	0.1012	0.0067	0.0663	0.0553	0.0045	0.0809
TMEM61	0.4517	0.0478	0.1059	0.4791	0.0208	0.0435	0.2438	0.023	0.0945	0.9456	0.0334	0.0353
TMEM92	1.0055	0.0435	0.0432	0.7783	0.0223	0.0286	0.9934	0.0287	0.0289	0.9984	0.0287	0.0287
TNFAIP8L3	0.1598	0.0167	0.1043	0.3013	0.006	0.0199	0.0982	0.0061	0.0624	0.1119	0.0045	0.0404
TNFSF9	0.3135	0.0379	0.1209									
TNIP3	0.4325	0.049	0.1133	0.3261	0.0113	0.0347	0.3186	0.0179	0.0563	0.4902	0.018	0.0367
TNS3	0.1171	0.013	0.1111	0.1243	0.0025	0.0198	0.1897	0.0118	0.062	0.1729	0.0112	0.0649
TOP3A	0.2198	0.0159	0.0722	0.1022	0.0031	0.0306	0.2515	0.0121	0.0483	0.1543	0.0101	0.0657
TRAIP	0.418	0.0169	0.0405	0.9268	0.0028	0.003	0.4049	0.0157	0.0387	0.2618	0.0056	0.0215
TRIM39	0.0552	0.0026	0.0464	0	0	0.0161	0.1593	0.0036	0.0229	0.0948	0.0026	0.0271
TSPAN15	0.0709	0.0075	0.1063	0	0	0.0095	0.0443	0.0015	0.0339	0.0734	0.0039	0.0538
TSPAN8	1.576	0.0949	0.0602	0.7423	0.0186	0.025	1.4414	0.0421	0.0292	2.7118	0.0762	0.0281
TSSK2	0.1414	0.0129	0.0912	1.5189	0.0061	0.004	0.1263	0.0073	0.0582	0.395	0.0156	0.0394
TSSK4	0.365	0.0285	0.078	0.6111	0.0052	0.0085	0.5941	0.0188	0.0317	0.4418	0.0285	0.0645
TTC29	0.3457	0.0183	0.0528	0.2788	0.0039	0.0139	0.6058	0.0118	0.0195	0.3041	0.01	0.0328
TTF1	0.4278	0.046	0.1074	0.2662	0.0088	0.033	0.3529	0.0216	0.0611	0.3509	0.0203	0.0578
TTLL9				0.5115	0.0263	0.0514	0.1004	0.0049	0.049	0.2182	0.023	0.1053
TTYH1	0.0924	0.0102	0.1105	0.1539	0.0032	0.0206	0.0899	0.0034	0.0375	0.1387	0.0073	0.0529
TUBB	0.0105	0.001	0.0936	0	0	0.0165	0.3851	0.0244	0.0635	0	0	0.0333
TXNDC11	0.2169	0.0174	0.0803	0.3188	0.0036	0.0113	0.2604	0.0116	0.0445	0.2301	0.0093	0.0402
UBLCP1	0	0	0.0444	0	0	0.0243	0.0927	0.0027	0.0292	0	0	0.0243
UGT1A3	0.3697	0.0314	0.0849				0.2322	0.0133	0.0571			
UNC13C	0.0898	0.0076	0.0843				0.1365	0.0056	0.0407	0.0977	0.0053	0.0546
UPF2	0.0414	0.0021	0.0509	0.1238	0.0019	0.015	0.046	0.0014	0.0302	0.0783	0.0027	0.0341
USP1	0.321	0.0109	0.0341				0.0906	0.0027	0.03	0.1507	0.0054	0.0362
USP18	0.3172	0.0343	0.1081				0.3774	0.0258	0.0683	0.3205	0.0234	0.073
USP26	0.5017	0.0354	0.0705	0.8837	0.0184	0.0208	0.9752	0.0326	0.0334	0.6703	0.0414	0.0618
USP7	0.014	0.0008	0.056	0	0	0.0207	0	0	0.0182	0	0	0.0264
VCX2	0.5649	0.0974	0.1724				0.9165	0.1105	0.1205			
VPREB1	0.5435	0.0358	0.0659	0.1231	0.0062	0.0501	0.3105	0.0156	0.0503	0.3433	0.0263	0.0766
VPS13D	0.0762	0.0055	0.0717				0.0881	0.0033	0.0372	0.1326	0.005	0.038
VPS52	0.0414	0.0031	0.0743	0.0655	0.0006	0.0094	0.0603	0.0021	0.0346	0.0464	0.0012	0.0265
VSIG1	0.4305	0.019	0.044	0.3788	0.0063	0.0166	0.6314	0.0084	0.0133	0.3834	0.0117	0.0306
WDFY2	0.1047	0.0043	0.0415	0.1476	0.0011	0.0073	0	0	0.0454	0.0486	0.0011	0.0223
WDR33	0.0479	0.0023	0.0482	0.0859	0.001	0.0115	0.0553	0.001	0.0178	0.0194	0.0007	0.0339
WDR5B	0.1688	0.0107	0.0632	0.2004	0.0053	0.0265	0.0835	0.0053	0.0635	0.2141	0.0066	0.031
WDR63	0.3477	0.0188	0.0542	0.2402	0.0039	0.0162	0.2549	0.0086	0.0339	0.2281	0.0083	0.0364
WDR74	0.1844	0.0105	0.0571	0.2423	0.007	0.0288	0.15	0.0056	0.0373	0.5375	0.019	0.0353
WFDC11	0.7436	0.0606	0.0815	0.1403	0.0072	0.0517	0.1537	0.0097	0.0629	0.1528	0.0097	0.0632
WFDC6							0.6734	0.0363	0.054	0.4114	0.0337	0.082
WISP3	0.1644	0.0117	0.0711	0.1151	0.0023	0.0202	0.231	0.0047	0.0202	0.1073	0.0035	0.0325
WSB2	0	0	0.0351	0.1023	0.0015	0.0142	0.0311	0.0011	0.0353	0.031	0.0011	0.0354
YLPM1	0.1178	0.0053	0.0451	0.0937	0.0012	0.0132	0.1615	0.0028	0.0174	0.0928	0.0029	0.0313
YTHDC1	0.0318	0.0012	0.0373	0.5856	0.0012	0.002	0.0482	0.0006	0.0126	0.0363	0.0006	0.0164
ZBP1	0.621	0.0569	0.0916	1.1788	0.0114	0.0097	0.5129	0.0272	0.0531	0.5834	0.0414	0.0709
ZBTB38	0.1014	0.0061	0.0603	0.1091	0.0025	0.023	0.2281	0.0063	0.0276	0.1224	0.0054	0.0441
ZC3H12D	0.2902	0.0262	0.0904	0.3926	0.0079	0.0201	0.2934	0.0159	0.0541	0.2434	0.0163	0.0669
ZC3H13	0.1194	0.0066	0.0557	0.1084	0.0018	0.0168	0.079	0.0026	0.0335	0.0647	0.0022	0.0345
ZC4H2	0	0	0.0562	0	0	0	0	0	0	0	0	0.0137
ZCCHC17	0.0334	0.0018	0.0531	0	0	0.0072				0	0	0.0604
ZFP37	0.8407	0.0249	0.0296	0.935	0.0047	0.005	0.3828	0.0088	0.0229	0.5678	0.0153	0.0269
ZFP57	0.4069	0.0253	0.0621	0.3261	0.0064	0.0198	0.5908	0.0125	0.0212	0.3287	0.0117	0.0357
ZFP64	0.0308	0.0032	0.1039	0	0	0.0192	0.0842	0.0038	0.0456	0.0689	0.0036	0.0521
ZFYVE20	0.1561	0.0086	0.0549	0.2413	0.0045	0.0185	0.1845	0.0084	0.0453	0.2235	0.0084	0.0375
ZMYND17	0.2087	0.0186	0.0893	0.5557	0.0049	0.0087	1.2288	0.0107	0.0087	0.4042	0.0107	0.0266
ZNF117	0.7316	0.0372	0.0509	0.801	0.0715	0.0893	0.9128	0.0621	0.068	0.5628	0.1014	0.1802
ZNF157	0.1276	0.008	0.0627	0.2769	0.0027	0.0096	0.2689	0.0073	0.0273	0.644	0.0093	0.0145
ZNF192	0.2088	0.0098	0.047	0.2962	0.0016	0.0055	0.3149	0.0106	0.0335	0.4714	0.0121	0.0256
ZNF20	0.4634	0.0287	0.062				0.4429	0.0096	0.0217	0.3321	0.0108	0.0326
ZNF235	0.1878	0.0138	0.0735	0.3095	0.0069	0.0222	0.1809	0.0111	0.0612			
ZNF275	0.0589	0.0081	0.1379	0.1297	0.0041	0.0319	0.0513	0.0041	0.0789	0.0944	0.0071	0.0752
ZNF30	0.2326	0.0243	0.1043	0.4885	0.0196	0.0401	0.4918	0.0191	0.0389	0.3563	0.0218	0.0613
ZNF302				1.0327	0.0085	0.0083	0.4757	0.0663	0.1395	0.2008	0.0128	0.0639
ZNF324B	0.2731	0.0262	0.0959	0.2767	0.0098	0.0353	0.2015	0.0152	0.0753	0.3169	0.0354	0.1118
ZNF335	0.1093	0.0093	0.0853	0.1891	0.0041	0.0214	0.1274	0.0068	0.0532	0.1365	0.0079	0.0577
ZNF528	0.2515	0.024	0.0956				0.2308	0.0102	0.0441	0.3666	0.0171	0.0465
ZNF540	0.4116	0.0195	0.0473				0.2831	0.0077	0.0272	0.2743	0.0109	0.0399
ZNF561	0.2951	0.0233	0.0789	0.4035	0.0737	0.1828	0.9118	0.08	0.0877	0.3337	0.02	0.0598
ZNF569	0.0677	0.0043	0.0631	0.4391	0.0043	0.0097	0.0828	0.0018	0.0221	0.1557	0.0052	0.0334
ZNF570	0.0279	0.0024	0.0848	0.0649	0.0017	0.0263	0.0926	0.004	0.0427			
ZNF574	0.0321	0.003	0.0935	0.1452	0.0025	0.0172	0.0343	0.0015	0.0439			
ZNF575	0.1612	0.0117	0.0726	-1	0.0116	0	0.3502	0.0114	0.0326	0.4085	0.0134	0.0329
ZNF592	0.1094	0.008	0.0731	0.0402	0.001	0.0258	0.1258	0.0032	0.0252	0.067	0.0024	0.0362
ZNF625												
ZNF652	0.0541	0.0021	0.0391	0.055	0.0007	0.0128	0.4757	0.013	0.0274	0	0	0.0232
ZNRD1	0.4544	0.0105	0.0231	0	0	0.012	0.1454	0.0105	0.0722	0.3007	0.007	0.0232

Gene	CMng_w	CM_dN	CM_dS	GOng_w	GO_dN	GO_dS	GSng_w	GS_dN	GS_dS	GMng_w	GM_dN	GM_dS
SYNPO2L	0.2142	0.0142	0.0665	0.536	0.0153	0.0285	0.2141	0.0121	0.0564	0.2548	0.0155	0.061
TAC4				0.4623	0.0307	0.0664	0.7805	0.0523	0.0671			
TACR2	0.2515	0.018	0.0717	0.24	0.0101	0.0422	0.3955	0.0121	0.0306	0.2458	0.0158	0.0643
TAGLN	0.0277	0.0022	0.0778	0	0	0.038	0	0	0.0459	0.0309	0.0022	0.0697
TBC1D17	0.0523	0.0062	0.1191	0.0384	0.0029	0.0767	0.0398	0.003	0.0742	0.0463	0.0052	0.1116
TBC1D9	0	0	0.081	0	0	0.0381	0.0266	0.0011	0.0406	0	0	0.0769
TBCB	0.0233	0.0018	0.0778	0.0599	0.0042	0.0708	0.0555	0.0045	0.0812	0.0455	0.0042	0.0933
TBR1	0.0164	0.0007	0.0434	0	0	0.0249	0	0	0.0327	0.0155	0.0007	0.0457
TBRG1	0.2405	0.0108	0.0449	0.1346	0.0032	0.0239	0.3156	0.0043	0.0136	0.2257	0.0114	0.0503
TBXA2R	0.125	0.0124	0.0988	0.229	0.0123	0.0538	0.2356	0.0158	0.0669	0.2226	0.0248	0.1116
TEKT5	0.1592	0.0196	0.123	0.0988	0.009	0.0914	0.3383	0.0265	0.0782	0.1482	0.0191	0.1288
TFEC	0.326	0.0139	0.0427	0.2005	0.0064	0.0321	0.2506	0.008	0.0321	0.4525	0.0195	0.043
TGM1	0.0878	0.0088	0.0997	0.061	0.004	0.0662	0.0936	0.0067	0.0715	0.0854	0.0093	0.1085
THY1	0.0327	0.0029	0.0876	0.0958	0.0056	0.0588	0.1353	0.0056	0.0416	0.0327	0.0029	0.0876
TIAF1	1.0399	0.0556	0.0535									
TJP2	0.108	0.0092	0.0849	0.1224	0.0073	0.0598	0.1179	0.007	0.0591	0.0935	0.008	0.0855
TMC8	0.2172	0.0132	0.0609	0.2936	0.0146	0.0497	0.2678	0.0181	0.0678	0.2069	0.014	0.0675
TMCC3	0.0382	0.0023	0.0612	0.0673	0.0035	0.0515	0.0294	0.0012	0.0393	0	0	0.0796
TMED4	0.1393	0.0098	0.0703	0.0767	0.0039	0.0508	0	0	0.0423	0.1111	0.0078	0.0704
TMEM105	0.5528	0.0329	0.0596				1.0105	0.0406	0.0401	0.7379	0.0366	0.0496
TMEM106B	0.0715	0.0048	0.0667	0.1478	0.0032	0.0215	0.1971	0.0032	0.0161	0.0715	0.0048	0.0667
TMEM121				0.0902	0.0043	0.0481	0.0512	0.0029	0.0564	0.0372	0.0029	0.0777
TMEM139	0.7914	0.0345	0.0436	0.4663	0.017	0.0364	0.5884	0.0136	0.0232	0.9841	0.0367	0.0373
TMEM178				0.564	0.0197	0.035				0	0	0.0767
TMEM179				0.2246	0.0284	0.1266	0	0	0.0499			
TMEM18				0.1113	0.0071	0.0641	0.09	0.0107	0.1193			
TMEM194A	0.2162	0.0129	0.0597									
TMEM208	0.0524	0.0026	0.0491	0.1612	0.0026	0.016	0.1608	0.0026	0.016	0.1044	0.0051	0.0493
TMEM232	0.4058	0.0242	0.0596	0.3353	0.0123	0.0368	0.2073	0.0082	0.0397	0.3895	0.0227	0.0583
TMEM38B	0.1596	0.0122	0.0762	0.3614	0.0106	0.0295	0.1905	0.0076	0.0398	0.1191	0.0091	0.0764
TMEM42				0.0823	0.0033	0.0399						
TMEM43	0.11	0.0158	0.1432	0.1607	0.0101	0.0628	0.1014	0.0078	0.0773	0.1114	0.0169	0.1516
TMEM61	0.4535	0.0559	0.1232	0.1596	0.0157	0.0981	0.6484	0.0247	0.038	0.5057	0.0501	0.0992
TMEM92	1.1556	0.045	0.0389	0.4652	0.02	0.043	0.6727	0.0229	0.0341	0.9408	0.0406	0.0431
TNFAIP8L3	0.1599	0.019	0.1186	0.1102	0.0061	0.0555	0.1109	0.0045	0.0406	0.1798	0.0204	0.1137
TNFSF9										0.2618	0.0272	0.104
TNIP3	0.4094	0.0464	0.1133	0.353	0.0252	0.0714	0.4155	0.0253	0.0608	0.4369	0.0509	0.1165
TNS3	0.1222	0.013	0.1065	0.2029	0.0124	0.061	0.1749	0.0115	0.066	0.1283	0.0137	0.1065
TOP3A	0.1615	0.0127	0.0785	0.2974	0.0137	0.0462	0.1829	0.0117	0.0639	0.1498	0.0118	0.0785
TRAIP	0.4246	0.0132	0.031	0.3981	0.0166	0.0417	0.2676	0.0066	0.0245	0.414	0.0141	0.0341
TRIM39	0.0391	0.0017	0.0437	0.1596	0.0036	0.0228	0.0789	0.0026	0.0325	0.0368	0.0017	0.0464
TSPAN15	0.0836	0.0075	0.0901	0.0342	0.0015	0.0438	0.0612	0.0039	0.0645	0.0747	0.0075	0.1009
TSPAN8	1.6378	0.099	0.0605	1.0246	0.0454	0.0443	2.533	0.0793	0.0313	1.7877	0.1022	0.0571
TSSK2	0.1548	0.0141	0.0913	0.0978	0.0061	0.0625	0.3276	0.0143	0.0437	0.1346	0.0129	0.0959
TSSK4	0.398	0.0312	0.0784	0.5967	0.0189	0.0316	0.4007	0.0257	0.0643	0.3643	0.0285	0.0781
TTC29	0.3403	0.0192	0.0564	0.6977	0.0097	0.0139	0.3698	0.0078	0.021	0.3917	0.0166	0.0424
TTF1	0.4461	0.0473	0.1059	0.4604	0.0221	0.0481	0.4477	0.0217	0.0484	0.4982	0.0497	0.0997
TTLL9				0.3983	0.0293	0.0737	0.0659	0.0049	0.0749			
TTYH1	0.0737	0.0081	0.1106	0.1205	0.0034	0.0279	0.1649	0.0066	0.0398	0.0771	0.0074	0.0963
TUBB	0.0097	0.001	0.1011	0.3649	0.0244	0.067	0	0	0.0367	0.0109	0.001	0.0899
TXNDC11	0.2007	0.0154	0.0766	0.2476	0.0125	0.0506	0.2706	0.0113	0.0419	0.2046	0.0163	0.0795
UBLCP1	0	0	0.0494	0.079	0.0027	0.0342	0	0	0.0293	0	0	0.0546
UGT1A3	0.3466	0.0314	0.0907									
UNC13C	0.0882	0.0074	0.0836									
UPF2	0.0383	0.0021	0.0551	0.1053	0.0027	0.0259	0.1236	0.0041	0.033	0.042	0.0023	0.0552
USP1	0.2569	0.0093	0.0361									
USP18	0.3108	0.0369	0.1188									
USP26	0.6162	0.0501	0.0813	0.8519	0.0203	0.0239	0.6848	0.0297	0.0434	0.516	0.0353	0.0685
USP7	0.0072	0.0004	0.0545	0	0	0.0275	0	0	0.039	0.006	0.0004	0.0656
VCX2	0.599	0.1121	0.1871									
VPREB1	0.5896	0.0326	0.0553	0.2574	0.0156	0.0607	0.3025	0.0265	0.0877	0.3757	0.0329	0.0876
VPS13D	0.0686	0.0052	0.0751									
VPS52	0.0451	0.0031	0.0682	0.0755	0.0028	0.0369	0.0648	0.0018	0.0285	0.0525	0.0037	0.0703
VSIG1	0.4001	0.019	0.0474	0.4022	0.0094	0.0234	0.2847	0.0117	0.0412	0.3262	0.019	0.0581
WDFY2	0.0642	0.0022	0.0337	0.0204	0.0011	0.0531	0.0728	0.0022	0.0298	0.0966	0.0033	0.0337
WDR33	0.0392	0.002	0.0504	0.0853	0.002	0.0232	0.0443	0.0016	0.0372	0.0552	0.003	0.0537
WDR5B	0.1768	0.012	0.0679	0.0727	0.0053	0.0729	0.1658	0.0066	0.04	0.1206	0.0093	0.0773
WDR63	0.3875	0.0203	0.0524	0.1823	0.0073	0.0402	0.1623	0.007	0.0429	0.2985	0.0177	0.0594
WDR74	0.2039	0.0133	0.0654	0.0276	0.0012	0.0422	0.3033	0.0123	0.0406	0.1326	0.0088	0.0662
WFDC11	0.9829	0.0603	0.0614	0.2333	0.017	0.0731	0.2318	0.017	0.0734	0.4359	0.0552	0.1267
WFDC6												
WISP3	0.1811	0.0105	0.058	0.192	0.0047	0.0243	0.0951	0.0035	0.0367	0.1685	0.0105	0.0624
WSB2	0	0	0.0463	0.1228	0.0029	0.0238	0.1015	0.0029	0.0287	0.03	0.0015	0.0485
YLPM1	0.1048	0.0051	0.0487	0.1758	0.0028	0.016	0.1267	0.0031	0.0247	0.1114	0.0051	0.0458
YTHDC1	0.0481	0.0012	0.0247	0.0413	0.0006	0.0147	0.0322	0.0006	0.0185	0.0525	0.0012	0.0226
ZBP1	0.7507	0.058	0.0772	0.5277	0.0262	0.0496	0.5547	0.0439	0.0792	0.7327	0.0591	0.0807
ZBTB38	0.1312	0.0072	0.0549	0.1572	0.0052	0.0329	0.0923	0.0043	0.0468	0.0875	0.0054	0.0617
ZC3H12D	0.2869	0.0254	0.0884	0.2345	0.0114	0.0488	0.2092	0.0119	0.0569	0.2677	0.0227	0.0848
ZC3H13	0.1063	0.0061	0.0577	0.1294	0.004	0.0307	0.103	0.0033	0.0325	0.1279	0.0074	0.0578
ZC4H2	0	0	0.0346	0	0	0	0	0	0.0144	0	0	0.0365
ZCCHC17	0.0296	0.0018	0.06				0	0	0.0683	0.029	0.002	0.0674
ZFP37	0.662	0.0204	0.0308	0.4713	0.0108	0.023	0.6438	0.0173	0.0269	0.7286	0.0225	0.0309
ZFP57	0.3049	0.0209	0.0686	0.3777	0.0129	0.0343	0.2818	0.0121	0.043	0.2775	0.0231	0.0832
ZFP64	0.006	0.0006	0.1063	0.0886	0.0038	0.0434	0.0656	0.0036	0.0546	0.0059	0.0006	0.1087
ZFYVE20	0.1382	0.0083	0.0599	0.1599	0.0072	0.0453	0.1842	0.0073	0.0394	0.1355	0.0074	0.0548
ZMYND17	0.2607	0.0216	0.0829	0.8358	0.0098	0.0117	0.3299	0.0098	0.0296	0.2589	0.0206	0.0796
ZNF117	0.8544	0.0811	0.0949	0.5012	0.0386	0.0769	0.5517	0.1241	0.225	0.887	0.0668	0.0753
ZNF157	0.187	0.0098	0.0524	0.2299	0.0063	0.0273	0.4186	0.0077	0.0183	0.1419	0.0089	0.0627
ZNF192	0.1765	0.0083	0.047	0.3178	0.0106	0.0332	0.4131	0.0114	0.0276	0.1703	0.0081	0.0477
ZNF20	0.4359	0.0271	0.0622									
ZNF235	0.1908	0.0162	0.0851	0.2222	0.0121	0.0546				0.2506	0.0196	0.0784
ZNF275	0.059	0.0081	0.1377	0.0736	0.0062	0.0844	0.1158	0.0093	0.0807	0.0722	0.0109	0.1512
ZNF30	0.2732	0.0292	0.107	0.5657	0.0222	0.0393	0.4157	0.0189	0.0455	0.289	0.0277	0.0959
ZNF302				0.4647	0.065	0.1398	0.1672	0.0106	0.0634			
ZNF324B	0.3015	0.0311	0.1033	0.2042	0.0115	0.0564	0.2624	0.0266	0.1012	0.2812	0.0254	0.0902
ZNF335	0.1279	0.0107	0.0836	0.11	0.0057	0.0514	0.1093	0.006	0.0546	0.1072	0.0087	0.0808
ZNF528	0.2519	0.0226	0.0899									
ZNF540	0.3692	0.0175	0.0473									
ZNF561	0.3263	0.0224	0.0685	0.5826	0.1119	0.192	0.408	0.0761	0.1865	0.4754	0.0793	0.1668
ZNF569	0.0707	0.0043	0.0605	0.1906	0.0061	0.0321	0.2473	0.0095	0.0384	0.1207	0.0086	0.071
ZNF570	0.0269	0.0024	0.0881	0.1742	0.0034	0.0196				0.0401	0.0026	0.064
ZNF574	0.0388	0.0035	0.0904	0.0414	0.002	0.0483				0.0414	0.004	0.0967
ZNF575	0.1995	0.0134	0.0673	0.5064	0.0147	0.029	0.6154	0.0205	0.0332	0.3004	0.0204	0.0681
ZNF592	0.1026	0.008	0.0779	0.1056	0.0035	0.0333	0.0594	0.0028	0.0467	0.1055	0.0083	0.0791
ZNF625				0.2328	0.0084	0.036	0.1241	0.0098	0.0791			
ZNF652	0.058	0.0021	0.0364	0.4971	0.0123	0.0248	0	0	0.0199	0.0417	0.0014	0.0338
ZNRD1	0.4544	0.0105	0.0231	0.1265	0.0112	0.0884	0.2038	0.0074	0.0365	0.3082	0.0112	0.0364

Gene	OSng_w	OS_dN	OS_dS	OMng_w	OM_dN	OM_dS	SMng_w	SM_dN	SM_dS
SYNPO2L	0.3464	0.0221	0.0637	0.4309	0.0231	0.0537	0.2175	0.0204	0.0937
TAC4	1.0409	0.0502	0.0482						
TACR2	0.283	0.0108	0.0383	0.2365	0.0169	0.0715	0.2183	0.0145	0.0664
TAGLN	0	0	0.038	0.0277	0.0022	0.0779	0.025	0.0022	0.0862
TBC1D17	0.0682	0.0035	0.0507	0.0565	0.0055	0.098	0.0762	0.0062	0.0819
TBC1D9	0.0253	0.0014	0.0548	0	0	0.0877	0.0127	0.0011	0.0837
TBCB	0.1132	0.0076	0.0676	0.0349	0.0036	0.1039	0.0715	0.0077	0.107
TBR1	0	0	0.0327	0.0173	0.0007	0.041	0.0252	0.0008	0.0328
TBRG1	0.189	0.0032	0.017	0.2408	0.0108	0.0449	0.287	0.0119	0.0414
TBXA2R	0.0478	0.0027	0.0571	0.1301	0.0124	0.095	0.1198	0.0137	0.1147
TEKT5	0.2103	0.0228	0.1083	0.1099	0.0173	0.1571	0.2979	0.0312	0.1046
TFEC	0.2488	0.0063	0.0253	0.3309	0.0127	0.0383	0.364	0.0139	0.0383
TGM1	0.0712	0.0058	0.0811	0.0779	0.0082	0.1054	0.0849	0.0091	0.1072
THY1	0.1128	0.0056	0.05	0.0367	0.0029	0.078	0.0477	0.0029	0.0601
TIAF1	1.2156	0.0283	0.0233	0.7102	0.0557	0.0784	1.4422	0.078	0.0541
TJP2	0.1862	0.0114	0.0614	0.1384	0.0121	0.0872	0.1468	0.0118	0.0801
TMC8	0.2441	0.0175	0.0716	0.1908	0.0148	0.0775	0.1931	0.0169	0.0874
TMCC3	0.1052	0.0046	0.0435	0.0671	0.0047	0.0698	0.0158	0.0012	0.074
TMED4	0	0	0.069	0.0799	0.0078	0.0979	0	0	0.0874
TMEM105							1.6178	0.0482	0.0298
TMEM106B	0.1175	0.0032	0.027	0.0609	0.0048	0.0783	0.0781	0.0048	0.061
TMEM121	0.0301	0.0014	0.048	0.0223	0.0014	0.0647	0	0	0.0732
TMEM139	2.1597	0.0164	0.0076	1.2015	0.0369	0.0307	1.6613	0.0393	0.0236
TMEM178				0.036	0.0019	0.052			
TMEM179	0.1943	0.0284	0.1463						
TMEM18	0.1026	0.0107	0.1048						
TMEM194A	0.19	0.0049	0.026	0.1488	0.0089	0.0599	0.2421	0.0124	0.0512
TMEM208	0	0	0.0321	0.039	0.0026	0.066	0.0389	0.0026	0.0661
TMEM232	0.2416	0.013	0.0539	0.3986	0.0252	0.0632	0.2395	0.0204	0.0853
TMEM38B	0.2223	0.0122	0.0548	0.1828	0.0168	0.0919	0.082	0.0076	0.0925
TMEM42									
TMEM43	0.0304	0.0022	0.0735	0.0892	0.0135	0.1512	0.0786	0.0112	0.1428
TMEM61	0.2215	0.0153	0.0693	0.3205	0.042	0.1311	0.4319	0.043	0.0997
TMEM92	0.1967	0.0085	0.0432	0.6025	0.0316	0.0524	0.7985	0.0346	0.0433
TNFAIP8L3	0.0737	0.0041	0.0556	0.1516	0.0185	0.1223	0.1508	0.0167	0.1107
TNFSF9									
TNIP3	0.3658	0.024	0.0657	0.3771	0.0522	0.1384	0.4258	0.0445	0.1046
TNS3	0.261	0.0203	0.078	0.1765	0.0216	0.1224	0.1629	0.0209	0.1283
TOP3A	0.2708	0.0175	0.0647	0.2385	0.0207	0.0869	0.1495	0.0131	0.0879
TRAIP	0.325	0.0156	0.0481	0.3607	0.0233	0.0647	0.3012	0.0132	0.0437
TRIM39	0.1054	0.0036	0.0345	0.0657	0.0036	0.0554	0.0519	0.0026	0.0493
TSPAN15	0.0791	0.0055	0.0699	0.0947	0.009	0.0955	0.1123	0.0103	0.0918
TSPAN8	1.6584	0.0732	0.0441	1.3626	0.0959	0.0704	1.481	0.0991	0.0669
TSSK2	0.1326	0.0081	0.0608	0.0508	0.0067	0.1326	0.0975	0.0074	0.0763
TSSK4	1.246	0.0397	0.0318	0.6186	0.034	0.055	0.5951	0.0411	0.069
TTC29	0.4854	0.0127	0.0262	0.3677	0.0182	0.0496	0.3826	0.0164	0.0429
TTF1	0.5286	0.0196	0.0371	0.5552	0.0476	0.0857	0.5089	0.0419	0.0824
TTLL9	0.2295	0.026	0.1134						
TTYH1	0.1117	0.0052	0.0467	0.0503	0.0056	0.1118	0.0809	0.0073	0.0906
TUBB	0.4344	0.0244	0.0563	0.2866	0.0255	0.0888	0.0105	0.001	0.0935
TXNDC11	0.1704	0.0077	0.0452	0.1547	0.0134	0.0869	0.2135	0.015	0.0701
UBLCP1	0.0791	0.0027	0.0342	0.0611	0.0027	0.0442	0	0	0.0443
UGT1A3				0.3062	0.0345	0.1126			
UNC13C	0.1549	0.0077	0.0496	0.1151	0.0094	0.0813	0.1014	0.0092	0.0909
UPF2	0.0635	0.0021	0.0329	0.0269	0.0015	0.0548	0.0374	0.0021	0.0565
USP1	0.1117	0.0038	0.0341	0.1918	0.0065	0.0341	0.2567	0.0093	0.0362
USP18	0.4883	0.027	0.0552	0.3598	0.0409	0.1137	0.2871	0.0342	0.1192
USP26	0.7129	0.0258	0.0362	0.4386	0.03	0.0683	0.4927	0.0366	0.0743
USP7	0	0	0.0275	0.0081	0.0004	0.0496	0.0065	0.0004	0.0608
VCX2				0.36	0.0965	0.2682			
VPREB1	0.6601	0.0299	0.0453	0.8034	0.0364	0.0453	0.6139	0.0374	0.0608
VPS13D	0.1167	0.005	0.0431	0.0711	0.0056	0.0786	0.0898	0.007	0.0784
VPS52	0.0762	0.0035	0.0457	0.0761	0.0056	0.0733	0.0719	0.0043	0.06
VSIG1	0.3459	0.0106	0.0308	0.3975	0.0189	0.0476	0.3862	0.0214	0.0555
WDFY2	0.0203	0.0011	0.0532	0.0332	0.0022	0.0653	0.0785	0.0033	0.0414
WDR33	0.0265	0.001	0.0372	0.0429	0.0023	0.0537	0.0315	0.002	0.0627
WDR5B	0.1651	0.0066	0.0402	0.1547	0.012	0.0776	0.2999	0.0134	0.0445
WDR63	0.2381	0.0073	0.0307	0.3981	0.0193	0.0486	0.3739	0.0157	0.042
WDR74	0.3764	0.0105	0.028	0.1294	0.0076	0.0587	0.2669	0.0152	0.0571
WFDC11	0.1135	0.0097	0.0851	0.812	0.07	0.0863	0.5522	0.0708	0.1283
WFDC6	0.8002	0.05	0.0624						
WISP3	0.159	0.0058	0.0367	0.2398	0.0129	0.0537	0.2016	0.0117	0.058
WSB2	0.194	0.0071	0.0368	0.0206	0.0011	0.0531	0.1264	0.006	0.0477
YLPM1	0.0864	0.0022	0.0253	0.0967	0.0041	0.0425	0.0811	0.0041	0.0504
YTHDC1	0	0	0.0255	0.0178	0.0006	0.0341	0.018	0.0006	0.0331
ZBP1	0.5329	0.0401	0.0752	0.7149	0.0602	0.0843	0.7428	0.0631	0.0849
ZBTB38	0.1438	0.0063	0.0438	0.1319	0.0078	0.0589	0.1051	0.0072	0.0686
ZC3H12D	0.2012	0.0108	0.0537	0.3161	0.0249	0.0787	0.2726	0.0219	0.0802
ZC3H13	0.1471	0.0042	0.0288	0.1467	0.0085	0.0578	0.1306	0.0077	0.0588
ZC4H2	0	0	0.0137	0	0	0.0346	0	0	0.0489
ZCCHC17							0.0258	0.002	0.0761
ZFP37	0.5408	0.0159	0.0295	0.5448	0.0211	0.0387	0.7001	0.0258	0.0368
ZFP57	0.2814	0.0121	0.0431	0.2993	0.024	0.08	0.2142	0.0214	0.0997
ZFP64	0.1243	0.0065	0.052	0.0476	0.0045	0.0942	0.0389	0.0043	0.1108
ZFYVE20	0.1409	0.0061	0.0434	0.1081	0.0068	0.0633	0.1295	0.0068	0.0529
ZMYND17	0.5549	0.0098	0.0176	0.2548	0.0186	0.0731	0.2706	0.0211	0.078
ZNF117	0.4538	0.097	0.2137	0.5805	0.0402	0.0693	0.5378	0.1104	0.2053
ZNF157	0.9919	0.0116	0.0117	0.2124	0.0126	0.0594	0.3286	0.0157	0.0477
ZNF192	0.402	0.0113	0.0282	0.2288	0.0113	0.0496	0.2186	0.0091	0.0415
ZNF20	0.3455	0.0124	0.036	0.4367	0.0287	0.0657	0.3849	0.0259	0.0674
ZNF235				0.2592	0.0204	0.0785			
ZNF275	0.0748	0.0051	0.0677	0.0573	0.0081	0.1418	0.0812	0.0112	0.1379
ZNF30	0.6843	0.0183	0.0268	0.3161	0.0273	0.0862	0.2853	0.0257	0.0902
ZNF302	0.4648	0.0684	0.1471						
ZNF324B	0.2511	0.0267	0.1063	0.1878	0.0212	0.1126	0.3059	0.0422	0.138
ZNF335	0.08	0.0049	0.0614	0.1031	0.0083	0.0808	0.0923	0.0074	0.08
ZNF528	0.3723	0.0184	0.0495	0.2048	0.0226	0.1104	0.3763	0.0296	0.0788
ZNF540	0.3989	0.0129	0.0323	0.6179	0.0214	0.0346	0.4797	0.0227	0.0474
ZNF561	0.6811	0.0805	0.1182	0.8793	0.0793	0.0902	0.3779	0.0367	0.0971
ZNF569	0.1353	0.0052	0.0384	0.0581	0.0037	0.0631	0.1165	0.0073	0.0631
ZNF570				0.0636	0.0047	0.0747			
ZNF574				0.021	0.002	0.0951			
ZNF575	0.1904	0.0101	0.0532	0.1209	0.0101	0.0839	0.1801	0.0168	0.0932
ZNF592	0.1095	0.0035	0.0322	0.1139	0.0085	0.0744	0.0952	0.0069	0.073
ZNF625	0.1563	0.0098	0.0627						
ZNF652	0.4307	0.0152	0.0354	0.318	0.0138	0.0433	0.0432	0.0017	0.0403
ZNRD1	0.0735	0.0035	0.0474	0.1481	0.007	0.0472	-1	0.0035	0

Seminal free estimates of *ω, Ka,* and *Ks*

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
A1BG	0.2567	0.0068	0.0265	0.2295	0.0019	0.0083	0.1649	0.0023	0.0142	0.3115	0.0138	0.0444	0.4788	0.0383	0.08			
a4GALT	0.0001	0	0.0256	0.2566	0.0049	0.019	0.0001	0	0.023	0.1218	0.0068	0.0559				0.09	0.015	0.1663
ABP1	0.1658	0.0034	0.0206	0.0588	0.0011	0.019	0.2308	0.0034	0.0145	0.1151	0.0037	0.0325	0.1812	0.0057	0.0312	0.2044	0.0174	0.0852
ACAT2	0.2086	0.0011	0.0054	999	0.0023	0	999	0.0025	0	0.2134	0.0034	0.016	0.9755	0.0139	0.0142	0.3638	0.019	0.0522
ACE	0.0983	0.0014	0.0141	0.2509	0.0057	0.0226	0.1274	0.0023	0.0182	0.0762	0.0044	0.0584	0.2001	0.0098	0.0491	0.0591	0.007	0.1176
ACE2	0.3221	0.0017	0.0053	0.8068	0.0029	0.0036				1.3048	0.0689	0.0528	0.3806	0.0066	0.0174	0.4097	0.0159	0.0389
ACLY	0.0704	0.0004	0.0056	0.2005	0.0033	0.0164	0.3501	0.0004	0.0012	0.0397	0.0009	0.0215	0.0123	0.0004	0.034	0.0562	0.0027	0.0476
ACO1	0	0	0.0087	0.1487	0.0006	0.0037	0.1108	0.0011	0.01	0.2758	0.0033	0.012	0.5149	0.0044	0.0086	0.0691	0.0039	0.056
ACP5	0.5047	0.0042	0.0084	0.1736	0.0054	0.0311	0	0	0.0042	0.1991	0.0058	0.0291	0.0326	0.0014	0.043	0.0906	0.0057	0.0624
ACPP	0	0	0.0052	1.8407	0.0048	0.0026	0.2297	0.0012	0.0052	0.1442	0.0026	0.0178	0.6791	0.0074	0.011	1.0925	0.029	0.0265
ACR	0.1816	0.0046	0.0092	0.7296	0.0094	0.0207	0.5477	0.0058	0.0259	0.8343	0.008	0.0154	0.4765	0.0163	0.0385	0.358	0.0232	0.0675
ACRBP	0.5051	0.0026	0.0141	0.452	0.0017	0.0023	0.2238	0.0026	0.0047	0.5171	0.0163	0.0196	0.4217	0.0295	0.0619	0.344	0.0121	0.0337
ACRV1	0.8949	0.0085	0.0095	999	0.0039	0	0.8712	0.0096	0.011	0.1056	0.0049	0.0467	0.4191	0.017	0.0406	0.3681	0.0315	0.0856
ACTN1	0	0	0.0082	0	0	0.0212	0.0708	0.0005	0.0064	0.0676	0.0041	0.0609	0.0128	0.0005	0.035	0.0327	0.0027	0.0836
ACTN4	0	0	0.0204	0	0	0.0209	0	0	0.0231	0.0065	0.0004	0.067	0.0201	0.0022	0.1091	0	0	0.1449
ACTR1A	0	0	0.0066	0	0	0.0066	0	0	0.0066	0	0	0.0236	0	0	0.0285	0	0	0.0645
ACYP1	0	0	0	0	0	0	0	0	0	0	0	0.011	0	0	0.0109	0.9046	0.0378	0.0418
ADAM10	0	0	0.0038	0	0	0.0019	0.4152	0.0025	0.006	0.0392	0.0006	0.0151	0	0	0.0131	0.0839	0.003	0.0353
ADAM7	1.9991	0.0033	0.0017	0.4546	0.0053	0.0117	0.8932	0.0062	0.007	0.2484	0.0062	0.0251	1.0571	0.0092	0.0087	0.5647	0.0266	0.0471
ADAMTS1	0	0	0.0092	0.1838	0.0005	0.0026	0.0909	0.0014	0.0158	0.16	0.0062	0.0388	0.0916	0.0024	0.026	0.0476	0.0029	0.0601
ADAMTSL1	0.2491	0.0013	0.0052	0.2325	0.001	0.0045	0.0591	0.0005	0.0088	0.2143	0.0049	0.0228	0.1762	0.0031	0.0173	0.1158	0.0055	0.0479
AGA	0.1762	0.0013	0.0075	0.117	0.0013	0.0113	0.5255	0.004	0.0076	1.2166	0.0092	0.0075	0.3748	0.0074	0.0198	0.3836	0.0175	0.0457
AGR2	999	0.0029	0	0	0	0	999	0.0029	0	999	0.0057	0	0	0	0.0062	0.0654	0.0029	0.044
AGRN	0.1266	0.0015	0.0116	0.1823	0.0034	0.0184	0.1682	0.0036	0.0213	0.1302	0.0068	0.0523	0.1749	0.0086	0.0495	0.1169	0.0148	0.1265
AGT	0.0559	0.0019	0.0346	0.289	0.0039	0.0134	0	0	0.0028	0.2201	0.0076	0.0345	0.1284	0.0053	0.0413	0.2608	0.0287	0.1099
AHCY	0	0	0.0064	0	0	0.0089	0	0	0.0312	0.0178	0.001	0.0558	0.8561	0.0454	0.053	0.1212	0.0103	0.0846
AKR1A1	0	0	0.0107	416.1491	0.0015	0	0.4226	0.0016	0.0038	0.2492	0.0045	0.0179	0	0	0.0217	0.0451	0.0015	0.0329
AKR1B1	999	0.0014	0	0.6462	0.0029	0.0044	0	0	0	0.0793	0.0029	0.0362	0.0495	0.0014	0.0289	0.0995	0.0057	0.0573
AKR7A2	0.1447	0.0013	0.0088	0.2041	0.0047	0.0233	0.1339	0.0013	0.0095	0.192	0.0132	0.0686	0.2421	0.0172	0.0711	0.1859	0.0156	0.0838
ALAD	0.4385	0.0027	0.0062	0.0862	0.0014	0.0157	0.6548	0.0042	0.0064	0.1062	0.0027	0.0255	0.2739	0.0054	0.0199	0.2568	0.0124	0.0484
ALB	0.5372	0.0023	0.0042	0.6051	0.0033	0.0055	0.3125	0.002	0.0063	0.2285	0.0058	0.0252	0.2767	0.0069	0.0248	0.5726	0.0277	0.0484
ALCAM	0.0896	0.0008	0.009	0	0	0.0143	0	0	0.0058	0.1535	0.0016	0.0105	0.1251	0.0016	0.0129	0.1097	0.004	0.0368
ALDH1A1	0	0	0.0067	0	0	0.0099	0	0	0.0064	0.2399	0.0029	0.0119	0.1052	0.0029	0.0271	0.0816	0.0038	0.0468
ALDH7A1	0.1765	0.0009	0.0051	0.2391	0.0018	0.0075	0.0643	0.0011	0.0175	0.1841	0.0041	0.0221	0.2284	0.0059	0.0258	0.0944	0.0032	0.0334
ALDH9A1	0.1066	0.0009	0.0088	690.9412	0.0009	0	0.4222	0.0038	0.0089	0.29	0.0038	0.013	0.1983	0.0066	0.0333	0.165	0.0075	0.0457
ALDOA	0	0	0.0065	0	0	0.0097	0.0408	0.0011	0.0267	0.0464	0.0011	0.0231	0.0237	0.0011	0.0457	0.0293	0.0022	0.0741
ALDOC	0.0001	0	0.0031	999	0.0013	0	0.0001	0	0.0061	0.2404	0.0054	0.0223				0.0594	0.0027	0.0452
AMBP	0.3122	0.0025	0.0082	0.155	0.0013	0.0082	0.9558	0.0038	0.004	0.0766	0.0013	0.0165	0.1195	0.0057	0.0476	0.1743	0.0132	0.0759
ANG	0.0001	0	0.0083	3.7675	0.0029	0.0008	8.585	0.0031	0.0004	2.8816	0.0186	0.0065				0.0019	0.1182	60.7818
ANPEP	0.1994	0.0038	0.0191	0.2144	0.0027	0.0127	0.8852	0.0049	0.0055	0.1758	0.0065	0.0367	0.4226	0.0085	0.02	0.1035	0.0104	0.1007
ANTXR2	0.1033	0.001	0.0092	0.5178	0.0019	0.0037	1.3672	0.0085	0.0062	0	0	0.0202	0.1189	0.0029	0.0248	0.1517	0.0041	0.0267
ANXA1	0	0	0.0063	0	0	0.0094	0.2789	0.0014	0.0063	0.1076	0.0014	0.0253	0.89	0	0.0064	0.1377	0.003	0.0418
ANXA11	0	0	0.0062	0	0	0.0032	0.2257	0.0023	0.0084	0.0565	0.002	0.0182	0	0.3002	0.3373	0.0719	0.0103	0.0747
ANXA2	0	0	0.0137	0	0	0.0195	0	0	0.0154	0.0771	0.0013	0.0168	0	0	0.0094	0	0	0.0629
ANXA3	0.3044	0.0029	0.0096	0.2088	0.0044	0.0209	0	0	0.0132	0.2588	0.0044	0.0169	0.2261	0.0058	0.0258	0.2266	0.0088	0.0386
ANXA4	5.9233	0.0014	0.0002	0	0	0.01	0.0927	0.0016	0.0168	0.1552	0.0016	0.01	0.3411	0.0047	0.0138	0.1709	0.0047	0.0274
ANXA5	0	0	0.0037	0	0	0.0037	0.2024	0.0015	0.0074	0.2026	0.0015	0.0074	0.2648	0.006	0.0227			
ANXA6	0.3756	0.0019	0.0052	0.1825	0.0019	0.0106	0.0463	0.0006	0.0139	0.0863	0.0019	0.0224	0.0464	0.0006	0.0139	0.3248	0.0364	0.1119
ANXA7	999	0.002	0	0.4196	0.001	0.0024	0.8373	0.0024	0.0029	0.6108	0.003	0.0049	0.2367	0.004	0.0169	0.0824	0.003	0.0362
APCS	0.818	0.0043	0.0053	0.8111	0.0043	0.0053	0.825	0.0044	0.0053	0.1042	0.0028	0.0272	3.4559	0.0191	0.0055	0.4825	0.0268	0.0556
APEH	20.1446	0.0006	0	0	0	0.0033	0.0776	0.0006	0.0083	0.1009	0.0013	0.0128	0.0272	0.0006	0.0237	0.1255	0.0045	0.036
APLP2	0.0811	0.0006	0.0077	1.1948	0.0019	0.0016	0.1336	0.0006	0.0047	0.1577	0.002	0.0125	0.1463	0.004	0.0276	0.1162	0.0074	0.0637
apoa1BP	0.1759	0.0016	0.0091	70.9756	0.0016	0	0.521	0.0048	0.0093	0.1523	0.0018	0.0117	0.0497	0.0016	0.0317	0.3241	0.0097	0.0298
APOA2	0	0	0.0125	999	0.0192	0	0	0	0.0125	0.3797	0.0148	0.0389	999	0.0096	0	0	0	0.0782
APOB	0.787	0.0037	0.0046	0.6875	0.0035	0.0052	0.715	0.0047	0.0066	0.4006	0.0057	0.0143	0.4691	0.0074	0.0158	0.4289	0.0191	0.0445
APOD	0.8477	0.0052	0.0061	0.4236	0.0026	0.0061	999	0.0052	0	3.6344	0.0219	0.006	1.4087	0.017	0.0121	1.5386	0.0677	0.044
APOE	0.314	0.0067	0.0212	0.4025	0.0215	0.0534	0.4224	0.006	0.0142	0.4	0.0063	0.0157	0.2841	0.0229	0.0805	0.1111	0.0183	0.1648
APOH	0.3651	0.0013	0.0037	0.1226	0.0013	0.0109	0.3559	0.0017	0.0048	0.4924	0.0093	0.019	0.1583	0.0054	0.0342	0.5957	0.0179	0.0301
APP	0.1216	0.0006	0.0048	0	0	0.0048	0.1988	0.0006	0.0029	0	0	0.0195	0.0947	0.0013	0.0138	0.3027	0.0226	0.0746
ARF1	0	0	0.0174	0	0	0.0241	0	0	0.0281	0	0	0.0223	0	0	0.0421	0	0	0.0629
ARF6	0	0	0	0	0	0	0	0	0.0189	0	0	0	0	0	0.019	0	0	0.0095
ARHGDIA	0.1774	0.0013	0.0075	0.2393	0.0027	0.0111	0.35	0.0027	0.0076	0.2042	0.0054	0.0262				0.4591	0.0176	0.0384
ARSA	0.0627	0.0009	0.0143	0.9948	0.0118	0.0119	0.3063	0.0088	0.0287	0.1721	0.0031	0.018	0.1637	0.003	0.0184	0.1447	0.0112	0.0771
ASAH1	1.7836	0.0055	0.0031	0.1359	0.0013	0.0094	1.775	0.0055	0.0031	0.37	0.0058	0.0157	0.0731	0.0024	0.0326	0.5129	0.0265	0.0517
ASRGL1	0.3995	0.0015	0.0039	1.6311	0.0062	0.0038				0.1611	0.0038	0.0234	0.3294	0.0133	0.0405	0.2652	0.0116	0.0436
ATRN	0.0689	0.0008	0.0113	0.8765	0.0243	0.0278	0.227	0.0018	0.008	0.1828	0.0023	0.0127	0.234	0.0077	0.0329	0.1	0.0045	0.0447
AZGP1	0	0	0.009	0.116	0.0015	0.0134	1.0617	0.0046	0.0044	0.2151	0.0037	0.0171	0.7254	0.0284	0.0392	0.3932	0.029	0.0737
B2M	0	0	0	999	0.0039	0	0	0	0	0.789	0.0078	0.0099	0.3708	0.0082	0.0221	0.4957	0.0317	0.064
B4GALT1	0.1854	0.0023	0.0124	0.9608	0.007	0.0072	0.1031	0.0023	0.0224	0	0	0.0137	0.3682	0.0191	0.052	0.2099	0.015	0.0716
B4GALT4	999	0.0072	0	999	0.0029	0	0.3588	0.0058	0.016	2.2544	0.0072	0.0032	0.1381	0.0029	0.0208	0.1288	0.0072	0.0561
BAIAP2	0.0897	0.0015	0.0168	0	0	0.0193	0.0546	0.0008	0.0138	0.0238	0.0015	0.0635	0.0207	0.0016	0.0772	0.0566	0.0076	0.1342
BASP1	0.2056	0.0021	0.0102	0	0	0.0051	0.4332	0.0024	0.0055	0.6261	0.0063	0.0101	0.1997	0.0023	0.0113	0.1331	0.0042	0.0317
BCAN	0.2761	0.001	0.0038	0.0585	0.0005	0.009	0.207	0.001	0.0051	0.2548	0.0044	0.0174	0.2326	0.0037	0.0159	0.1828	0.0128	0.07
BGN	0.0482	0.0011	0.0228	0	0	0.0179	0.069	0.0011	0.0161	0.0691	0.0033	0.0479	0.0428	0.0011	0.0258	0.007	0.0011	0.1597
BPIL1	999	0.0012	0	0.161	0.0018	0.0114	0.1402	0.0033	0.0233	0.3373	0.0064	0.019	0.2536	0.0091	0.0359	0.1995	0.0121	0.0606
BPNT1	0	0	0	0	0	0.0043	0	0	0.0043	0	0	0.0131	0.8623	0.015	0.0174	0.0592	0.0034	0.0574
BTD	0.3124	0.0027	0.0085	0.2085	0.0009	0.0042	1.6739	0.0035	0.0021	0.3545	0.0087	0.0246	0.4447	0.0055	0.0125	0.3788	0.0135	0.0357
C19orf10	0.0001	0	0.0152	0.0001	0	0.0273				0.0632	0.0029	0.046	0.2374	0.0026	0.0109	0.0217	0.0029	0.1353
C1RL	0.1735	0.0027	0.0157	0.8726	0.0027	0.0031	0.4327	0.0055	0.0126	0.1255	0.0061	0.0487	0.429	0.0113	0.0264	0.3644	0.0225	0.0619
C3	0.1346	0.0022	0.0164	0.4526	0.0046	0.0102				0.2379	0.0074	0.0311	0.316	0.0105	0.0332	0.122	0.0105	0.0859
C9	1.2316	0.003	0.0024	0.5322	0.0026	0.0049	0.1522	0.0029	0.0192	0.302	0.011	0.0364	0.1768	0.0072	0.0406	0.6193	0.0269	0.0434
CA2	999	0.0018	0	999	0.0037	0	0.3999	0.0058	0.0144	0.8061	0.0074	0.0092	0.1544	0.0037	0.0237	0.1272	0.0074	0.058
CA4	999	0.0014	0	0.9084	0.0043	0.0047	0.5084	0.0073	0.0143	0.747	0.0175	0.0234	0.2297	0.0126	0.0548	1.1077	0.0563	0.0508
CA6	0.6852	0.009	0.0132	0.0693	0.0015	0.0215	0	0	0.0385	0.4773	0.0197	0.0412	0.0769	0.0015	0.02	0.2776	0.0227	0.0819
CAB39	0	0	0	0	0	0.0029	0	0	0.0059	0	0	0.0058	0	0	0.0059	0.0755	0	0.0179
CAB39L	0	0	0.0059	0	0	0	0	0	0.0061	0	0	0.0061	0	0	0.0092	0	0.003	0.0402
CACNA2D1	0.6739	0.0008	0.0012	0	0	0.006	0	0	0.0155	0	0	0.0151	0.2628	0.0034	0.0131	0.0857	0.0027	0.0321
CACYBP	0	0	0	0	0	0	1.4275	0.0096	0.0067	0	0	0.0068	0.1338	0.0019	0.0142	0.0451	0.0019	0.0422
CALR	0	0	0.003	0	0	0	0.2466	0.0022	0.0089	0	0	0.0184	0.0407	0.0011	0.0271	0.0147	0.0011	0.0752
CAMP	0	0	0.008	0.3307	0.0027	0.008	999	0.0053	0	1.572	0.0253	0.0161	999	0.0185	0	1.1778	0.0582	0.0494
CANT1	0.0814	0.002	0.0251	0.4111	0.0041	0.0099	0.0213	0.001	0.0476	0.0572	0.0031	0.0541	0.2336	0.0232	0.0992	0.096	0.0135	0.1406
CAP1	1.2168	0.006	0.005	0	0	0	0.2676	0.002	0.0075	0.3996	0.003	0.0075	0.1052	0.003	0.0285	0.0256	0.001	0.0389
CAPG	0.3269	0.0013	0.004	0	0	0.0119	0.1084	0.0013	0.012	0.1105	0.0026	0.0234	0.0667	0.0026	0.0392	0.0282	0.0013	0.046
CAPN1	0.0561	0.0012	0.0207	0	0	0.0132	0.02	0.0006	0.0288	0.0128	0.0006	0.045	0.0268	0.0012	0.0446	0.0348	0.0041	0.1173
CAPNS1	0.1335	0.0028	0.021	0.9011	0.0042	0.0047	0.1564	0.0043	0.0277	0	0	0.0411	0.0325	0.0017	0.0532	0.0301	0.0014	0.0467
CAPZA1	0	0	0	0	0	0.0321	0	0	0.0284	0.0017	0.0001	0.0408	0.0014	0.0001	0.0425	0	0	0.0607
CAPZA2	0	0	0.0093	18.3133	0.0047	0.0003	0	0	0.0093	0	0	0.0141	0	0	0.0046	0	0	0.0187
CAPZB	0.1371	0.0014	0.0104	0	0	0.0157	0	0	0.0117	0	0	0.0303	0.253	0.0306	0.121	1.0411	0.0584	0.0561

Gene	HC_ω	HC_*Ka*	HC_*Ks*	GO_ω	GO_*Ka*	GO_*Ks*	Ogi_ω	Ogi_*Ka*	Ogi_*Ks*
A1BG	0.1071	0.0013	0.0123	0.4227	0.0052	0.0124			
a4GALT	0.5866	0.0034	0.0057	0.0609	0.0011	0.0179			
ABP1	31.4053	0.0005	0	0.225	0.0035	0.0156	0	0	0.0045
ACAT2	0.6899	0.0046	0.0066	0.3165	0.0023	0.0072	999	0.0022	0
ACE	0.0981	0.0005	0.005	0.0914	0.0018	0.0201	999	0.0005	0
ACE2	0.1198	0.0017	0.0141				0.1947	0.0007	0.0034
ACLY	0	0	0.0023	0.0799	0.0008	0.0099	0	0	0.0059
ACO1	0	0	0	0.2039	0.0011	0.0054	0	0	0
ACP5	0	0	0	0	0	0.0091	0	0	0.008
ACPP	0	0	0	2.0476	0.006	0.0029	96.7115	0.0011	0
ACR	830.1173	0	0.0024	0.206	0.0065	0.0126	0.1224	0.0031	0.0004
ACRBP	0	0.0017	0	0.5142	0.0052	0.0252	7.7622	0.0009	0.0077
ACRV1	0	0	0.0084	999	0.0108	0	0.2846	0.0008	0.0029
ACTN1	0	0	0	0	0	0.0158	0	0	0.0104
ACTN4	0	0	0.0059	0	0	0.0381	0	0	0.0075
ACTR1A	0	0	0.0034	0	0	0.0069	0	0	0.0055
ACYP1	0	0	0.0154	0	0	0.0154	0	0	0
ADAM10	0	0	0	0	0	0.0022	0	0	0
ADAM7	0.2182	0.0007	0.0033	0.4178	0.0033	0.008	0	0	0.005
ADAMTS1	0.1175	0.0005	0.004	0.1734	0.001	0.0055	0.0522	0.0005	0.0091
ADAMTSL1	113.6735	0.0008	0	0.0798	0.0006	0.0073	0	0	0.0031
AGA	999	0.0013	0	1.0968	0.0041	0.0038	999	0.0007	0
AGR2	0	0	0	0	0	0.0061	0	0	0.006
AGRN	0.0723	0.0004	0.0059	0.158	0.0037	0.0233	0.0544	0.0007	0.0132
AGT	0	0	0	0.3693	0.0041	0.011	999	0.0068	0
AHCY	0	0	0.0148	0.1395	0.002	0.0142	0.1612	0.0008	0.0053
AKR1A1	0	0	0	0.4089	0.0015	0.0036	0	0	0.0033
AKR1B1	0	0	0.0044	0.2999	0.0029	0.0095	0	0	0.0031
AKR7A2	0	0	0.0048	0.2429	0.0035	0.0143	0	0	0.0123
ALAD	0.4329	0.0014	0.0032	0.4095	0.0027	0.0066	0	0	0.0021
ALB	0.4959	0.001	0.0021	0.0278	0.0003	0.0093	0.3701	0.003	0.0081
ALCAM	0.407	0.0008	0.002	0	0	0.0026	0	0	0.0061
ALDH1A1	0.4003	0.0009	0.0024	0.1218	0.001	0.0078	0	0	0.0018
ALDH7A1	999	0.0023	0	0.1128	0.0018	0.0155	0	0	0.0011
ALDH9A1	0	0	0.0044	0	0	0.0048	0	0	0.0061
ALDOA	0	0	0.0035	0	0	0.0216	0	0	0.0024
ALDOC	0.0001	0	0	0.0001	0	0.0221			
AMBP	128.8287	0.0013	0	0	0	0.0163	0	0	0
ANG	79.3461	0	0	0.8186	0.0145	0.0177			
ANPEP	0	0	0.0024	0.7038	0.0048	0.0068	0.4297	0.0029	0.0068
ANTXR2	0	0	0	0	0	0.0069	0	0	0.0076
ANXA1	0.625	0	0.003	0.3516	0	0.0032	999	0.0014	0
ANXA11	0	0.0022	0.0035	0	0.0019	0.0055	999	0.0006	0
ANXA2	0	0	0	0	0	0.026	0	0	0.0004
ANXA3	0	0	0.0038	0.3502	0.0015	0.0042	0.5553	0.0015	0.0026
ANXA4	0	0	0	0	0	0.0033	0	0	0.0031
ANXA5	0	0	0	0	0	0.0112			
ANXA6	0	0	0.0048	0	0	0.0109	0	0	0.0069
ANXA7	0	0	0	0.0704	0.001	0.0141	0.407	0.001	0.0024
APCS	999	0.0021	0	0.894	0.0146	0.0163	0.9824	0.0048	0.0049
APEH	14.1706	0.0006	0	0	0	0.0059	0	0	0.0031
APLP2	0.1006	0.0006	0.0062	0.0656	0.0005	0.0079	0	0	0.003
apoa1BP	0.7119	0.0032	0.0045	0.3815	0.0048	0.0127	0	0	0.0043
APOA2	0	0	0	0.4441	0.0056	0.0126	999	0.0285	0
APOB	0.9466	0.0009	0.0009	0.5363	0.0034	0.0063	0.7051	0.0025	0.0035
APOD	0	0	0	999	0.0094	0	999	0.0079	0
APOE	0	0	0	0.264	0.0016	0.0059	0	0	0.0206
APOH	0	0	0	0.1255	0.0027	0.0219	0	0	0.0107
APP	0	0	0.0051	0	0	0.0105	0	0	0.0013
ARF1	0	0	0	0	0	0.0334	0	0	0
ARF6	0	0	0	0	0	0	0	0	0.0095
ARHGDIA	0.0001	0	0.0074	0.0849	0.0013	0.0157			
ARSA	0	0	0.0027	0.0967	0.0018	0.0185	0.7315	0.0015	0.002
ASAH1	0.3619	0.0011	0.0031	0.5423	0.0034	0.0062	0.4121	0.0023	0.0055
ASRGL1	0.2339	0.0055	0.0236				0.0001	0	0.0071
ATRN	0	0	0.0007	0.0932	0.0011	0.0119	0	0	0.0014
AZGP1	0	0	0.0045	0.729	0.0105	0.0145	0.2722	0.0037	0.0138
B2M	0	0	0	999	0.0078	0	0	0	0.0192
B4GALT1	0	0	0	0.3324	0.0023	0.0069	0.228	0.0012	0.0051
B4GALT4	0	0	0.0032	0	0	0.0031	0.3523	0.0043	0.0122
BAIAP2	0	0	0	0	0	0.0182	0	0	0.0051
BASP1	0	0	0.0065	0.107	0.0021	0.0196	0	0	0
BCAN	0.1364	0.0005	0.0038	0.2747	0.0021	0.0076	0.1305	0.0005	0.0038
BGN	0.0573	0.0011	0.0192	0	0	0.0111	0	0	0.0171
BPIL1	0.7848	0.002	0.0026	0.343	0.0056	0.0164	0	0	0.0027
BPNT1	0	0	0	0	0	0.0086	0	0	0
BTD	0	0	0	0.1996	0.0029	0.0146	0.3061	0.002	0.0065
C19orf10	0.0001	0	0.0322				999	0	0
C1RL	0.294	0.0009	0.0031	0.1881	0.0037	0.0199	0.1389	0.0014	0.0102
C3	0.5312	0.005	0.0094				0.3989	0.0037	0.0093
C9	999	0.0011	0	1.3039	0.0152	0.0117	999	0.0037	0
CA2	0.4081	0.0019	0.0045	0	0	0	0	0	0.004
CA4	999	0.0042	0	0.8721	0.0129	0.0148	0.1586	0.0049	0.0308
CA6	0.3674	0.003	0.0082	0	0	0.0085	0.1765	0.0015	0.0082
CAB39	0	0	0.003	0	0.0015	0.003	0	0	0
CAB39L	0	0	0.0029	0.5059	0	0.021	0	0	0.0057
CACNA2D1	0	0	0.0087	0	0	0.0056	0	0	0.006
CACYBP	0	0	0	0	0	0.0067	0	0	0.0062
CALR	0	0	0.0031	0	0	0.006	0	0	0.0067
CAMP	999	0.0027	0	0.3049	0.0074	0.0244	999	0.0045	0
CANT1	0	0	0.0096	0	0	0.0353	0	0	0
CAP1	0	0	0.0025	0.5318	0.004	0.0075	0	0	0.0019
CAPG	999	0.0013	0	0	0	0.0113	0.1358	0.0013	0.0095
CAPN1	0	0	0.0112	0	0	0.0159	0.335	0.0011	0.0034
CAPNS1	0	0	0	0.0578	0.0014	0.0242	0	0	0.0194
CAPZA1	0	0	0.0233	0	0	0	0	0	0
CAPZA2	0	0	0	0	0	0	0	0	0
CAPZB	999	0.0014	0	0	0	0.0052	0.9943	0.0613	0.0617

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
CAT	0.1023	0.0012	0.0119	0.5973	0.0014	0.0024	0.3218	0.0023	0.0072	0.3727	0.0044	0.0119	0.2752	0.0075	0.0271	0.2263	0.012	0.0529
CCT2	0	0	0	0	0	0.005	0	0	0.005	0	0	0.0231	0.0658	0.0009	0.0129	0	0	0.0415
CCT3	0	0	0.005	0.1649	0.0008	0.005	0.4892	0.0409	0.0835	0	0	0.0128	0.2087	0.0041	0.0197	0.0775	0.0042	0.0541
CCT4	0	0	0.0047	0	0	0.0024	0.3611	0.0009	0.0026	0	0	0.0213	0	0	0.0121	0.0971	0.0026	0.0266
CCT5	0	0	0.0024	0	0	0.0024	0	0	0.0121	0.1017	0.0017	0.0165	0	0	0.0125	0	0	0.0715
CCT7	0	0	0.0083	0	0	0.0021	0	0	0.0104	0.2179	0.0036	0.0166	0.0351	0.0009	0.0257	0	0	0.0587
CCT8	0	0	0.0023	1.0877	0.0025	0.0023	0	0	0.0165	0	0	0.0136	0.0959	0.0017	0.0176	0.0903	0.0025	0.0281
CD109	0.1853	0.0016	0.0086	0.5599	0.0029	0.0051	0.2618	0.0026	0.01	0.2785	0.0048	0.0172	0.3075	0.0055	0.0179	0.4339	0.0243	0.056
CD14	0.8059	0.0025	0.0031	0.5029	0.0063	0.0126	0.4024	0.0013	0.0031	0.322	0.0051	0.0158	0.6455	0.0102	0.0159	0.326	0.018	0.0553
CD151	0	0	0.0237	0	0	0.0078	0	0	0.0079	0.0489	0.0016	0.0319	0.4312	0.0052	0.012	0.0526	0.0082	0.1562
CD38	0.3865	0.0016	0.0041	0.3856	0.0031	0.0082	0.2556	0.0032	0.0123	0.5691	0.007	0.0124	3.7845	0.0152	0.004	1.053	0.028	0.0266
CD44	1.0801	0.0032	0.003	0.3542	0.0039	0.011	0.4948	0.0039	0.0079	0.3739	0.007	0.0187	0.4372	0.0103	0.0235	0.5396	0.0188	0.0348
CD47	0.3981	0.0015	0.0037	0.7714	0.003	0.0039	0	0	0.0038	0.0872	0.0015	0.0172	0	0	0.0212	0.1542	0.0045	0.0291
CD59	0	0	0	999	0.0154	0	999	0.0354	0	1.016	0.0269	0.0265	6.1225	0.0532	0.0087	1.303	0.0624	0.0479
CD63	0	0	0	999	0.002	0	0	0	0	0.1467	0.004	0.027	0.1242	0.002	0.0159	0	0	0.0437
CD81	0	0	0.0082	0	0	0.0343	0	0	0.0186	0	0	0.0522	0	0	0.0822	0.0437	0.0071	0.1616
CD9	0	0	0	0.1549	0.002	0.0127	0	0	0	0.0878	0.0044	0.0497	0	0	0.0127	0.0881	0.0063	0.0714
CDC42	0.0001	0	0.0045	101.7164	0	0				0.0001	0	0.0045				0.158	0.0021	0.0135
CDH1	0	0	0.0133	0.1597	0.0016	0.0102	0.0765	0.0011	0.0142	0.1892	0.0076	0.04	0.105	0.0028	0.0263	0.3111	0.0174	0.056
CFB	0.1797	0.001	0.0056	0.8041	0.005	0.0063	0.8861	0.006	0.0068	0.1638	0.0035	0.0215	0.2012	0.0046	0.0227	0.301	0.0187	0.062
CFL1	0	0	0.0101	0	0	0	0	0	0.0524	0	0	0.0209	0	0	0.0578	0.024	0.0026	0.1062
CKB	0	0	0.0075	0	0	0.015	0	0	0.0098	0	0	0.0296	0.0663	0.003	0.0455	0.0191	0.002	0.1044
CLIC1	0	0	0.0149	0	0	0.0149	0.3961	0.002	0.0049	0.0965	0.002	0.0202	999	0.0025	0	0.4433	0.0159	0.0358
CLN5	0.5364	0.0068	0.0128	0.746	0.0023	0.0031	1.3865	0.0055	0.004	0.9033	0.0057	0.0063	0.642	0.0081	0.0126	0.4644	0.0244	0.0525
CLSTN1	0.0866	0.0009	0.0107	0.0794	0.0009	0.0116	0.0503	0.0009	0.0183	0.1134	0.0042	0.0366	0.0249	0.0009	0.0379	0.0474	0.0042	0.0879
CLTC	0	0	0.0048	0	0	0.0021	0	0	0.0014	0	0	0.0103	0.08	0.0006	0.0072	0.0138	0.0004	0.0274
CLU	0.2235	0.0037	0.0167	0.4565	0.003	0.0067	0.2034	0.002	0.01	0.2114	0.0056	0.0266	0.173	0.0055	0.0317	0.2191	0.017	0.0774
CNDP2	0.2934	0.0033	0.0112	0.05	0.0011	0.0226	0.1765	0.0033	0.0185	0.0222	0.0009	0.0391	1.0495	0.9876	0.9411	0.087	0.0079	0.0906
CNP	0	0	0.0076	0	0	0	0.5302	0.002	0.0038	0.0995	0.002	0.0203	0	0	0.0322	0.135	0.0081	0.0601
CNTN3	0.1229	0.0014	0.0112	0	0	0.0102	0.1108	0.0014	0.0124	0.2682	0.0047	0.0177	0.2121	0.0032	0.0152	0.1104	0.0065	0.0501
CNTNAP2	0.0485	0.0007	0.0141	0.1017	0.0014	0.0134	0.4514	0.0162	0.0359	0.2048	0.0054	0.0264	0.0935	0.0039	0.0413	0.0646	0.004	0.0624
col12A1	0.0599	0.0005	0.0078	0.1334	0.0006	0.0047	0.1032	0.0006	0.006	0.0794	0.0012	0.015	0.238	0.0056	0.0237	0.124	0.0045	0.036
COL18A1	0.2967	0.0052	0.0175	0.1679	0.0033	0.0196	0.5946	0.0152	0.0256	0.3587	0.0117	0.0325				0.2354	0.0207	0.0881
COL6A1	0.0905	0.0015	0.0168	0.1693	0.0022	0.0129	0.0001	0	0.0214				0.3069	0.0522	0.1701	0.0468	0.0071	0.1526
COL6A2	0.0397	0.0008	0.0204	0.0124	0.0004	0.0327	0.0458	0.0012	0.0265	0.0167	0.0009	0.0543	0.4621	0.0561	0.1213	0.1429	0.0218	0.1527
COL9A1	0	0	0.0108	0	0	0.0136	0	0	0.0287	0	0	0.0264	0	0	0.0497	0	0	0.0656
COLEC12	0.1749	0.0013	0.0072	0.0429	0.0006	0.0146	0.1125	0.0013	0.0111	0.1889	0.0034	0.0181	0.0287	0.0006	0.0218	0.0646	0.0039	0.0598
COMP	0.294	0.0016	0.0054	0.3189	0.01	0.0313				0.1386	0.0027	0.0197	0.0788	0.0045	0.057	0.1048	0.0142	0.1353
COPB2	14.3416	0.0009	0.0001	0.1058	0.0007	0.0066	0.3557	0.0014	0.0039	0.1754	0.0021	0.012	0.0557	0.0005	0.0094	0.0155	0.0005	0.0339
CP	0	0.001	0.0034	0.1197	0.0012	0.0068	0.3328	0.0033	0.005	0	0.0054	0.0148	0.2786	0.0018	0.018	0.024	0.0117	0.0358
CPAMD8	0.2805	0.0039	0.0139	0.1207	0.0025	0.0204				0.1947	0.0067	0.0342	0.1961	0.0096	0.0492	0.1662	0.0124	0.0749
CPD	0.1386	0.001	0.0072	0.6559	0.0033	0.005				0.2971	0.0038	0.0128	0.2071	0.0054	0.0259			
CPE	0.7675	0	0.0081	0.3831	0.001	0.0085	0	0.002	0.0061	0.128	0	0.015	0.3465	0.0051	0.0183	0.3402	0.001	0.0423
CPM	0.3203	0.0021	0.0027	999	0.0021	0.0055	0.2134	0	0.0195	0.4719	0.0021	0.0165	0.3112	0.0035	0.0102	0.5468	0.0148	0.0435
CPO	0.3099	0.0012	0.0037	0.1738	0.0048	0	0.6591	0.0024	0.0113	0.3616	0.0072	0.0153	0.0986	0.0024	0.0077	0.3267	0.0707	0.1293
CPVL	0.8518	0.0024	0.0028	1.4976	0.006	0.004	0.2961	0.0028	0.0096	0.4931	0.0105	0.0213	0.3186	0.0098	0.0308	0.5223	0.0166	0.0318
CPZ	0.058	0.0027	0.0461	0.1868	0.0061	0.0325	0.0474	0.0032	0.0677	0.0507	0.0031	0.0619						
CREG1	0	0	0.0238	999	0.0021	0	999	0.0042	0	0.0433	0.0021	0.0484	0.0694	0.0021	0.0301	0.3513	0.0148	0.0422
CRISP1	0	0	0	0.4697	0.0054	0.0115	0.462	0.0054	0.0116	0.0901	0.0036	0.0397	0.1287	0.0036	0.0278	1.9214	0.0909	0.0473
Crisp2	0.2914	0.0032	0.0108	0	0	0	0.2908	0.0016	0.0054	0.3721	0.0108	0.029	0.3022	0.0096	0.0316	0.8221	0.0253	0.0308
CRISP3	0.7105	0.0037	0.0053	0.172	0.0019	0.0109	0.2565	0.0037	0.0146	0.6962	0.0037	0.0054	999	0.0037	0	0.5968	0.0405	0.0678
CRTAC1	0.0845	0.0016	0.019	0.1468	0.0025	0.017	0.0894	0.0009	0.0105	0.1291	0.0037	0.0285	0.0343	0.0019	0.0562			
CRYZ	0.129	0.0042	0.0327	0	0	0.0205	0.7591	0.0155	0.0204	0.6132	0.0073	0.0119	1.0977	0.0129	0.0118	0.239	0.0057	0.0238
CST1	0.193	0.0041	0.021	1.1016	0.0192	0.0175				0.8233	0.0506	0.0615	0.2181	0.0273	0.125	0.5488	0.0618	0.1126
CST3	0.0001	0	0.0629							0.0001	0	0.0155	0.2057	0.0057	0.0279	0.0498	0.0058	0.117
CST6	0	0	0	999	0.0027	0	0.1739	0.0054	0.0311	0	0	0.0329	0.0815	0.0027	0.0331	0.2112	0.0164	0.0778
CTBS	999	0.0012	0	0.1945	0.0035	0.0181	0.3258	0.0035	0.0108	0.3949	0.0072	0.0182	0.0501	0.0015	0.0295	0.4413	0.0211	0.0479
CTSB	0.0521	0.0013	0.0246	0.0379	0.0013	0.0337	0	0	0.0235	0.0599	0.0025	0.0425	0.1691	0.0108	0.0638	0.1112	0.0066	0.0594
CTSD	0.09	0.002	0.0218	0.078	0.003	0.038	0	0	0.0438	0.0282	0.0025	0.0874	0.0511	0.0055	0.108	0.1213	0.0165	0.1359
CTSF	0.1073	0.0021	0.0193	0.657	0.0063	0.0096	0.569	0.0036	0.0063	0.1936	0.0055	0.0285	0.5324	0.0127	0.0239	0.1259	0.01	0.0794
CTSH	0.0657	0.0014	0.0214	0	0	0	0.491	0.0042	0.0086	0.1821	0.0084	0.0463	0.1107	0.002	0.0179	0.1672	0.0094	0.0562
CTSO	0.3756	0.0015	0.0039	0	0	0.0116	1.5209	0.0058	0.0038	0.2219	0.0015	0.0066	0.4551	0.005	0.011	0.5223	0.0177	0.034
CTSZ	0	0	0.0059	0	0	0.0149	0.2628	0.0043	0.0164	0.5219	0.025	0.0479	0.2191	0.0087	0.0396	0.2212	0.0186	0.084
CUL3	0	0	0.0034	0	0	0.0068	0.3446	0.0006	0.0017	0	0	0.0051	0.034	0.0006	0.0173	0.0354	0.0012	0.0329
CYB561	0.2102	0.0044	0.0209	0.2827	0.0015	0.0052	0	0	0	0.3195	0.0045	0.0142	0.6087	0.1253	0.2058	0.0825	0.0122	0.1475
CYB5R2	0.4204	0.0081	0.0193	0.6287	0.0034	0.0054	1.4868	0.0081	0.0054	0.6746	0.0066	0.0098	0.1598	0.0049	0.0307	0.1473	0.0099	0.0673
DAG1	2.0637	0.0027	0.0013	0.1025	0.0005	0.0052	0.1252	0.0011	0.0085	0.4355	0.0087	0.0199	0.1163	0.0032	0.0276	0.1108	0.0038	0.034
DBI	0.3282	0.0035	0.0107	0.0001	0	0.0107	0.0001	0	0.0107	0.446	0.0141	0.0317				0.3155	0.0213	0.0676
DCD	0	0	0.0087	999	0.0042	0	0	0	0	0.9388	0.0083	0.0089	0.941	0.0155	0.0165	0.9787	0.0388	0.0397
DCXR	0.9885	0.0127	0.0128	0	0	0.0064	0.0924	0.0018	0.0193	0.1849	0.0079	0.0428	0.1023	0.0054	0.0531	0.3056	0.0224	0.0732
DDAH1	0	0	0	0.3901	0.0016	0.0042	999	0.0016	0	0.297	0.0033	0.011	0.0491	0.0019	0.0395	0	0	0.0494
DDB1	0	0	0.0032	0	0	0.0043	0	0	0.0129	0.1538	0.0021	0.0135	0.0179	0.0004	0.0231	0	0	0.0414
DDR1	0	0	0.0035	0	0	0.0082	0.1002	0.0005	0.0049	0.0575	0.001	0.0172	0.0451	0.001	0.0219	0.0456	0.0025	0.054
DDT	0.0001	0	0.0151	0.0001	0	0				0.2307	0.0145	0.0628	999	0.0051	0	0.0389	0.0049	0.1252
DEFB129	0	0	0	0	0	0	999	0.0026	0	1.2425	0.0079	0.0064	1.2589	0.0161	0.0128	0.6273	0.0243	0.0388
DNAJB9	0	0	0	0.34	0.002	0.006	0.3376	0.002	0.006	0.4834	0.0041	0.0085	0.3149	0.0104	0.033	0.3856	0.0084	0.0217
DNAJC3	0	0	0.0319	0	0	0.0177	0	0	0.0157	0.0014	0.0001	0.052	0.001	0.0001	0.0946	0.0017	0.0003	0.1741
DNASE1	999	0.0032	0	0.2075	0.0032	0.0153	0	0	0.0206	0.1876	0.0108	0.0575	0.1012	0.0049	0.0479	0.1157	0.0098	0.085
DNASE2	999	0.0025	0	0.1173	0.0025	0.021	0.2968	0.0037	0.0125	0.5825	0.0098	0.0169	0.2525	0.0075	0.0298	0.382	0.0266	0.0696
DPEP3	0.2843	0.0027	0.0097	0	0	0.005	1.1532	0.0055	0.0048	0.157	0.0037	0.0239	0.6371	0.0113	0.0177	0.3867	0.0263	0.0679
DPP4	0.0764	0.0006	0.008	0.7757	0.0012	0.0016	1.1589	0.0037	0.0032	0.3711	0.0012	0.0033	0.228	0.0018	0.0081	0.2115	0.0062	0.0292
DPP7	0.1016	0.0017	0.0163	0.1326	0.0017	0.0125	0.4546	0.0071	0.0156	0.1124	0.0056	0.0502	0.0977	0.0089	0.0914	0.1198	0.0141	0.1177
DSC2	0.4645	0.0028	0.0059	0.4531	0.004	0.0089	0.6131	0.0036	0.0059	0.2242	0.0039	0.0173	0.5088	0.011	0.0217	0.3735	0.0148	0.0396
DSC3	0.2455	0.0026	0.0105	0.3232	0.0021	0.0064	0.0001	0	0.0137	0.5672	0.0082	0.0145				0.2095	0.0139	0.0663
ECM1	999	0.0017	0	0.4039	0.0025	0.0062	0.4057	0.0034	0.0084	0.378	0.0047	0.0124	0.4172	0.0073	0.0174	0.5982	0.0208	0.0347
EDIL3	0.168	0.001	0.0058	0	0	0.0072	0	0	0.0177	0	0	0	0.1256	0.002	0.0156	0.1586	0.0059	0.0371
EEF1A1	0	0	0.0025	0	0	0.0025	0	0	0.005	0	0	0.0137	0	0	0.0215	0	0	0.0377
EEF1G	0.3665	0.001	0.0026	0	0	0.0052	0.1197	0.0023	0.0193	0.1808	0.0029	0.0159	0.2243	0.0068	0.0302	0.1172	0.0048	0.041
EEF2	0	0	0.0276	0.0168	0.0006	0.0331	0	0	0.0379	0	0	0.0678	0	0	0.1271	0.0022	0.0005	0.2191
EFEMP1	0	0	0.0023	0	0	0	0.1374	0.001	0.0071	0.0729	0.001	0.0134	0.2248	0.002	0.0087	0.0486	0.001	0.0199
EFHD2	0	0	0	999	0.0016	0	0	0	0.0519	0.0927	0.0197	0.2125	0.0617	0.0097	0.1573	0	0	0.1484
EGF	0.6627	0.0042	0.0064	0.3398	0.0025	0.0073	0.6309	0.0029	0.0046	0.8127	0.0055	0.0068	0.7277	0.0083	0.0115	0.5485	0.0216	0.0394
ELSPBP1	0.2252	0.0042	0.0185	0.6628	0.0045	0.0068	0.3414	0.0021	0.0061	0.2219	0.0052	0.0235				0.1128	0.0104	0.0921
ENO1	0	0	0.0068	0	0	0.0169	0	0	0.0169	0	0	0.0465	0.0293	0.0011	0.0364	0.0168	0.0011	0.0637
ENPP3	0.3508	0.0011	0.0032	0.4104	0.0021	0.0051	0.298	0.0014	0.0048	0.2276	0.0044	0.0194	0.3255	0.0097	0.0299	0.3366	0.0118	0.0349
ENPP5	0.0001	0	0.0062	0.5251	0.0031	0.0058	0.2991	0.001	0.0034	0.0001	0	0.0193				0.5325	0.0181	0.0339
EPHA5	0.1356	0.0009	0.0068	0.136	0.0005	0.0034	0.7818	0.008	0.0102	0.0979	0.0014	0.0141	0.1396	0.0014	0.0099	0.0489	0.0014	0.0282
ESD	0.0001	0	0.0225	999	0.0017	0				0.1269	0.002	0.0154	0.0001	0	0.0046	0.1606	0.0067	0.0416
EXTL2	999	0.0014	0	999	0.0014	0	0.1881	0.0014	0.0076	0.076	0.0014	0.0188	0.1221	0.0014	0.0116	0.1875	0.0043	0.0228
F11R	999	0.003	0	0	0	0	0	0	0.0067	999	0.0045	0	0.1089	0.003	0.0279	0.3856	0.0121	0.0315

Gene	HC_ω	HC_*Ka*	HC_*Ks*	GO_ω	GO_*Ka*	GO_*Ks*	Ogi_ω	Ogi_*Ka*	Ogi_*Ks*
CAT	0	0	0.0024	0.1762	0.0021	0.0119	51.8906	0.0005	0
CCT2	0	0	0	0	0	0.0052	0	0	0.002
CCT3	0	0	0.0046	0.0543	0.0008	0.0151	0	0	0
CCT4	0	0	0	0	0	0.0118	0	0	0.0024
CCT5	0	0	0	0	0	0.0201	0	0	0
CCT7	999	0.0009	0	0	0	0.0022	999	0.0009	0
CCT8	0	0	0	0	0	0.0102	0	0	0.0046
CD109	999	0.0004	0	0.2943	0.0019	0.0063	0.4067	0.0009	0.0023
CD14	0	0	0	0.807	0.0025	0.0031	999	0.0012	0
CD151	0	0	0	0.1597	0.0066	0.0414	66.0601	0.0016	0
CD38	0	0	0.0041	1.8134	0.0073	0.004	0.6947	0.003	0.0042
CD44	0	0	0	0.3415	0.0028	0.0083	0.2124	0.0005	0.0025
CD47	0	0	0	0	0	0.0056	0	0	0.0035
CD59	999	0.0037	0	1.4624	0.0126	0.0086	999	0.0121	0
CD63	0	0	0.0053	0	0	0	0	0	0
CD81	0	0	0	0	0	0.0427	0	0	0.0197
CD9	0	0	0	0	0	0	0	0	0
CDC42	82.5231	0	0						
CDH1	0	0	0.0013	0.1197	0.0012	0.0097	999	0.0028	0
CFB	0	0	0.0019	0.8061	0.0079	0.0098	0.4888	0.0019	0.0038
CFL1	0	0	0	0	0	0.0103	0	0	0.0078
CKB	0	0	0	0.0656	0.001	0.0152	0	0	0
CLIC1	0	0	0	0	0	0.0048	0	0	0
CLNS	0.0888	0.0011	0.0127	0	0	0	0.0817	0.001	0.0128
CLSTN1	0	0	0.0064	0.0352	0.0009	0.0262	61.7183	0.0005	0
CLTC	0	0	0.0021	0	0	0.0056	0.4069	0.0002	0.0005
CLU	0	0	0	0.1594	0.0034	0.0213	0.2266	0.0008	0.0034
CNDP2	0	0	0.0116	0.0916	0.002	0.0219	0	0	0
CNP	0	0	0	0.0956	0.001	0.0105	0.0869	0.001	0.0116
CNTN3	0.1997	0.0005	0.0023	0.0993	0.0014	0.0139	0	0	0.0018
CNTNAP2	0	0	0.0033	0.0808	0.0014	0.0177	0.0572	0.0003	0.0059
col12A1	0.2475	0.0005	0.0019	0.0654	0.0007	0.0103	0.054	0.0002	0.0028
COL18A1	0.0001	0	0.002	0.1937	0.0062	0.032			
COL6A1	0.0001	0	0.0064						
COL6A2	0.076	0.0004	0.0053	0.1046	0.0015	0.014	0	0	0.0144
COL9A1	0	0	0	0	0	0.0177	0	0	0.0071
COLEC12	0	0	0.0085	0	0	0.0071	0	0	0.0085
COMP	0.038	0.0005	0.0136				0.3225	0.0011	0.0035
COPB2	0	0	0	0.1751	0.0007	0.004	0	0	0.0024
CP	0	0.0008	0.0017	0.1375	0.0022	0.0051	999	0	0.0034
CPAMD8	0.1327	0.0023	0.0176				0.3104	0.0022	0.007
CPD	0.4071	0.0038	0.0095						
CPE	0	0	0	0.1817	0.001	0.0074	0	0.001	0
CPM	999	0	0	0.0707	0.0011	0.0058	0	0	0.0025
CPO	0.4537	0.0012	0	0.429	0.0024	0.0339	0	0	0
CPVL	999	0.001	0	0.3005	0.0024	0.008	0	0	0
CPZ	999	0.0014	0						
CREG1	0	0	0	0	0	0.0238	0	0	0
CRISP1	0	0	0.0116	0	0	0.0131	0	0	0
Crisp2	0	0	0	0.1935	0.0023	0.0121	999	0.0072	0
CRISP3	0	0	0.016	0.2441	0.0019	0.0077	0	0	0.0053
CRTAC1	0	0	0	0.0679	0.0006	0.0084			
CRYZ	0.1755	0.0016	0.0092	0	0	0.0144	0.6769	0.0026	0.0038
CST1	0.4352	0.0407	0.0935				0.174	0.0076	0.0436
CST3									
CST6	0.0899	0.0027	0.03	0	0	0	0	0	0
CTBS	0	0	0	999	0.0034	0	0	0	0
CTSB	0	0	0.0002	0.2594	0.0038	0.0147	0.1233	0.001	0.0084
CTSD	0	0	0	0.1141	0.0034	0.0299	0.0857	0.0018	0.0215
CTSF	999	0.0052	0	0.1108	0.0018	0.0162	999	0.0018	0
CTSH	0	0	0.0043	0.1731	0.0023	0.0135	0.6484	0.0028	0.0043
CTSO	0	0	0.0038	0.3287	0.0029	0.0089	999	0.0014	0
CTSZ	0	0	0.0143	0.102	0.0015	0.0143	0	0	0.0104
CUL3	0	0	0	0	0	0.0017	0	0	0.0017
CYB561	0	0	0	0.2419	0.0042	0.0175	153.7023	0.0029	0
CYB5R2	0	0	0	0.1202	0.0017	0.0145	0.33	0.0016	0.0049
DAG1	0	0	0.0006	0.3596	0.0026	0.0072	36.3933	0.0006	0
DBI	38.3393	0	0	0.5596	0.0071	0.0126			
DCD	0	0	0	0.9809	0.0087	0.0089	0.2771	0.0057	0.0204
DCXR	0	0	0	0.1738	0.0035	0.02	0	0	0
DDAH1	0	0	0	0	0	0.006	0	0	0
DDB1	0	0	0	0	0	0.0106	0	0	0
DDR1	0	0	0	0.0276	0.0005	0.0179	0	0	0.0059
DDT	0.0001	0	0				0.5653	0.0096	0.017
DEFB129	0	0	0	0.1365	0.0026	0.0194	0	0	0
DNAJB9	0	0	0	0.8615	0.0082	0.0095	0	0	0
DNAJC3	0	0	0	0	0	0.0441	0	0	0.0361
DNASE1	0.305	0.0016	0.0052	0.2849	0.0054	0.0188	3.5024	0.0063	0.0018
DNASE2	0	0	0	0	0	0.0126	999	0.0023	0
DPEP3	1.1461	0.0027	0.0024	0.1716	0.0017	0.0101	353.662	0.0016	0
DPP4	0.5729	0.0018	0.0032	0	0	0.0079	999	0.0012	0
DPP7	0	0	0	0.0734	0.0027	0.0361	0	0	0.0136
DSC2	999	0.0005	0	0.1959	0.0019	0.0096	0	0	0.0054
DSC3	999	0.001	0	0.2292	0.0023	0.0098			
ECM1	999	0.0008	0	1.2219	0.008	0.0065	0	0	0.004
EDIL3	0	0	0.0026	0	0	0.0057	0	0	0
EEF1A1	0	0	0	0	0	0.009	0	0	0
EEF1G	0	0	0	0.7227	0.0019	0.0027	0.513	0.001	0.0019
EEF2	0	0	0.0067	0	0	0.0379	0	0	0.0053
EFEMP1	0	0	0.0023	0.6179	0.002	0.0032	0	0	0.0023
EFHD2	0	0	0	0	0	0.051	0	0	0
EGF	0.7703	0.0008	0.0011	0.6527	0.0062	0.0095	0.4722	0.0009	0.0019
ELSPBP1	0.0001	0	0.0061	0.0001	0	0.0215			
ENO1	0	0	0	0	0	0.0097	0	0	0
ENPP3	0.282	0.0011	0.0038	0.1013	0.0009	0.0092	0.2823	0.0016	0.0056
ENPP5	999	0.002	0	0.2153	0.002	0.0094			
EPHA5	0	0	0.0013	0.0733	0.0005	0.0063	0	0	0.0021
ESD	0.0001	0	0.0046				0.3818	0.0017	0.0044
EXTL2	0	0	0	0.705	0.0028	0.004	0	0	0
F11R	0	0	0	0.4465	0.0076	0.017	0.2338	0.0015	0.0063

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
FAM12A	999	0.0034	0	999	0.0034	0				0.2293	0.0053	0.0231	0.8507	0.0288	0.0338	1.2854	0.0544	0.0424
FAM12B	0.3034	0.003	0.01	999	0.003	0				999	0.003	0	0.914	0.0091	0.01	0.6086	0.0183	0.0301
fam3B	0.1891	0.0018	0.0096	999	0.0018	0	0.3792	0.0018	0.0048	0.9165	0.0138	0.015	0.8557	0.0087	0.0102	0.527	0.0236	0.0447
FAM3C	0	0	0	0.3589	0.002	0.0057	0	0	0.0057	0	0	0.0113	0.1201	0.002	0.017	0	0	0.023
FASN	0.1096	0.002	0.018	0.0874	0.0022	0.0249	0.1475	0.0029	0.0196	0.1587	0.0088	0.0555	0.0973	0.0073	0.0752	0.122	0.0214	0.1752
FBLN2	0.1544	0.0025	0.0164	0.1988	0.003	0.015	0.1059	0.0024	0.0226	0.0961	0.0032	0.0338	0.0801	0.0038	0.0469			
FBP1	0.6967	0.0027	0.0039	0.1198	0.0014	0.0114	0	0	0.0086	0	0	0.0181	0.1574	0.005	0.0319	0.064	0.0081	0.1271
FCGBP	0.2531	0.0049	0.0192	0.1962	0.0048	0.0244	0.2743	0.0047	0.0171	0.1639	0.0059	0.0359	0.1799	0.0079	0.044			
FDPS	0	0	0.0029	0	0	0.0056	0.3358	0.0078	0.0232	0.2364	0.0038	0.0161	0.2511	0.0046	0.0184	0.1551	0.0058	0.0372
FH	0.3378	0.0009	0.0027	0.151	0.0018	0.0121	0.074	0.0009	0.0123	0.0374	0.0009	0.0243	0.1954	0.0018	0.0093	0.1096	0.0055	0.0501
FKBP4	0.1923	0.001	0.0053	106.6329	0.003	0	0.4323	0.0093	0.0215	0.244	0.0051	0.0208	0.1263	0.0022	0.0175	0.1778	0.0078	0.0438
FLNB	0.081	0.001	0.0124	0.0889	0.0008	0.0091	0.0809	0.0009	0.0109	0.0964	0.002	0.0208	0.0267	0.0006	0.0228	0.052	0.0031	0.0594
FMOD	0	0	0	0	0	0.0132	0	0	0.0174	0.0264	0.0013	0.0507	0.041	0.0013	0.0324	0.0311	0.0021	0.0671
FN1	0.1347	0.0012	0.0087	0.0801	0.0008	0.0096	0.1385	0.0015	0.0112	0.0793	0.0013	0.0167	0.1125	0.0023	0.0202	0.1344	0.0052	0.0385
FOLH1	0.5005	0.0025	0.0049	0.2294	0.0031	0.0134	4.5856	0.0082	0.0018	0.3289	0.0061	0.0186	0.2341	0.0037	0.0159	0.2108	0.0086	0.0408
FSTL1	0	0	0.0083	0.1842	0.0015	0.0083	0	0	0.0044	0.1829	0.0015	0.0083	0	0	0.0256	0	0	0.0299
FTH1	0.0001	0	0.0129	0.0001	0	0.0064				0.1998	0.0026	0.0129	0.1967	0.0026	0.0132	0.0427	0.0026	0.0607
FUCA1	0.7662	0.002	0.0026	0.3809	0.0061	0.016	0.3824	0.003	0.0079	0.2985	0.0056	0.0188	0.3064	0.0058	0.019	0.2462	0.0136	0.0553
FUCA2	0	0	0.0104	0	0	0	0.1956	0.001	0.0052	0.1583	0.002	0.0129	0.7852	0.0051	0.0065	0.2682	0.0113	0.0422
FUT3	0.14	0.0028	0.0203	0.1272	0.0064	0.0499	0.0935	0.004	0.043	0.1933	0.0104	0.054	0.2493	0.0437	0.1752	0.1822	0.024	0.1319
GAA	0.1345	0.0035	0.026	0.1535	0.0026	0.0171	0.1535	0.0034	0.0224	0.0898	0.0054	0.0607	0.1284	0.0056	0.0432	0.1321	0.0142	0.1072
GALC	0.0768	0.0007	0.009	0.0001	0	0.0055				0.1829	0.002	0.0108	0.2591	0.0053	0.0203	0.3635	0.0129	0.0354
GALNS	0.4142	0.0058	0.0141	0.1023	0.0025	0.0244	0.1735	0.0034	0.0196	0.1283	0.008	0.0627	0.1617	0.0131	0.081	0.0755	0.0084	0.1117
GALNT6	0	0	0.0066	0.4851	0.0023	0.0047	999	0.0015	0	0.0292	0.0007	0.0249	0.1492	0.0015	0.0097	0.1313	0.0081	0.0619
GALNT7	0.3249	0.0007	0.0022	0.1144	0.0014	0.0126	0	0	0.0035	0	0	0.0056	0.506	0.003	0.006	0.1034	0.0023	0.022
GANAB	0	0	0.0023	0.3511	0.002	0.0058	0.4393	0.001	0.0023	0.4669	0.0046	0.0098	0.1284	0.0015	0.0119	0.2121	0.0071	0.0335
GAPDH	0	0	0.0129	0	0	0.0043	0	0	0.0136	0.0667	0.0027	0.0402	0.0219	0.0013	0.0613	0.0419	0.0027	0.0635
GAPDHS	0.1254	0.0016	0.0126	1.2968	0.0041	0.0031	0.4101	0.0027	0.0066	0.0769	0.0023	0.0294	0.3318	0.008	0.024	0.2219	0.016	0.0722
GAS6	0.1004	0.0031	0.0304	0.2122	0.0026	0.0123				0.0986	0.0049	0.0497	0.2326	0.0166	0.0712	0.0686	0.0112	0.1637
GBA	1.0097	0.0025	0.0025	0.0838	0.0008	0.0101	1.5553	0.0971	0.0625	0.0871	0.0034	0.0386	0.0513	0.0017	0.0336	0.4991	0.0276	0.0553
GC	0	0.001	0.0025	0	0.001	0.0094	0	0	0.0025	0	0	0.0077	0.1025	0.0039	0.0224	0.1601	0.0316	0.0414
GCHFR	0.3893	0	0.017	0.1016	0	0	0	0	0	0	0	0.0169	0.1723	0.0054	0.0529	0.762	0.0055	0.0342
GDF15	0.4056	0.0057	0.014	0.3628	0.0086	0.0237	0.509	0.0072	0.0141	0.1283	0.0043	0.0334	0.9075	0.0129	0.0142	0.4812	0.0328	0.0682
GDI2	0	0	0.0149	0.3425	0.0011	0.0031	0.1091	0.0011	0.0098	0.1026	0.0011	0.0104	0	0	0.0131	0.1064	0.0056	0.0526
GFRA2	0.0001	0	0.0197	0.222	0.0012	0.0056	0.1089	0.0009	0.0082	0.0501	0.0027	0.0535				0.0211	0.0023	0.1095
GGH	0.3832	0.0015	0.0039	0	0	0.0076	0.7534	0.0031	0.0041	0.6872	0.0031	0.0046	3.9052	0.0259	0.0066	0.2289	0.0135	0.0591
GGT1	0.2471	0.0037	0.0152	0.0279	0.0007	0.0268	0.5596	0.0092	0.0164	0.083	0.0051	0.0616	0.1685	0.0063	0.0374	0.0927	0.0121	0.1309
GLA	0	0	0	999	0.0064	0	999	0.0012	0	0.3257	0.0042	0.013	0.2111	0.0042	0.02	0.1549	0.0056	0.0359
GLB1	1.0379	0.0035	0.0033	0.3186	0.0015	0.0047	0.3278	0.0015	0.0045	0.1676	0.0033	0.0194	0.3719	0.0053	0.0143	0.5775	0.0329	0.0569
GLB1L	0.4111	0.0015	0.0036	0.3746	0.0045	0.012				0.4363	0.0052	0.012	2.3411	0.0088	0.0038	0.3678	0.009	0.0245
GLG1	0	0	0.0066	0.1725	0.0008	0.0047	0.0938	0.0008	0.0085	0.048	0.0009	0.0188	0.0284	0.0005	0.0162	0	0	0.0464
GLO1	0.1082	0.0025	0.0227	0	0	0.0075	0	0	0.0075	0.3268	0.0049	0.015	0.1049	0.0024	0.0232	0.0886	0.0049	0.0553
GM2A	0.7372	0.0048	0.0065	0	0	0.0065	0.3699	0.0024	0.0065	0.4999	0.0101	0.0201	0.1052	0.0028	0.0263	0.697	0.0375	0.0538
GMPPA	0	0	0	999	0.001	0	0.0837	0.001	0.0123	0.1783	0.0031	0.0173	0.2218	0.0035	0.016	0.0256	0.001	0.04
GNAI3	0	0	0	0	0	0.0136	0	0	0.0102	0	0	0.0136	0	0	0.0172	0	0	0.0172
GNB1	0	0	0.0107	999	0.0016	0	0	0	0.0038	0	0	0.0315	0	0	0.0103	0	0	0.0563
GNB2	0	0	0.0051	0	0	0.0151	0	0	0.0199	0	0.005	0.0413	0	0	0.0134	0	0.0012	0.0595
GNB2L1	0	0	0.0104	0	0	0.0099	0	0	0.006	0.1199	0	0.0124	0	0	0.0346	0.0208	0	0.0434
GNG12	0	0	0	0	0	0	0	0	0	0	0	0	0.2255	0.0131	0.058	0	0	0.0374
GNMT	0	0	0.0101	0	0	0.0049	0	0	0.0102	0.117	0.0051	0.0439	0.0969	0.0045	0.0465	0.0556	0.003	0.0533
GNPDA1	0	0	0.005	0	0	0.0049	0.3104	0.0015	0.005	0	0	0.0049	0.0407	0.0017	0.0428	0.0325	0.0015	0.0475
GNPTG	0.2582	0.0042	0.0162	0.5118	0.0028	0.0054	0.1669	0.0056	0.0335	0.0919	0.007	0.0757	0.0868	0.0088	0.101	0.1268	0.0167	0.1317
GNS	0.1351	0.0008	0.006	0.2033	0.0008	0.004	0	0	0.006	0.2452	0.004	0.0164	0.1122	0.0025	0.0223	0.1303	0.0056	0.0434
GOT1	0	0	0.0082	0	0	0	0	0	0.014	0.1072	0.0035	0.0331	0	0	0.022	0.2298	0.0095	0.0413
GP2	0.1464	0.0019	0.013	0.3203	0.0026	0.0081	0.3395	0.0044	0.0128	0.6286	0.0061	0.0097	0.391	0.0087	0.0222	0.4979	0.0313	0.0629
GPC1	0.0748	0.0021	0.0284	0.0323	0.0009	0.0292	0.0296	0.0008	0.0261	0.0473	0.0032	0.0677	0.0778	0.0048	0.0612	0.0584	0.0095	0.1619
GPC4	0	0	0.0023	0	0	0	0.3607	0.0017	0.0046	0.0594	0.0008	0.0139	0.5848	0.0055	0.0094	0.1407	0.005	0.0355
GPD1L	0.0001	0	0.0106				0.253	0.0062	0.0246	0.0958	0.0013	0.014	0.1239	0.0041	0.0331	0.0458	0.0027	0.0587
GPI	0.5874	0.0015	0.0025	0.359	0.0045	0.0125	0	0	0.0129	0.1682	0.0045	0.0265	0.0193	0.0009	0.0442	0.0921	0.0067	0.073
GPR115	0.4298	0.0029	0.0067	0.4303	0.0021	0.005	0.2867	0.0029	0.01	0.432	0.0058	0.0135	0.5378	0.0232	0.0432	0.3953	0.0205	0.0519
GPR56	0.3689	0.0037	0.01	0.3351	0.0039	0.0116	0.1783	0.0043	0.0242	0.2516	0.009	0.0358				0.1378	0.013	0.094
GPR64	0.3092	0.001	0.0032	999	0.001	0	0.7763	0.0025	0.0032	0.1414	0.002	0.0139	0.4498	0.0025	0.0055	0.3978	0.0099	0.0248
GPRC5C	0.2125	0.0027	0.0125	0.1188	0.0018	0.0149	0.135	0.0027	0.0197	0.0425	0.0018	0.0433	0.1039	0.0048	0.0458	0.0668	0.008	0.1194
GPX3	0	0	0	0	0	0	0	0	0.0118	0	0	0.0241	0.224	0.0042	0.0186	0.2638	0.0187	0.0707
GRHPR	0.1199	0.0014	0.0117	0.363	0.0028	0.0078	0.1822	0.0014	0.0078	0.2432	0.003	0.0124	0.3437	0.0047	0.0135	0.2816	0.0219	0.0777
GRN	0.9431	0.0022	0.0024	0.1602	0.0007	0.0046	0.1777	0.003	0.0169	0.1992	0.005	0.0252	0.6467	0.0071	0.011	0.4024	0.0262	0.0652
GSN	0.0619	0.0006	0.0091	0.0949	0.0006	0.0059	0.294	0.0051	0.0174	0.2012	0.0051	0.0254	0.1132	0.004	0.0351	0.0391	0.0028	0.0725
GSR	0.1228	0.0018	0.0146	0.2292	0.0027	0.0118	0.1897	0.0028	0.0147	0.2633	0.0086	0.0327	0.283	0.0074	0.0261	0.1669	0.015	0.0896
GSS	0.4386	0.001	0.0024	0.1456	0.001	0.0071	0.1085	0.001	0.0095	0.2177	0.0021	0.0095	0.0881	0.0012	0.0133	0.3414	0.0125	0.0366
GSTM3	0	0	0.0138	0	0	0.0495	0	0	0.051	0	0	0.0871	0.001	0.0001	0.1096	0.0012	0.0003	0.2936
GSTO1	0.1584	0.0018	0.0117	69.767	0.0018	0	0.317	0.0018	0.0058	0.3175	0.0056	0.0175	0.3168	0.0037	0.0117	0.233	0.0112	0.0479
GSTP1	0.263	0.002	0.0078	0	0	0	0.2624	0.002	0.0078	0.0479	0.002	0.0428	0.3024	0.0102	0.0338	0	0	0.1057
GSTT1	0	0	0	0	0	0.0056	999	0.0019	0	0.2989	0.0122	0.0409	0.1518	0.0026	0.0171	0.2025	0.0108	0.0534
GSTZ1	999	0.0065	0	0.3593	0.0022	0.006	1.4466	0.0087	0.006	999	0.0021	0	0.1409	0.0044	0.0309	0.3525	0.0132	0.0376
GUSB	0.4852	0.0021	0.0043	0	0	0.0042	0.6067	0.0145	0.0239	0.2092	0.0081	0.0387	0.3895	0.0192	0.0493	0.2469	0.0207	0.0836
HDHD2	0.9595	0.0039	0.0041	0	0	0	0.9683	0.0039	0.004	0.7172	0.0059	0.0082	0	0	0.0208	0.1332	0.0039	0.0296
HEBP2	12.8231	0.0024	0.0002	0.4577	0.0024	0.0053	0	0	0.0161	0	0	0.0163	0.222	0.0049	0.022	0.2733	0.0123	0.045
HEXA	0.366	0.0017	0.0047	0	0	0.0071	0	0	0.0047	0.1213	0.0009	0.0071	0.3623	0.0086	0.0238	0.1653	0.0069	0.0418
HEXB	0.6117	0.004	0.0065	1.6968	0.0037	0.0022	0.3525	0.0028	0.0079	0.379	0.0058	0.0154	0.4211	0.0157	0.0374	0.5162	0.0171	0.0331
HINT1	0	0	0	0	0	0.009	0	0	0	0	0	0.0167	0.1517	0.0078	0.0518	0	0	0.0135
HIST2H2BE	0	0	0	0	0	0.0429	0	0	0.0214	0	0	0.0229	0	0	0.0705	0	0	0.0696
HPRT1	0	0	0	0	0	0.0141	0.56	0.0149	0.0266	0	0	0.0141	0.8261	0.0212	0.0257	0	0	0.0355
HPX	0.3684	0.001	0.0027	0	0	0.0055	1.066	0.0633	0.0594	0.799	0.0044	0.0055	0.2668	0.0075	0.028	0.7407	0.0224	0.0303
HRSP12	0.4322	0.0036	0.0084	0	0	0	0	0	0	0	0	0.0255	0	0	0.0082	0.3612	0.0222	0.0616
HSPA1L	0.2227	0.0022	0.0099	0.3715	0.0007	0.002	0	0	0.0097	0.0364	0.0007	0.0201	0.0356	0.0392	1.1026	0.0404	0.0022	0.0543
HSPA4	999	0.0005	0	0.179	0.0005	0.003	0.0591	0.0006	0.0095	0.0921	0.0011	0.0118	0.1203	0.0016	0.0137	0.0391	0.0016	0.0418
HSPA5	0	0	0.0061	0	0	0.0061	0	0	0.0061	0	0	0.0157	0.1859	0.0056	0.03	0	0	0.0344
HSPA8	0	0	0.013	0	0	0.0117	0	0	0.017	0	0	0.0187	0	0	0.0203	0	0	0.0619
HSPB1	0.0001	0	0	0.1806	0.0039	0.0217	0.0001	0	0.0216	0.2229	0.0138	0.0618				0.0001	0	0.1532
HSPG2	0.1289	0.0024	0.019	0.1663	0.0027	0.0164	0.1109	0.0018	0.0165	0.0705	0.0031	0.0434	0.7944	0.2772	0.349	0.0625	0.0055	0.0879
Hyou1	0.4303	0.0015	0.0034	0.5375	0.0024	0.0045	0.1941	0.0014	0.0075	0.1837	0.0024	0.0131	0.0461	0.001	0.0218	0.1112	0.0055	0.0498
IDE	0	0	0.0049	0.3376	0.0005	0.0013	0.3364	0.0014	0.004	0.164	0.0027	0.0166	0.0421	0.0005	0.0117	0.0713	0.0027	0.0381
IDH1	0.1619	0.0011	0.0067	0.0536	0.0011	0.0203	0.1607	0.0033	0.0203	0.1084	0.0022	0.0201	0.725	0.0319	0.0441	0.1306	0.0033	0.0251
IDI1	0.9599	0.0044	0.0046	0.1416	0.0021	0.015	0.6789	0.0036	0.0053	0.185	0.0037	0.02	1.6606	0.0124	0.0075	0.1494	0.0108	0.0722
IDS	0.4217	0.0009	0.0021	2.1182	0.0044	0.0021	0	0	0.0044	0.1795	0.0044	0.0246	0.3514	0.0036	0.0103	0.2983	0.0124	0.0416
IDUA	0.207	0.0019	0.0092	1.2448	0.0116	0.0093	0.7096	0.0067	0.0095	0.3452	0.0084	0.0242	0.1486	0.0072	0.0486	0.1994	0.0226	0.1133
IGF2R	0.0838	0.0009	0.0111	0.3711	0.0021	0.0057	0.1694	0.0021	0.0121	0.1281	0.0032	0.0247				0.2748	0.0194	0.0707
IGFBP2	0.0001	0	0.0127	0.0001	0	0.0055				0.5644	0.0013	0.0023	0.0001	0	0.0435	0.0512	0.0039	0.0761
IGFBP5	0.1913	0.0015	0.0077	0.3665	0.003	0.0081				0.0616	0.0015	0.024	0.0617	0.0015	0.024	0.0304	0.0015	0.0488
IGHG2	0.435	0.0252	0.0579	0.1595	0.0093	0.0581				0.3284	0.0069	0.0209				0.3232	0.0502	0.1554

Gene	HC_ω	HC_*Ka*	HC_*Ks*	GO_ω	GO_*Ka*	GO_*Ks*	Ogi_ω	Ogi_*Ka*	Ogi_*Ks*
FAM12A	999	0.0048	0				0.0001	0	0.0065
FAM12B	0.1515	0.003	0.0199				0.0001	0	0
fam3B	0	0	0	1.4241	0.0069	0.0049	1.702	0.0103	0.0061
FAM3C	0	0	0	999	0.002	0	0	0	0
FASN	0.1041	0.0012	0.0115	0.1119	0.0031	0.028	0.2607	0.0028	0.0109
FBLN2	0.259	0.0009	0.0033	0.2776	0.0032	0.0116			
FBP1	0	0	0	0	0	0.0166	0	0	0.0012
FCGBP	0.0962	0.0005	0.0055	0.154	0.0031	0.0201			
FDPS	0.6852	0.0015	0.0022	0.9092	0.0046	0.0051	0.0863	0.0008	0.0088
FH	0	0	0.0024	0.1454	0.0009	0.0063	0	0	0.0047
FKBP4	0	0	0	0	0	0.0033	0	0	0.0046
FLNB	0	0	0.0011	0.0185	0.0002	0.0134	0.0862	0.0002	0.0026
FMOD	0	0	0	0.3495	0.0043	0.0124	0	0	0.004
FN1	0	0	0.0032	0.1052	0.0009	0.0082	0.2724	0.0004	0.0013
FOLH1	0	0	0.004	62.8601	0.0008	0	0	0	0.0043
FSTL1	0	0	0	0	0	0.0083	0	0	0.0037
FTH1	0.0001	0	0				0.0001	0	0.0063
FUCA1	0	0	0	0.0663	0.0013	0.0189	0	0	0.0077
FUCA2	0	0	0.0026	0.2491	0.002	0.0082	0	0	0.0045
FUT3	0	0	0	0.0946	0.0018	0.0186	0	0	0.04
GAA	44.3008	0.0006	0	0.0621	0.0019	0.0304	3.6146	0.0004	0.0001
GALC	0.1988	0.0029	0.0145				0.0001	0	0.0031
GALNS	0	0	0	0	0	0.0219	0.3004	0.0027	0.0091
GALNT6	0	0	0	0	0	0.0141	0.3928	0.0007	0.0018
GALNT7	0	0	0	0.1233	0.0007	0.0058	0	0	0
GANAB	0	0	0	0.1216	0.0015	0.0124	0	0	0.0045
GAPDH	0	0	0.0036	3.7996	0.0012	0.0003	0	0	0.0014
GAPDHS	0	0	0.0061	0.1879	0.0029	0.0156	0	0	0.0023
GAS6	0.0001	0	0.0303				0.1852	0.0011	0.0062
GBA	0.2585	0.0008	0.003	62.7699	0.0018	0	0	0	0.0041
GC	999	0	0.0024	0	0.0019	0.0114	0	0.001	0.0044
GCHFR	0	0.011	0	0.1691	0	0	0.2164	0	0
GDF15	0	0	0	0	0	0.0046	0	0	0.0046
GDI2	0	0	0.005	0	0	0.0186	0	0	0
GFRA2	0.0001	0	0	0.0001	0	0.021			
GGH	0	0	0	0.2117	0.0058	0.0272	0.1676	0.0016	0.0097
GGT1	0	0	0.0078	0.08	0.001	0.0125	0.0493	0.0008	0.0153
GLA	0	0	0	999	0.0021	0	0.1106	0.001	0.0095
GLB1	0.424	0.0014	0.0034	0.2353	0.0029	0.0125	1.8478	0.0017	0.0009
GLB1L	0.3936	0.0039	0.01				0.269	0.0014	0.0054
GLG1	0.1506	0.0004	0.0027	0.1244	0.0015	0.0122	0.0645	0.0005	0.0075
GLO1	0	0	0	1.6246	0.0049	0.003	0	0	0.0045
GM2A	0	0	0	0.1658	0.0021	0.0127	0	0	0
GMPPA	0	0	0.0022	0.0693	0.001	0.0147	0	0	0.0073
GNAI3	0	0	0	0	0	0	0	0	0.0033
GNB1	0	0	0	0	0	0.0082	0	0	0
GNB2	0	0	0	0	0	0.0163	0	0	0.0074
GNB2L1	0	0	0	0	0	0.0146	0	0	0.007
GNG12	0	0	0	0	0	0	0	0	0
GNMT	0	0	0.0156	0.0687	0.003	0.0433	0	0	0
GNPDA1	0	0	0	0	0	0.005	0	0	0.0034
GNPTG	0	0	0	0.1284	0.0042	0.0326	0	0	0
GNS	0	0	0	0.0876	0.0009	0.01	0	0	0
GOT1	0	0	0.0026	0.1293	0.0024	0.0182	0	0	0.0078
GP2	104.3916	0.0017	0	0.1055	0.0009	0.0086	0.5515	0.0035	0.0064
GPC1	0	0	0	0.0269	0.0016	0.059	999	0.0009	0
GPC4	0	0	0	0	0	0.0023	0	0	0.0055
GPD1L							0.0001	0	0.0067
GPI	0	0	0.0023	0	0	0.0125	0	0	0.0133
GPR115	0	0	0	0.2684	0.0044	0.0165	0.1997	0.001	0.005
GPR56	0.1967	0.0006	0.0031	0.1683	0.0033	0.0198			
GPR64	999	0.001	0	0.2725	0.0015	0.0054	0.735	0.0015	0.002
GPRC5C	0.1306	0.0009	0.0068	0.0341	0.0009	0.026	2.261	0.0045	0.002
GPX3	0	0	0	0.3468	0.002	0.0059	0.1059	0.0019	0.0183
GRHPR	0	0	0	0.0956	0.0026	0.0275	0	0	0.0036
GRN	7.4154	0.0034	0.0005	0.3697	0.0032	0.0088	0	0	0.001
GSN	0.1437	0.0006	0.0039	0.0253	0.0006	0.0221	0	0	0.0009
GSR	0.2693	0.0027	0.01	0.1311	0.0015	0.0114	0.502	0.0058	0.0115
GSS	0	0	0	0	0	0.0023	0	0	0
GSTM3	0	0	0.0286	0	0	0.0157	0	0	0
GSTO1	0	0	0	0	0	0	0	0	0
GSTP1	535.9046	0.002	0	0.6016	0.0083	0.0137	0.0562	0.002	0.0362
GSTT1	0	0	0.0056	999	0.0031	0	0	0	0
GSTZ1	999	0.0022	0	0	0	0.0182	0	0	0.0183
GUSB	0.1276	0.0021	0.0165	0.1814	0.0037	0.0201	0.1236	0.0027	0.0216
HDHD2	999	0.0019	0	0	0	0.0081	0	0	0.0039
HEBP2	0	0	0	0	0	0.0107	0	0	0.0108
HEXA	999	0.0009	0	0.2711	0.0026	0.0095	0	0	0.0042
HEXB	0	0	0	0.1434	0.0012	0.0087	0	0	0
HINT1	0	0	0	0.1339	0.0039	0.0291	0	0	0
HIST2H2BE	0	0	0	0	0	0.0231	0	0	0.0465
HPRT1	0	0	0	0	0	0	0	0	0
HPX	999	0.001	0	0.3363	0.0037	0.011	0.3628	0.0019	0.0053
HRSP12	0	0	0	0	0	0	0	0	0.0087
HSPA1L	0.3422	0.0007	0.0021	0.0763	0.0015	0.0191	0	0	0.0254
HSPA4	0	0	0	0	0	0.0035	0	0	0.0044
HSPA5	0	0	0	0	0	0.0089	0	0	0.0063
HSPA8	0	0	0	0	0	0.0124	0	0	0.0073
HSPB1	153.0202	0	0	0.0001	0	0.0534			
HSPG2	0.1276	0.0003	0.0022	0.029	0.0007	0.0224	0.0736	0.001	0.0138
Hyou1	0	0	0.0027	0.0576	0.0005	0.0084	0	0	0.0035
IDE	0	0	0.0035	0	0	0.0083	0	0	0.0014
IDH1	0	0	0	0	0	0.0037	0	0	0.0058
IDI1	0	0	0.0128	0.3232	0.0122	0.0378	999	0.0017	0
IDS	0.4197	0.0009	0.0021	0.3039	0.0009	0.0029	0	0	0.002
IDUA	0	0	0.0024	0.2726	0.0064	0.0236	0.4206	0.0006	0.0015
IGF2R	0.142	0.0007	0.0046	0.2641	0.0047	0.0177			
IGFBP2	0.0001	0	0.0435				0.0001	0	0.0075
IGFBP5	0.0001	0	0.0161				40.9554	0	0
IGHG2	0.1117	0.0056	0.05						

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
IGHG4	0.3134	0.0262	0.0837	0.1003	0.0067	0.0671				0.219	0.0076	0.0349				0.2311	0.031	0.1342
IGJ	0.4098	0.0028	0.0067	999	0.0028	0	0.8275	0.0055	0.0067	0.8172	0.011	0.0135	2.0906	0.014	0.0067	1.0907	0.0222	0.0204
IGKC	999	0.0058	0	0	0	0	999	0.0191	0	1.8625	0.0518	0.0278	999	0.0152	0	3.6585	0.0916	0.025
IGLV1-40	0.4262	0.022	0.0517	999	0.0043	0							1.8291	0.041	0.0224	0.5048	0.0465	0.092
IL1R1	999	0.0008	0	0.3832	0.0008	0.0022	0.1516	0.0016	0.0109	0.3244	0.0049	0.0152	0.4014	0.0059	0.0147	0.6022	0.0213	0.0354
IL1RAP	0	0	0.0049	0	0	0.0083	0.1286	0.0014	0.011	0.1158	0.0021	0.0183	0.036	0.0007	0.0196	0.0726	0.0028	0.039
IL1RL1	0.4265	0.0032	0.0076	0.3159	0.0032	0.0102	0.798	0.004	0.0051	0.5616	0.0105	0.0187	0.7594	0.1419	0.1869	0.226	0.0184	0.0815
IL6ST	0.3672	0.0015	0.0041	0.2312	0.001	0.0044				0.2732	0.002	0.0074	0.1804	0.003	0.0168	0.1722	0.0076	0.0443
IMPA1	0.3187	0.0027	0.0084	0.32	0.0027	0.0084				0.1653	0.0042	0.0253	2.2485	0.0094	0.0042	0.2182	0.0094	0.043
INHBB	0.0001	0	0.0054	0.3737	0.0056	0.015	0.0001	0	0.0057				0.0001	0	0.0068	0.0096	0.0011	0.112
IQGAP1	0.0487	0.0003	0.0058	0	0	0.0029	0.1064	0.0007	0.0065	0.1042	0.0017	0.0164	0.0356	0.0006	0.016	0.0485	0.0015	0.0301
IQGAP2	0.2513	0.0013	0.005	0.1967	0.0006	0.0032	0.1844	0.0006	0.0034	0.1232	0.0013	0.0102	0.1558	0.0025	0.0161	0.221	0.0059	0.0266
ITIH5	0.2633	0.0029	0.0112	0.2364	0.0033	0.0139	0.6318	0.0106	0.0168	0.1498	0.0052	0.0345	0.2357	0.0106	0.0449	0.1482	0.0103	0.0693
KAL1	0	0	0.0079	0.2316	0.0007	0.0032	0.1049	0.0007	0.007	0.2854	0.0044	0.0154	0.6389	0.0052	0.0082	0.1599	0.0089	0.0559
KIF5B	0.1301	0.0004	0.0034	0	0	0.0017	0	0	0.0034	0.0128	0.0004	0.0345	0	0	0.0139	0.1889	0.0129	0.0681
KLK11	1.3269	0.0076	0.0058	0.2461	0.003	0.0124	0	0	0.0072	0.2911	0.0138	0.0475	0.1783	0.006	0.0337	0.3221	0.0184	0.0572
KLK2	999	0.0055	0	0.3749	0.0018	0.0047				0.3494	0.0139	0.0398				0.2834	0.0176	0.0621
KLK3	0.4833	0.0063	0.0131	0.3858	0.0157	0.0408	0	0	0.0188	0.3363	0.0184	0.0546	0.3459	0.0139	0.0402	0.5759	0.0452	0.0786
KPNB1	0	0	0.0055	0	0	0.0069	0	0	0.011	0.2175	0.0027	0.0124	0	0	0.0152	0	0	0.0392
KRT1	0.4903	0.0007	0.0106	0.2916	0.0038	0.0293	0.0795	0	0.0088	0.3421	0.0045	0.015	0.0911	0.0019	0.021	0.0779	0.0045	0.0434
KRT10	0.0695	0.0038	0.0078	0.1282	0.0027	0.0091	0	0.002	0.0253	0.3012	0.0048	0.014	0.0884	0.0021	0.0229	0.1044	0.0054	0.0689
KRT5	0.0846	0.0022	0.0255	0.0558	0.0009	0.0163	0.0987	0.0017	0.017	0.0449	0.0015	0.0341	0.0812	0.0046	0.0566	0.0282	0.0023	0.0811
KRT8	0.1231	0.0017	0.0138	0.4606	0.0071	0.0153	0.2536	0.0017	0.0069	0.0944	0.0038	0.0405	0.3791	0.0482	0.1272	0	0	0.073
KRT9	0	0	0.0068	0.6144	0.0016	0.0026	0.6248	0.0125	0.0199	0.8878	0.025	0.0282	0.0965	0.0024	0.0245	0.2164	0.0081	0.0372
LAMA5	0.1382	0.0027	0.0192	0.145	0.0031	0.021				0.1636	0.0084	0.0513	0.1592	0.0096	0.06	0.1181	0.0159	0.1345
LAMB2	0.4131	0.0022	0.0052	0.3814	0.0039	0.0101	0.2878	0.003	0.0103	0.3708	0.0078	0.0211	0.265	0.0056	0.021	0.2298	0.0121	0.0528
LAMC1	0.4087	0.002	0.0049	0.1137	0.0012	0.0108	0.2642	0.0023	0.0087	0.0933	0.0021	0.0221	0.0693	0.0018	0.0255	0.0522	0.0029	0.0565
LAMP1	0.2398	0.0042	0.0177	0.2601	0.0043	0.0164	0.2388	0.0053	0.0222	0.0905	0.0036	0.0398	0.2977	0.0074	0.0249	0.1427	0.0105	0.0736
LAMP2	1.1437	0.0034	0.003	0.3812	0.0014	0.0035	0.7648	0.003	0.0039	0	0	0.003	0.634	0.0058	0.0091	0.3284	0.0081	0.0247
LAP3	0	0	0.0183	0	0	0.0121	0	0	0.0159	0.1807	0.0018	0.0097	0.8492	0.0897	0.1056	0.1193	0.0054	0.0453
LCN1	999	0.0024	0	0.2646	0.0049	0.0185	0.1291	0.0049	0.038	0.5441	0.0304	0.0558	0.3359	0.0265	0.0788	0.245	0.0221	0.0903
LCN2	0	0	0.007	0.6453	0.0046	0.0071	0	0	0.0064	0.2014	0.0072	0.0355	0.2665	0.0077	0.0288	0.7035	0.0426	0.0605
LCP1	0.1032	0.0008	0.0074	0	0	0.0072	0	0	0.0021	0	0	0.0172	0	0	0.0262	0.044	0.0015	0.0348
LDHA	0.2092	0.0013	0.0064	0.4191	0.0013	0.0032	0	0	0.0032	0	0	0.0129	0.0823	0.0013	0.0162	0.1227	0.004	0.0328
LDHB	0	0	0.0029	0	0	0.0042	0	0	0.008	0	0	0.0132	0	0	0.0378	0	0	0.0347
LDHC	0	0	0.0039	0	0	0.0039	999	0.0014	0	0.1556	0.0028	0.0179	0.1496	0.0028	0.0186	0.1789	0.0099	0.0552
LDLR	0.0726	0.0024	0.0333	0.0675	0.002	0.0294	0.2028	0.0026	0.0131	0.0495	0.0028	0.0564				0.1758	0.0207	0.1177
LEFTY2	0	0	0.0125	0	0	0.0448	0.0739	0.0033	0.0444	0.0518	0.0053	0.1024	0.0454	0.0082	0.1808	0.0887	0.0158	0.1777
LGALS3	0.2449	0.002	0.0043	0.1924	0.008	0.0043	0.1415	0.004	0.013	0.2127	0.0029	0.0086	0.1858	0.013	0.0131	0.1552	0.0216	0.0496
LGALS3BP	0.4627	0.0036	0.0147	1.8576	0.0015	0.0076	0.3067	0.0022	0.0154	0.3402	0.0175	0.0822	0.9934	0.0121	0.065	0.4361	0.0148	0.0954
LGMN	0.1653	0.0031	0.019	0	0	0.0064	0.8292	0.028	0.0337	0.0858	0.0031	0.0366	0.1552	0.0057	0.0369	0.0348	0.0021	0.0599
LIFR	0.27	0.0012	0.0045	0.3702	0.0008	0.0022	0.3162	0.002	0.0064	0.2367	0.0037	0.0155	0.1733	0.0032	0.0187	0.2161	0.0086	0.0398
LIPA	1.0588	0.0066	0.0062	0.3708	0.0031	0.0084	1.1407	0.0038	0.0034	0.59	0.0154	0.0261	0.4581	0.0101	0.0222	0.3208	0.0156	0.0487
LIPG	999	0.0009	0	0	0	0.018	0.4839	0.0207	0.0428	0.0479	0.0011	0.0226	0.3289	0.0028	0.0085	0.1123	0.0065	0.0583
LIPI	0.3833	0.0034	0.0088	0.1912	0.0022	0.0117				0.747	0.0152	0.0203	0.6518	0.0062	0.0096	0.8518	0.0462	0.0542
LMAN2	0	0	0.0052	0.1132	0.0012	0.0103	0	0	0.0155	0.0243	0.0012	0.048	0.0705	0.0012	0.0174	0.0235	0.0012	0.0495
LNPEP	0.1018	0.0005	0.0046	0.4107	0.0014	0.0035	0	0	0.0092	0.4728	0.0071	0.0151	0.6142	0.0065	0.0105	0.2183	0.0077	0.0351
LPL	0.0979	0.001	0.0102	0	0	0.0102	0.0658	0.001	0.0152	0.4799	0.0088	0.0184	0.1065	0.003	0.0282	0.0183	0.001	0.0546
LRG1	0.2486	0.0027	0.0108	0.3813	0.0013	0.0035	0.2775	0.004	0.0145	0.4505	0.0082	0.0181	0.1344	0.0068	0.0508	0.3752	0.0291	0.0777
LSAMP	0	0	0.0031	0	0	0.0031	0	0	0.0061	0	0	0.0031	0	0	0.0123	0.0721	0.0016	0.0218
LTA4H	0	0	0	0	0	0.0056	0	0	0.0075	0.1759	0.0024	0.0135	0.3441	0.0025	0.0073	0.4173	0.0058	0.0139
LTF	0.801	0.0056	0.0069	0.6234	0.0043	0.007	0.5546	0.0068	0.0123	0.4407	0.0102	0.0232	0.2432	0.0132	0.0542	0.6463	0.0591	0.0914
LYZ	0	0	0.0081	0	0	0.0082	0.7943	0.0065	0.0082	0.397	0.0033	0.0083	0.2086	0.007	0.0335	2.0817	0.0548	0.0263
LZTFL1	0.5486	0.0017	0.0032	999	0.0017	0	0.5532	0.0017	0.0031	0	0	0.0031	999	0.0017	0	0.2311	0.0052	0.0226
MAMDC2	0.2225	0.0007	0.0032	0	0	0.0016	0.1099	0.0007	0.0065	0.2546	0.0029	0.0112	0.1119	0.0029	0.0256	0.1055	0.0043	0.0408
MAN2A1	0.0788	0.0004	0.005	0.072	0.0004	0.0055	0.1639	0.001	0.0062	0.2058	0.0022	0.0106	0.2647	0.0059	0.0224	0.2615	0.0079	0.0303
MAN2B1	0.5834	0.0018	0.003	0.135	0.0013	0.0098	0.2666	0.0022	0.0083	0.1922	0.0053	0.0276	0.1252	0.0039	0.0311	0.1228	0.0093	0.076
MAN2B2	0.2051	0.0022	0.0109	0.1366	0.0046	0.0336	0.3643	0.004	0.0109	0.3219	0.013	0.0403	0.3225	0.036	0.1115	0.2168	0.0157	0.0722
MANBA	0.2868	0.0012	0.004	0.196	0.0021	0.0108	0.1432	0.0012	0.0081	0.3294	0.0049	0.015	0.2945	0.0044	0.0149	0.2426	0.0113	0.0465
MARCKS	0.27	0.0015	0.0055	0.5583	0.003	0.0053				0.0732	0.0029	0.0401	0.4171	0.0089	0.0213	0.03	0.0015	0.049
MATN2	0.2434	0.002	0.008	0.1474	0.0015	0.0099	0.0719	0.0005	0.0068	0.296	0.0048	0.0163	0.2143	0.004	0.0186	0.1758	0.0072	0.0407
MDH1	0	0	0.028	0	0	0	0	0	0.0293	0	0	0.0208	0.0014	0.0001	0.0442	0.0006	0.0001	0.0974
MDH2	0	0	0.0073	0.1879	0.0014	0.0073	0.2495	0.0028	0.011	0.1359	0.0028	0.0204	0	0	0.0481	0.1052	0.0083	0.0792
MFAP4	0.0001	0	0.0053				0.0001	0	0.0117	0.0881	0.0015	0.0175	0.0001	0	0.0311	0.0555	0.0049	0.0877
MGAM	0.2172	0.003	0.0138	0.17	0.0021	0.0125	0.192	0.0028	0.0147	0.2867	0.0055	0.0193	0.1187	0.0031	0.026	0.2518	0.0127	0.0506
MINPP1	0.1462	0.001	0.0069	0.5459	0.005	0.0092	0.215	0.001	0.0046	0.496	0.008	0.0162	0.2898	0.0091	0.0312	0.2787	0.0121	0.0435
MLPH	0.7484	0.0091	0.0122	0.256	0.0045	0.0175	0.8883	0.007	0.0079	0.5659	0.0165	0.0292	0.6719	0.0675	0.1005	0.5371	0.028	0.0522
MME	0.1502	0.0012	0.0083	0	0	0.0033	0	0	0.0154	0.0787	0.0012	0.0159	0.1703	0.0031	0.0184	0.0791	0.0038	0.0475
MMP14	999	0.0008	0	999	0.0008	0	0.0773	0.0009	0.0113	0.1584	0.0023	0.0145	0	0	0.0198	0.0545	0.0023	0.0424
MMP2	0.0359	0.0007	0.0184	0	0	0.0049	0	0	0.016	0.0541	0.0016	0.0289	0.1974	0.0087	0.044	0.0075	0.0007	0.0883
MMP7	0.1908	0.0018	0.0092	0.2874	0.0053	0.0184	0	0	0.0115	0.7144	0.0106	0.0148	2.8334	0.0143	0.005	0.1598	0.0106	0.0662
MPI	0	0	0.0029	0.3937	0.0011	0.0029	0	0	0.0029	0.3879	0.0045	0.0116	0	0	0.0186	0.2236	0.0102	0.0457
MPST	0.1068	0.0038	0.0355	0.0958	0.0013	0.0131	0.0542	0.0013	0.0231	0.2832	0.0127	0.045	0.1517	0.0068	0.0446	0.1606	0.0271	0.1688
MSLN	1.3756	0.0065	0.0047	0.3549	0.0056	0.0158	0.7044	0.0089	0.0127	0.4291	0.0168	0.0392	0.3429	0.0269	0.0784	0.3779	0.0393	0.1041
MSMB	999	0.0083	0	0	0	0.0111	999	0.0041	0	999	0.0249	0	0.8766	0.0127	0.0144	2.733	0.1094	0.04
MUC5B	0.4902	0.0108	0.0221	0.3281	0.0124	0.0377				0.3898	0.0251	0.0645				0.3183	0.0409	0.1286
MUC6	0.4668	0.0109	0.0234	0.3545	0.0097	0.0274	0.5023	0.0116	0.0231	0.2576	0.0133	0.0517	0.3028	0.0152	0.0501			
MYH9	0	0	0.0201	0.0403	0.0011	0.0276	0	0	0.0198	0.0342	0.0012	0.036	0.007	0.0004	0.0599	0.0062	0.0006	0.0891
MYO1C	0.164	0.0024	0.0146	0.2828	0.0079	0.0278	0.1266	0.0016	0.013	0.0384	0.0016	0.0419	0.0376	0.0021	0.0553	0.0089	0.0011	0.1271
NAGA	0.2761	0.0021	0.0077	0	0	0	0.1643	0.0032	0.0194	0.3432	0.0049	0.0142	0.1139	0.0049	0.043	0.1304	0.0089	0.0684
NAGLU	0.0572	0.0006	0.0103	0	0	0.0021	0.3977	0.0016	0.0041	0.0816	0.0022	0.0267	0.0306	0.0016	0.0523	0.1149	0.0079	0.0689
NAPA	0.0001	0	0.0137	0.0001	0	0.0045	0.0001	0	0.0153	0.0001	0	0.0215				0.0001	0	0.0712
NBL1	0.0019	0.0003	0.1464				0.0003	0	0.0106	0.0001	0	0.051	0.0014	0.0001	0.0719	0.0012	0.0002	0.1955
NCSTN	0	0	0.0099	0.7774	0.0013	0.0017	0	0	0.0034	0.2894	0.0047	0.0163	0.3571	0.0139	0.0388	0.0615	0.0027	0.0447
NELL1	0.6159	0.0022	0.0036	0.3894	0.0028	0.0073	0.376	0.0068	0.0182	0.2586	0.0036	0.0139	0.0856	0.002	0.0231	0.1267	0.0043	0.0337
NEO1	0.1735	0.0007	0.0038	0.1084	0.0007	0.0062	0.0593	0.0007	0.0118	0.246	0.0029	0.0119	0.1521	0.0031	0.0202	0.1439	0.0043	0.0297
NEU1	0	0	0	0	0	0.0147	0	0	0.0088	0.2337	0.0043	0.0185	0.2424	0.0037	0.0151	0.1999	0.0112	0.0562
NIF3L1	0.1562	0.0013	0.0083	0.3746	0.0013	0.0035	0.4041	0.0026	0.0064	0.1829	0.0026	0.0143	0.4667	0.0105	0.0226	0.3568	0.0132	0.037
NME3	0	0	0.027	0	0	0	0.1708	0.0047	0.0276	0	0	0.0716	0	0	0	0.032	0.0025	0.0783
NP	0.2137	0.0017	0.0079	0.2175	0.0017	0.0078				0.1984	0.0053	0.0269	0.4109	0.0051	0.0124	0.6688	0.0198	0.0296
NPC2	0	0	0.0076	0	0	0	0	0	0	1.2896	0.0098	0.0076	0	0	0.0075	0	0	0.0733
NPEPPS	0.0001	0	0	0.0001	0	0.0012				0.2227	0.0016	0.0072	0.2127	0.003	0.0142	0.0354	0.0006	0.0164
NRCAM	0.0674	0.0004	0.0054	0	0	0.0045	0.1806	0.0015	0.0082	0.127	0.0023	0.018	0.1037	0.0018	0.0177	0.153	0.0044	0.0288
NRP1	0.1248	0.001	0.0083	0.1079	0.001	0.0096	0.0539	0.0005	0.0096	0.1685	0.0025	0.0149	0.1302	0.0016	0.0126	0.0875	0.0041	0.0465
NUCB1	0	0	0.0045	0.3197	0.0011	0.0033	0.1813	0.003	0.0163	0.1048	0.003	0.0282	0.1051	0.0036	0.0344	0.1678	0.0151	0.09
NUCB2	1.2928	0.0017	0.0013	0	0	0.0043	0	0	0.0043	0.0718	0.0009	0.0132	0.089	0.0019	0.0219	0.9334	0.0575	0.0617
NUTF2	0	0	0.0106	0	0	0	0	0	0	0	0	0.0214	0	0	0	0.3654	0.0552	0.1511
ODZ2	0.0521	0.0003	0.0064	0	0	0.008	0.0369	0.0003	0.0092	0.0161	0.0003	0.0207	0.0294	0.0008	0.0283	0.0136	0.0007	0.0489
OLFM1	0	0	0.0361	0.3943	0.0009	0.0023	0	0	0.0177	0.0404	0.0022	0.0534	0.059	0.001	0.0161	0.0282	0.003	0.108
OLFM4	0	0	0.0095	0.1308	0.0009	0.0071	0.2604	0.0037	0.0143	0.2672	0.0084	0.0314	0.5849	0.0105	0.018	0.6234	0.0276	0.0442
ORM1	0.3282	0.0068	0.0208	0.1096	0.0022	0.0205	0.404	0.0113	0.0279	0.2127	0.0186	0.0873	0.2433	0.0046	0.0191	0.5196	0.0363	0.0698
ORM2	0.6898	0.0377	0.0547	0.0991	0.0042	0.0419				0.2739	0.0224	0.0819	0.0717	0.0024	0.033	0.6666	0.038	0.057
OS9	0.0001	0	0.0035	0.83	0.0014	0.0017				0.1167	0.0031	0.0266	0.0998	0.0029	0.0287	0.1231	0.005	0.0407

Gene	HC_ω	HC_*Ka*	HC_*Ks*	GO_ω	GO_*Ka*	GO_*Ks*	Ogi_ω	Ogi_*Ka*	Ogi_*Ks*
IGHG4	0.0001	0	0.0446						
IGJ	0	0	0	0	0	0	0.8908	0.006	0.0067
IGKC	999	0.0182	0	0.7747	0.0267	0.0345	0.8274	0.0124	0.015
IGLV1-40	0.0001	0	0.0345						
IL1R1	0	0	0.0065	0	0	0.0052	0.0806	0.0007	0.0086
IL1RAP	0	0	0.004	0	0	0.0075	0.0963	0.0007	0.0074
IL1RL1	0.316	0.0008	0.0025	0.4047	0.0066	0.0163	649.0182	0.0035	0
IL6ST	0.216	0.0015	0.007				0.1919	0.0005	0.0024
IMPA1	0.321	0.0013	0.0042				999	0.0015	0
INHBB	0.3756	0.002	0.0052						
IQGAP1	0	0	0.0044	0.0396	0.0003	0.0072	0	0	0.0029
IQGAP2	0.4897	0.0003	0.0006	0	0	0.0035	1.0053	0.0006	0.0006
ITIH5	0	0	0.0041	0.1292	0.0026	0.0199	0.4045	0.0013	0.0033
KAL1	0	0	0.0025	0.2291	0.0015	0.0064	0.1745	0.0007	0.0038
KIF5B	0.1282	0.0004	0.0034	0.7538	0.0013	0.0018	0.1366	0.0004	0.0032
KLK11	0	0	0	0.2136	0.0061	0.0285	0	0	0.0081
KLK2	0.7994	0.0109	0.0137						
KLK3	999	0.002	0	0	0	0.0232	999	0.0068	0
KPNB1	0	0	0	0	0	0.0096	0	0	0
KRT1	999	0	0	0.0832	0.0007	0.0017	0.7954	0.0007	0.011
KRT10	0	0.0031	0	0.4296	0.0014	0.0169	0.0673	0.0088	0.011
KRT5	0	0	0.0033	0.2226	0.0022	0.0097	0	0	0.0082
KRT8	0	0	0.007	0.0133	0.0002	0.0187	0.303	0.0053	0.0176
KRT9	0.3308	0.0021	0.0063	0.8309	0.0035	0.0042	999	0.0007	0
LAMA5	0.1034	0.0033	0.0321				0.1582	0.0017	0.0109
LAMB2	0	0	0.0024	0.2484	0.0024	0.0099	226.8173	0.0006	0
LAMC1	0.0976	0.0003	0.003	0.0597	0.0006	0.0106	0	0	0.0013
LAMP1	0.1284	0.0011	0.0083	0	0	0.017	0	0	0.0095
LAMP2	0	0	0.0091	999	0.0034	0	999	0.0011	0
LAP3	0	0	0	0	0	0.0083	0.1436	0.0008	0.0053
LCN1	0	0	0	0.1488	0.005	0.0338	999	0.0109	0
LCN2	0.1528	0.0023	0.015	0.401	0.0066	0.0165	30.6787	0.0025	0.0001
LCP1	0	0	0	0	0	0.0121	0	0	0.0031
LDHA	0	0	0	0	0	0.0129	0	0	0
LDHB	0	0	0	0	0	0.0039	0	0	0.0078
LDHC	999	0.0014	0	0	0	0.002	0.3889	0.0014	0.0036
LDLR	20.6666	0.0003	0	0.3421	0.0061	0.0177			
LEFTY2	0	0	0	0.2003	0.0045	0.0227	0.0718	0.0019	0.027
LGALS3	0	0	0	0.3599	0.003	0	0.1361	0.0061	0.0091
LGALS3BP	0	0	0.0156	999	0.0032	0.009	0.6715	0.0019	0.0139
LGMN	0	0	0.0027	0.0468	0.001	0.0223	0.1043	0.001	0.01
LIFR	0.0809	0.0004	0.005	0.1595	0.002	0.0127	0.2292	0.0008	0.0037
LIPA	999	0.0015	0	0.1288	0.0016	0.0124	4.7959	0.0095	0.002
LIPG	0.8871	0.002	0.0023	0.0984	0.0009	0.0093	0.171	0.0017	0.0099
LIPI	0.3108	0.0027	0.0088				999	0.0009	0
LMAN2	999	0.0012	0	0	0	0.005	0	0	0.0051
LNPEP	0.3527	0.0014	0.004	0.5356	0.0022	0.0041	2.5613	0.0026	0.001
LPL	0	0	0.0052	0.0514	0.001	0.0194	0	0	0.0071
LRG1	0	0	0.0072	0.5098	0.0066	0.0129	0	0	0.0115
LSAMP	0	0	0	0.1099	0.0014	0.0123	0	0	0
LTA4H	999	0.0008	0	0.0709	0.0008	0.0111	0	0	0.004
LTF	0.7992	0.0041	0.0051	0.4354	0.0084	0.0192	4.3504	0.0097	0.0022
LYZ	0	0	0.0081	999	0.0066	0	999	0.0029	0
LZTFL1	0	0	0.0032	0.1819	0.0017	0.0095	0	0	0
MAMDC2	0	0	0.0065	0	0	0.0017	0	0	0.0041
MAN2A1	999	0.0007	0	0.1203	0.0012	0.0103	0.1699	0.0004	0.0022
MAN2B1	0.1492	0.0004	0.0029	0.0529	0.0009	0.0166	0.1154	0.0005	0.004
MAN2B2	999	0.0008	0	0.212	0.0041	0.0195	0.1093	0.0012	0.0113
MANBA	999	0.0005	0	0.3289	0.0027	0.0081	0.4014	0.0011	0.0027
MARCKS	0.058	0.0015	0.0253				0.0001	0	0
MATN2	0	0	0.0027	0.2219	0.002	0.0092	0	0	0.0022
MDH1	0	0	0	0	0	0.0148	0	0	0.0109
MDH2	0	0	0	0	0	0.0113	0	0	0
MFAP4							0.0001	0	0
MGAM	0.1478	0.0003	0.0023	0.1648	0.0025	0.0153	0.4497	0.0019	0.0042
MINPP1	0.4553	0.001	0.0022	0	0	0.0093	0.336	0.002	0.006
MLPH	0.2738	0.0011	0.0041	0.1494	0.0043	0.0288	0.2308	0.0036	0.0156
MME	0	0	0.0066	0	0	0.0023	0	0	0.0046
MMP14	0	0	0.0069	0.3086	0.0015	0.005	0	0	0.0023
MMP2	0	0	0.0023	0	0	0.0124	0	0	0
MMP7	0	0	0.0056	0	0	0.0167	0	0	0
MPI	0	0	0	0	0	0.0087	0.6201	0.0011	0.0018
MPST	0	0	0.0204	0	0	0.0157	0.0421	0.0008	0.0199
MSLN	1.5848	0.0037	0.0024	0.2809	0.0107	0.0382	999	0.003	0
MSMB	0	0	0	0.7611	0.0085	0.0111	0	0	0.0313
MUC5B	0.4499	0.0176	0.039						
MUC6	0.3161	0.0027	0.0084	0.2622	0.0069	0.0264			
MYH9	0	0	0.0061	0	0	0.04	0.0472	0.0003	0.0058
MYO1C	0	0	0.0063	0.0186	0.0004	0.0209	0.1704	0.0026	0.0153
NAGA	0	0	0.0077	0.264	0.0025	0.0095	0	0	0.0063
NAGLU	0.0878	0.0007	0.0084	0.0445	0.0012	0.027	0.1903	0.0017	0.009
NAPA	0.0001	0	0	0.0001	0	0.0148			
NBL1							0.0001	0	0
NCSTN	0	0	0.0016	0.2417	0.0013	0.0056	139.9078	0.002	0
NELL1	0	0	0.0019	0.4562	0.0023	0.0051	105.3628	0.0006	0
NEO1	0	0	0.0012	0.227	0.0011	0.0047	0	0	0.0007
NEU1	0	0	0	0.0797	0.0014	0.0174	0	0	0.0155
NIF3L1	0	0	0	999	0.0026	0	0.3946	0.0052	0.0131
NME3	0	0	0	0	0	0.0432	0	0	0.0438
NP	0.4079	0.0034	0.0083				0.0001	0	0.0036
NPC2	0	0	0.0153	0	0	0.0077	0	0	0.0156
NPEPPS	0.0001	0	0.0048				0.0001	0	0.0026
NRCAM	0.2043	0.0004	0.0018	0	0	0.0072	0	0	0.0052
NRP1	0	0	0	0.4613	0.0011	0.0024	0.4393	0.0005	0.0012
NUCB1	0	0	0.0048	0	0	0.0095	0	0	0.0196
NUCB2	0	0	0	0	0	0.0131	0	0	0
NUTF2	0	0	0.0106	0	0	0.0108	0	0	0.0105
ODZ2	0.0454	0.0002	0.0037	0.0266	0.0002	0.0062	0	0	0.0037
OLFM1	0	0	0.004	0	0	0.0221	0	0	0.0134
OLFM4	0	0	0.0023	0.0553	0.001	0.0175	1.2721	0.0018	0.0014
ORM1	999	0.0047	0	0	0	0.0107	999	0.0045	0
ORM2	999	0.0021	0				999	0.0027	0
OS9	0.058	0.0007	0.0123				999	0.0007	0

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
P4HB	0	0	0.008	0.1045	0.0018	0.0168	0	0	0.0246	0.0672	0.0026	0.0395	0.1687	0.0056	0.0332	0.1062	0.0062	0.0583
PACSIN2	0.0695	0.0008	0.012	0.3143	0.0025	0.008	0.1413	0.0017	0.0119	0	0	0.0268	0	0	0.0633	0.2207	0.0531	0.2407
PAEP	0.4288	0.0047	0.0109	0.2273	0.0047	0.0206				0.32	0.0115	0.0361	0.6769	0.0188	0.0278	0.7411	0.0648	0.0874
PAICS	0.3491	0.0032	0.0092	0.7081	0.0021	0.003	1.0557	0.0034	0.0032	1.0304	0.0031	0.003	0.2481	0.0091	0.0365	0.1373	0.0044	0.0318
PAM	0.1519	0.001	0.0063	0.3807	0.0005	0.0013	0.5695	0.0014	0.0025	0.2973	0.0038	0.0129	0.4082	0.0051	0.0124	0.2526	0.0067	0.0266
Park7	0.0001	0	0.0119	0.4491	0.0026	0.0058				0.8832	0.0052	0.0059	0.0001	0	0	0.0001	0	0.0362
PCMT1	14.8633	0.0017	0.0001	0	0	0	0.4575	0.002	0.0043	0	0	0.0037	0	0	0.0152	0.0808	0.0035	0.0428
PDCD6	0.2481	0.0019	0.0078	0.3835	0.0059	0.0153				0.0978	0.0039	0.0397	0.2463	0.0098	0.0399	0.1437	0.0098	0.0685
PDCD6IP	0.0479	0.0005	0.0112	0	0	0.0027	0.0869	0.0006	0.0071	0.0589	0.0005	0.0091	0	0	0.0144	0	0	0.0216
PDGFA	0.474	0.0115	0.0243	0.5654	0.0038	0.0068	0.102	0.0023	0.0228				0.2382	0.0104	0.0438	0.2657	0.0276	0.1037
PDIA3	0	0	0.0051	0	0	0.0026	1.2193	0.012	0.0098	0	0	0.0125	0.1623	0.0018	0.0112	0.0699	0.0036	0.052
PEBP4	0.1082	0.002	0.0184	0.3247	0.006	0.0185	999	0.002	0	0.2287	0.0057	0.0249	0.4941	0.0176	0.0357	0.5013	0.0314	0.0627
PFAS	0.221	0.0018	0.0081	0.1948	0.0029	0.0147	0.1856	0.0021	0.0114	0.3301	0.0052	0.0157	0.4332	0.0067	0.0156	0.1322	0.008	0.0604
PFKP	0.0195	0.0006	0.0285	0.0388	0.0012	0.0302	0	0	0.0267	0.0604	0.0017	0.0276	0.1817	0.0159	0.0873	0.027	0.0024	0.0884
PFN1	0	0	0.0118	999	0.0134	0	0	0	0	0.2559	0.0061	0.0238	999	0.0061	0	0	0	0.0483
PFN2	0	0	0	0	0	0.0076	0	0	0	999	0.0024	0	999	0.0024	0	0	0	0.0076
PGAM2	0	0	0	0	0	0.0082	0.0652	0.0016	0.0246	0	0	0.0345	0	0	0.0415	0.0546	0.0048	0.0884
PGC	0.2546	0.0011	0.0044	555.765	0.0033	0	0	0	0.0132	0.1411	0.0072	0.0512	0.2579	0.0094	0.0364	0.1097	0.0118	0.1072
PGCP	0.4139	0.0031	0.0074	999	0.002	0				0.867	0.0081	0.0094	0.1772	0.0042	0.0237	0.2699	0.0061	0.0224
PGD	0	0	0.0127	0.25	0.003	0.012	0.189	0.0013	0.0068	0.2591	0.0122	0.0472	0.1971	0.007	0.0356	0.0148	0.001	0.0673
PGK1	0	0	0.003	0	0	0	0	0	0	0	0	0.003	0.8599	0.0149	0.0174	0	0	0.0466
PGK2	0.0001	0	0.0122	0.3636	0.0022	0.0061				0.2527	0.0022	0.0088	0.4203	0.004	0.0096	0.196	0.0086	0.0439
PGLS	0.3615	0.0018	0.0049	0	0	0.0206	0.1764	0.0024	0.0139	0.1093	0.0036	0.0325	0.0432	0.0018	0.0407	0.1799	0.0082	0.0454
PGM1	0.3821	0.0026	0.0067	0.1318	0.0009	0.0065	0.4089	0.0034	0.0084	0	0	0.0124	0.0849	0.0017	0.0201	0.0656	0.0034	0.0521
PGM2	0.0387	0.0007	0.0184	0.2172	0.0015	0.0068	0.7549	0.1022	0.1354	0.0243	0.0007	0.0292	0.138	0.0021	0.0155	0.103	0.0072	0.0695
PHGDH	0	0	0.0071	0.1845	0.0009	0.0047	0.369	0.0035	0.0095	0.0404	0.0009	0.0217	0.0894	0.0017	0.0196	0.078	0.0053	0.0675
PI15	0	0	0.0047	0	0	0.0095	0	0	0	0.2857	0.0055	0.0193	0.1268	0.0037	0.0289	0.0469	0.0018	0.039
PIGR	0.8323	0.0068	0.0082	0.6622	0.0024	0.0036	0.1413	0.0024	0.0169	0.3411	0.0136	0.0397	0.3142	0.008	0.0254	0.7224	0.0431	0.0596
PIP	0.4425	0.0035	0.0079	1.6648	0.0132	0.0079	999	0.0119	0	999	0.0122	0	1.3297	0.0437	0.0329	3.0585	0.1549	0.0507
PITPNA	0	0	0	0	0	0	0	0	0.0125	0	0	0.0119	0.0072	0.0001	0.0181	0.013	0.0029	0.2228
PKM2	0.9948	0.0022	0.0022	0	0	0.0045	0.1647	0.0015	0.009	0.1424	0.003	0.021	0.2325	0.0127	0.0547	0.089	0.0031	0.0347
PLA1A	0.1342	0.001	0.0078	0	0	0.0078	0.344	0.0045	0.013	0.3572	0.0074	0.0207	0.4088	0.0078	0.0192	0.5548	0.0359	0.0647
pla2g2A	999	0.0125	0	0	0	0.0402	0	0	0.0099	0.4717	0.0094	0.0199	0.6839	0.0122	0.0179	0.4188	0.0368	0.0878
PLA2G7	0.3499	0.001	0.003	999	0.0021	0	0.2256	0.0025	0.0109	0.5251	0.0031	0.006	0.0537	0.0007	0.0133	0.3968	0.0262	0.0659
PLOD2	999	0.0006	0	0.083	0.0006	0.0072	0	0	0.0125	0.242	0.0047	0.0194	0.1087	0.0024	0.0218	0.1058	0.0036	0.0337
PLOD3	0	0	0.0133	1.2993	0.0018	0.0014	0.195	0.0018	0.009	0.0466	0.0018	0.0377	0.2843	0.0147	0.0518	0.0668	0.0064	0.0965
PLXNB2	0.0441	0.0009	0.0196	0.115	0.0021	0.0187	0.0149	0.0004	0.0298	0.0336	0.0023	0.0675	0.1303	0.0135	0.1037	0.0448	0.0074	0.166
PODXL2	0.256	0.0011	0.0041	0	0	0.0045	0.8103	0.0016	0.002	0.1983	0.0052	0.026	0.2174	0.0061	0.0281	0.2925	0.0086	0.0294
PPAP2A	0.0001	0	0.004	999	0.0017	0	0.0001	0	0.012				0.0001	0	0.0121	1.0654	0.0086	0.008
PPIA	0	0	0.0082	0	0	0.0164	0.6718	0.0056	0.0083	0	0	0.0324	0	0	0.0088	0	0	0.0324
PPIB	0	0	0	999	0.0021	0	0	0	0.0122	0	0	0.0308	0.0856	0.0025	0.0292	0	0	0.0515
PPIC	999	0.0095	0	0	0	0.0104	999	0.0024	0	0.0775	0.0024	0.0304	0.2389	0.0071	0.0298	0.1796	0.0095	0.053
PPP1CC	0	0	0.0072	0	0	0	0	0	0.0074	0	0	0.0036	0	0	0.015	0	0	0.0183
PPP1R7	0	0	0.0069	0.1837	0.0013	0.0069	0	0	0.007	0.1504	0.0013	0.0085	0.0818	0.0013	0.0156	0.0312	0.0013	0.0412
PPP2CA	0	0	0	0.9823	0.0044	0.0044	0	0	0.0089	0	0	0.0271	0	0	0.0184	0	0	0.0416
PPP2R4	0.3313	0.0048	0.0145	0.5063	0.0037	0.0072	0	0	0.0041	0.0557	0.0012	0.0219	0.6322	0.055	0.087	0.1525	0.0074	0.0488
PPP5C	0.0382	0.0009	0.0223	0	0	0.0155	0.055	0.0008	0.0154	0.0334	0.0008	0.0254	0.1206	0.0034	0.0282	0.0146	0.0008	0.058
PPT1	999	0.0032	0	0	0	0.0111	0	0	0.0186	0.2154	0.0032	0.0148	0.1434	0.0036	0.0248	0.1293	0.0064	0.0494
PRCP	0.6477	0.0017	0.0027	999	0.0009	0	0	0	0.0054	0.3763	0.0035	0.0092	0.6082	0.0354	0.0582	0.3219	0.0098	0.0306
PRDX1	0	0	0	0	0	0.0112	0.4416	0.0033	0.0076	0	0	0.0112	999	0.0025	0	0	0	0.0345
PRDX2	0	0	0.0072	0	0	0	0	0	0	0.105	0.0022	0.0214	0.2902	0.023	0.0793	0	0	0.0619
PRDX4	0	0	0	0.7173	0.0079	0.011	0.3968	0.0017	0.0044	999	0.0017	0	0.3966	0.0035	0.0088	0.3923	0.007	0.0179
PRDX5	0.9131	0.0046	0.0051	0	0	0	0.4516	0.0046	0.0102	0.4529	0.0023	0.0051	0.108	0.0031	0.029	0.3902	0.0165	0.0424
PRDX6	0	0	0	0	0	0.0098	0	0	0.0098	0	0	0.0198	0.074	0.0022	0.0298	0.1094	0.0044	0.0405
PRKACA	0.0001	0	0.0095	999	0.0159	0	0.0001	0	0.0238	0.2491	0.0201	0.0807				0.1447	0.0146	0.1012
PRKAR1A	0	0	0.0154	0	0	0.003	4.7257	0.0012	0.0002	0	0	0.0233	0	0	0.0108	0.0275	0.0013	0.0459
PRKAR2A	0	0	0	0.3217	0.0022	0.0069	0.1613	0.0012	0.0072	0.3469	0.0036	0.0103	0.1419	0.0025	0.0174	0.234	0.0198	0.0846
PRKCSH	0.0403	0.0008	0.0204	0.13	0.0018	0.0141	0.2186	0.0033	0.015	0.0412	0.0016	0.0399	0.1494	0.0071	0.0473	0.0961	0.0099	0.1032
PROM2	0.4164	0.0037	0.009	0.112	0.0016	0.0143	0.3034	0.0048	0.0159	0.1524	0.0055	0.0359	0.3545	0.0255	0.0718	0.219	0.0224	0.1024
PROS1	422.1504	0.0007	0	0.3423	0.002	0.0059	1.1145	0.0054	0.0049	0.5083	0.0067	0.0131	0.2828	0.0034	0.0119	0.3569	0.018	0.0506
PRSS22	0.4328	0.0041	0.0096	0.2879	0.0014	0.0048	1.7378	0.0083	0.0048	0.1984	0.0055	0.0279	0.1947	0.0237	0.1217			
PRSS8	0	0	0.0116	0.4378	0.0026	0.0059	0.3198	0.0052	0.0162	0.3001	0.0109	0.0363	0.1972	0.0125	0.0634	0.3379	0.0222	0.0656
PSAP	0.1656	0.0009	0.0052	0	0	0.0026	0	0	0.0086	0.0384	0.0009	0.0226	0.2689	0.0072	0.0267	0.0993	0.0052	0.0524
PSAT1	0	0	0.0031	0.6321	0.0039	0.0062	0	0	0.0075	0.278	0.0026	0.0094	0.0502	0.0013	0.026	0.184	0.0079	0.0427
PSCA	0	0	0.0292	999	0.0034	0	999	0.0034	0	0	0	0.0733	0.1995	0.0034	0.017	0.1009	0.0217	0.2153
PSMA1	0	0	0.0176	0	0	0	0	0	0.0058	0	0	0.0129	0.328	0.0081	0.0248	0	0	0.0584
PSMA2	0	0	0	0	0	0	3.481	0.0184	0.0053	0	0	0.0053	0	0	0.0324	0	0	0.0435
PSMA3	0	0	0.0139	0	0	0	0.7521	0.0498	0.0662	0	0	0.014	0	0	0.0211	0	0	0.0211
PSMA4	0	0	0.0052	0	0	0	0	0	0.0053	0	0	0	0.2218	0.0035	0.0157	0	0	0.0773
PSMA5	0	0	0.0052	0	0	0	0	0	0	0	0	0.0052	0	0	0.0104	0	0	0.0262
PSMA6	0	0	0	0	0	0.018	0	0	0.006	0	0	0.012	0.5443	0.0147	0.027	0	0	0.0242
PSMA7	0.4053	0.0019	0.0047	0	0	0.0095	0	0	0.0047	0.0667	0.0019	0.029	0.141	0.0058	0.0412	0	0	0.0509
PSMB1	0.0001	0	0.0118	0.0001	0	0.0089				0.0001	0	0.0249	0.0001	0	0.0401	0.0001	0	0.111
PSMB2	0	0	0	0	0	0.0111	0.3957	0.0022	0.0055	0.0987	0.0022	0.0221	0	0	0.0148	0.1476	0.0111	0.075
PSMB4	0	0	0	0.4222	0.0018	0.0043	0	0	0.0043	0.4264	0.0037	0.0086	0	0	0.0131	0.0293	0.0018	0.0631
PSMB5	0.0001	0	0.0106				0.2586	0.0018	0.0071	0.0001	0	0.0062	0.0825	0.0018	0.0222	0.0718	0.0036	0.0508
PSMB6	0.1547	0.0021	0.0135	0	0	0.0045	0	0	0.009	0.1163	0.0021	0.0181	0	0	0.0135	0.0369	0.0021	0.0568
PSMB7	999	0.0018	0	0	0	0.0123	0.2841	0.0035	0.0124	0	0	0.0295	0.4549	0.0018	0.0039	0.0314	0.0018	0.0561
PSMB8	0.1588	0.0017	0.0108	0.2204	0.0034	0.0155	0.5071	0.0034	0.0068	0.975	0.0086	0.0088	0.5802	0.0104	0.0179	0.2534	0.0069	0.0271
PSMD14	0	0	0	0	0	0	0	0	0	0	0	0.0039	0	0	0.0039	0	0	0.0238
PSMD2	0	0	0.0083	0	0	0.0023	0.744	0.0016	0.0022	0.0542	0.0011	0.0201	0.0854	0.0011	0.0128	0.0251	0.0011	0.0435
PSME4	0.1235	0.0005	0.0042	0.33	0.0016	0.0047	0.0655	0.0005	0.0083	0.1221	0.0013	0.0103	0.0451	0.0008	0.0184	0.0925	0.0028	0.0305
PTGDS	0.0412	0.0021	0.0518	0.0764	0.0021	0.0279	0.0433	0.0021	0.0494	0.1392	0.0065	0.0465	0.0927	0.0021	0.0229	0.5776	0.0196	0.0339
PTN	0	0	0.014	0	0	0	0	0	0.014	0	0	0.0158	0.1801	0.0029	0.0158	0.0697	0.0028	0.0409
PTPRD	0.061	0.0005	0.0081	0	0	0.0058	0.2849	0.0034	0.0118	0	0	0.0107	0.1221	0.0035	0.0291	0.0473	0.0017	0.0365
PTPRF	0.0227	0.0007	0.0302	21.6957	0.0004	0	0.057	0.0007	0.012	0.0677	0.0021	0.0304	0.0468	0.0013	0.0274	0.05	0.0045	0.09
PTPRJ	0.8021	0.0015	0.0018	0.2411	0.0018	0.0076	0.2338	0.0026	0.0111	0.6306	0.0096	0.0152	0.3694	0.0115	0.0312	0.5178	0.036	0.0695
PTPRS	0.0241	0.0004	0.0178	0.1571	0.002	0.0129	0.0431	0.0008	0.0186	0.0208	0.0008	0.0369	0.1656	0.0123	0.0744	0.0038	0.0005	0.1213
PURA	0	0	0.0073	0	0	0	0	0	0	0	0	0	0.3227	0.0024	0.0075	0.0795	0.0012	0.0151
PYGB	0	0	0.02	0	0	0.0192	0.0955	0.0048	0.0504	0.1471	0.0072	0.0489	0.2355	0.0367	0.1557	0.0222	0.0029	0.1287
QPCT	0	0	0.0094	0.6503	0.004	0.0062	0	0	0.0063	0.5488	0.0082	0.0149	0.2566	0.0041	0.0158	0.168	0.0082	0.0485
QSCN6	0.7517	0.0031	0.0041	1.1067	0.0023	0.0021				0.3442	0.0107	0.0312	0.2095	0.006	0.0286	0.1647	0.0105	0.0636
RAB10	0	0	0	0	0	0.0068	0	0	0	0	0	0.0068	0	0	0	0	0	0.0079
RAB11B	0	0	0	0	0	0.0238	0	0	0.049	0	0	0.0524	0	0	0.0614	0	0	0.1438
RAB13	0	0	0.0066	0	0	0.0067	0	0	0.0133	0	0	0.0266	0	0	0.0338	0	0	0.0482
RAB14	0	0	0.007	0	0	0	0	0	0.0141	0	0	0	0	0	0.0214	0	0	0.0214
Rab18	0	0	0	0	0	0	0	0	0.0051	0.1526	0.004	0.0265	0	0	0.0156	0	0	0.0158

Gene	HC_ω	HC_Ka	HC_Ks	GO_ω	GO_Ka	GO_Ks	Ogi_ω	Ogi_Ka	Ogi_Ks
P4HB	0.3219	0.0009	0.0027	0	0	0.0029	0.0597	0.0009	0.0147
PACSIN2	0	0	0.0041	0	0	0.0223	0.1704	0.0017	0.0098
PAEP	999	0.0023	0				999	0.0056	0
PAICS	0	0	0.003	0.1869	0.0011	0.0061	0	0	0.0023
PAM	999	0.0005	0	0.1889	0.0014	0.0076	0	0	0.0013
Park7	0.0001	0	0.018				0.0001	0	0
PCMT1	0	0	0	0.4598	0.0017	0.0038	0	0	0
PDCD6	0.0946	0.0039	0.0412				0.0001	0	0.0245
PDCD6IP	0	0	0.0061	0.5938	0.0011	0.0018	0	0	0.006
PDGFA	0.7192	0.0044	0.0061						
PDIA3	0	0	0.0051	0	0	0.0082	0	0	0.0088
PEBP4	0	0	0	0.1843	0.0023	0.0124	0.5421	0.0036	0.0066
PFAS	0.2345	0.0004	0.0017	0.1437	0.002	0.0136	0.3947	0.0017	0.0043
PFKP	0	0	0.0061	0	0	0.0279	0	0	0.0106
PFN1	0	0	0	0	0	0	0	0	0
PFN2	0	0	0	0	0	0	0	0	0
PGAM2	0	0	0	0	0	0.0252	0	0	0.009
PGC	147.7895	0.0011	0	0.1004	0.0017	0.0171	0	0	0.0014
PGCP	0.3676	0.0011	0.003				0.5117	0.001	0.002
PGD	0	0	0.0051	0.1817	0.001	0.0055	0	0	0
PGK1	0	0	0.003	0.3679	0.0011	0.003	0	0	0
PGK2	0.1722	0.0011	0.0064				0.1996	0.0018	0.0092
PGLS	0	0	0.0074	0	0	0.0238	0.3206	0.0018	0.0055
PGM1	0	0	0	0	0	0.0113	0	0	0
PGM2	0	0	0.0026	0.0706	0.0007	0.0101	51.0326	0.0007	0
PHGDH	0	0	0.0047	0	0	0.0073	0	0	0.002
PI15	0	0	0	0	0	0.0048	0	0	0
PIGR	0.1061	0.0012	0.011	1.0475	0.0079	0.0075	0.3381	0.003	0.009
PIP	999	0.0046	0	1.2038	0.0095	0.0079	0	0	0
PITPNA	0.0005	0.0001	0.2549	0	0	0.1511	0	0	0.0142
PKM2	999	0.0007	0	0	0	0.009	0	0	0
PLA1A	999	0.0039	0	0.1279	0.0011	0.0083	0.078	0.0008	0.0105
pla2g2A	999	0.0062	0	0.6214	0.0062	0.01	0.1555	0.0037	0.0235
PLA2G7	0	0	0	0.3493	0.001	0.003	0.7608	0.0014	0.0018
PLOD2	0	0	0.0036	0	0	0.0042	0.2335	0.0012	0.0051
PLOD3	0	0	0.0021	0.0376	0.0012	0.0312	0	0	0.0036
PLXNB2	0.1053	0.0012	0.011	0.0592	0.0018	0.0301	0.0425	0.001	0.0229
PODXL2	0	0	0.0021	1.5892	0.0047	0.0029	0	0	0.0017
PPAP2A	0.0001	0	0						
PPIA	0	0	0	0	0	0.0089	0	0	0
PPIB	0	0	0	0	0	0	0	0	0.0055
PPIC	0.4582	0.0024	0.0051	0	0	0.0126	0	0	0.0095
PPP1CC	0	0	0	0	0	0.0036	0	0	0.0035
PPP1R7	0	0	0	0	0	0.0124	0	0	0.0035
PPP2CA	0	0	0	0	0	0	0	0	0.004
PPP2R4	0	0	0	0	0	0	0	0	0.0067
PPP5C	0	0	0	0.0261	0.0008	0.0324	0	0	0.0065
PPT1	0	0	0	0	0	0.0113	0	0	0
PRCP	0	0	0.0027	0.0579	0.0009	0.0151	0	0	0
PRDX1	0	0	0	0.2215	0.0025	0.0112	0	0	0
PRDX2	0	0	0.0071	0	0	0.0075	0	0	0.0135
PRDX4	0	0	0.0044	0	0	0.0132	0	0	0.0044
PRDX5	0	0	0.0102	0	0	0	0	0	0
PRDX6	0	0	0	0	0	0	999	0.0022	0
PRKACA	0.0001	0	0	0.0001	0	0.0047			
PRKAR1A	0	0	0	0	0	0.0142	0	0	0.0027
PRKAR2A	0	0	0	999	0.002	0	999	0.0022	0
PRKCSH	0	0	0.0025	0.2647	0.0025	0.0093	999	0.0016	0
PROM2	0.7822	0.0016	0.002	0.126	0.0025	0.02	86.8851	0.0012	0
PROS1	0	0	0.0017	0	0	0.0053	0.1388	0.0007	0.0047
PRSS22	999	0	0	0.195	0.0055	0.0282			
PRSS8	0.287	0.0013	0.0044	0.2488	0.0037	0.0149	356.2649	0.0042	0
PSAP	0	0	0	0	0	0.0112	0.532	0.0009	0.0016
PSAT1	0	0	0.0038	0.1092	0.0013	0.012	0	0	0.0089
PSCA	999	0.0035	0	0.3133	0.0104	0.0331	0	0	0.0165
PSMA1	0	0	0	0	0	0.0283	0	0	0
PSMA2	0	0	0	0	0	0.0053	0	0	0
PSMA3	0	0	0.0137	0	0	0.0142	0	0	0.0068
PSMA4	0	0	0.0078	0	0	0.0078	0	0	0
PSMA5	0	0	0	0	0	0.0156	0	0	0
PSMA6	0	0	0	0	0	0	0	0	0
PSMA7	0	0	0	0	0	0	0	0	0.0031
PSMB1	0.0001	0	0.0169				0.0001	0	0.0108
PSMB2	0.1975	0.0022	0.0111	999	0.0044	0	0	0	0
PSMB4	0	0	0.0087	0.2088	0.0018	0.0088	0	0	0
PSMB5							0.0001	0	0.0077
PSMB6	999	0.0021	0	0.2326	0.0021	0.009	0	0	0
PSMB7	0	0	0	0.2135	0.0018	0.0082	0	0	0.0127
PSMB8	0	0	0	0.6277	0.0069	0.0109	0	0	0.0042
PSMD14	0	0	0	0	0	0	0	0	0
PSMD2	0	0	0.0025	0	0	0.005	0	0	0.0002
PSME4	0	0	0	0.055	0.0005	0.0099	0.135	0.0003	0.0025
PTGDS	0	0	0	0.0725	0.0021	0.0294	0	0	0.0222
PTN	0	0	0	0	0	0.012	0	0	0
PTPRD	0.2058	0.0002	0.0012	0	0	0.0072	0	0	0.0005
PTPRF	0	0	0.0239	0	0	0.0105	169.7691	0.0003	0
PTPRJ	0.1085	0.0008	0.0071	0.2967	0.0036	0.0122	0.7569	0.0035	0.0046
PTPRS	0	0	0.0065	0.0091	0.0002	0.0233	0	0	0.0029
PURA	0	0	0	0	0	0.0226	0	0	0
PYGB	0	0	0.0013	0.019	0.0005	0.0248	0	0	0
QPCT	0	0	0.007	0.8775	0.0027	0.0031	0.3448	0.0013	0.0039
QSCN6	0.4372	0.0036	0.0083				0.7348	0.0039	0.0053
RAB10	0	0	0	0	0	0	0	0	0.0068
RAB11B	0	0	0	0	0	0.0377	0	0	0.0239
RAB13	0	0	0	0	0	0.0205	0	0	0
RAB14	0	0	0	0	0	0	0	0	0
Rab18	0	0	0	0	0	0.0053	0	0	0.0049

Gene	H_ω	H_Ka	H_Ks	C_ω	C_Ka	C_Ks	G_ω	G_Ka	G_Ks	O_ω	O_Ka	O_Ks	gi_ω	gi_Ka	gi_Ks	M_ω	M_Ka	M_Ks
RAB1A	0	0	0	0	0	0	0	0	0	0	0	0.0143	0.2042	0.005	0.0245	0	0	0
RAB1B	0	0	0	16.5974	0.0042	0.0003	1.6434	0.0169	0.0103	0	0	0.0643	0	0	0.0351	0	0	0.1002
RAB27A	0.8812	0.0044	0.005	999	0.0022	0	0	0	0.0152	0.4343	0.0022	0.0051	0	0	0.0264	0.1049	0.0044	0.0424
RAB27B	0	0	0	999	0.0022	0	0	0	0.0111	999	0.0043	0	0.2529	0.0043	0.0172	0	0	0.0341
RAB2A	0.077	0	0	0.0001	0	0				0.0001	0	0.0203	0.0001	0	0	0.0001	0	0.0308
RAB3B	0.1837	0.0021	0.0116	0	0	0	0	0	0.0117	0.0725	0.0021	0.0294	0	0	0.0178	0	0	0.0548
RAB3D	0.0829	0.002	0.0236	0	0	0.0158	0.2709	0.0019	0.0072	0.1133	0.0022	0.0194	0	0	0.0262	0	0	0.0916
RAB5B	0	0	0.0067	0	0	0	0	0	0	0	0	0.0137	0	0	0.007	0.4411	0.0339	0.0768
RAB5C	0	0	0	0.4381	0.002	0.0045	0.2173	0.002	0.0091	0	0	0.0229	0.0703	0.002	0.0279	0.1215	0.004	0.0325
RAC1	0	0	0.0052	0	0	0.0105	0	0	0.0105	0	0	0.0052	0.6704	0.007	0.0104	0	0	0.0158
RAD23B	0	0	0.0056	0.3086	0.0036	0.0116	0	0	0	0.0831	0.0012	0.0142	0.3416	0.006	0.0174	0.0331	0.0012	0.0356
RALA	0	0	0	0	0	0.0102	0.2793	0.0399	0.1428	0	0	0	0	0	0.0154	0	0	0.0154
RALB	0	0	0	0	0	0	0.3485	0.002	0.0058	0	0	0.0226	0	0	0.0064	0.1163	0.004	0.0346
RAP1B	0	0	0	0	0	0.007	0	0	0.007	0	0	0.0146	0	0	0.0072	0	0	0.0218
RBP4	0.0001	0	0.0178	0.0001	0	0.0186	0.0001	0	0.0095	0.0001	0	0.1116	13.8138	0.0046	0.0003			
RDX	0	0	0.0095	0	0	0.0023	0.6615	0.024	0.0363	0	0	0.0115	0.028	0.0007	0.026	0	0	0.0389
RELN	0.0608	0.0004	0.0069	0.3143	0.0029	0.0092	0.0613	0.0004	0.007	0.1066	0.0017	0.0163	0.0579	0.0011	0.0196	0.0763	0.0036	0.0473
RHOA	0	0	0	0	0	0	0	0	0	0	0	0.0104	0	0	0.0052	0	0	0.0211
RNASE1	0.2794	0.0057	0.0203	0.2759	0.0028	0.0101	0.2779	0.0028	0.0101	0.8323	0.0084	0.0101	0.0816	0.0027	0.0331	0.6647	0.0381	0.0574
RNASE4	999	0.003	0	0	0	0	0.3083	0.003	0.0098	0.041	0.003	0.0736	1.5983	0.0154	0.0096	0.15	0.0061	0.0409
RNASET2	999	0.0018	0	0.354	0.0018	0.0051	0	0	0.0051	0.1599	0.0054	0.0338	0.3666	0.0334	0.0911	0.1354	0.0109	0.0809
RPLP0	0	0	0.0039	0	0	0.0039	0.254	0.003	0.0117	0	0	0	0	0	0.0121	0	0	0.028
RRBP1	0.1486	0.0023	0.0155	0.1804	0.0018	0.0102	0.0379	0.0005	0.0122	0.0486	0.0018	0.0366	0.3276	0.0164	0.0499	0.0703	0.0046	0.0655
RTN4RL1	0	0	0.0284	88.3791	0.0044	0.0001	0.0223	0.0012	0.0553	0.0544	0.0026	0.0473	0.0544	0.0029	0.0535	0.0917	0.017	0.1855
RUVBL1	0	0	0.0025	0	0	0	0	0	0.005	0	0	0.0196	0	0	0.02	0	0	0.0355
RUVBL2	0	0	0.0162	0	0	0	0	0	0.0285	0.0241	0.0009	0.0382	0.0484	0.0018	0.0369	0	0	0.122
s100A11	0	0	0.0222	0	0	0.011	0	0	0	0	0	0.011	0	0	0.011	0.1479	0.0142	0.0961
SCGB2A1	0	0	0	999	0.0159	0	0.8851	0.0105	0.0119	0.6651	0.008	0.012	0.5574	0.0133	0.0239	0.1893	0.0352	0.1859
SCPEP1	0	0	0.0077	1.258	0.0065	0.0051	0.1051	0.0011	0.0102	0.1374	0.0021	0.0155	0.0838	0.0011	0.013	0.3163	0.0152	0.0481
SDC1	1.4125	0.0062	0.0044	0	0	0.0201	0	0	0.0274	1.4812	0.0113	0.0076	0.4428	0.005	0.0114	0.4218	0.0258	0.0611
SDCBP	999	0	0.0042	0.1518	0	0	0.0567	0.0015	0.0173	0.153	0.003	0.0187	0.1248	0.0015	0.0145	0.1157	0.0077	0.0387
SDCBP2	0	0.0077	0	0	0.0046	0.0302	0.0885	0.0017	0.0301	0.1633	0.0031	0.0199	0.1054	0.0039	0.0317	0.1987	0.0122	0.1052
SDK2	0.0593	0.001	0.0162	0.033	0.0006	0.0175	0.0538	0.0013	0.0251	0.0562	0.0018	0.032				0.036	0.0039	0.1087
SELENBP1	0.7042	0.0018	0.0025	0.2046	0.0027	0.0131	62.8351	0.0009	0	0.0629	0.0027	0.0425	0.1187	0.0036	0.0302	0.1262	0.0099	0.0782
SEMA3C	0	0	0.0048	0.0959	0.0006	0.0063	0.2569	0.0012	0.0048	0.3152	0.001	0.0032	0.0843	0.0022	0.0264	0.0829	0.0033	0.0396
SEMA3F	0.318	0.0017	0.0054	0.4263	0.0023	0.0054	0.2045	0.0023	0.0113	0.1141	0.0024	0.021	0.0823	0.0029	0.0348	0.0604	0.004	0.0669
SEMA7A	0.1347	0.0006	0.0048	0.4928	0.0055	0.0111	0.291	0.0044	0.015	0.0715	0.0021	0.0297	0.136	0.0039	0.0287	0.083	0.0053	0.0639
SEMG1	0.8763	0.0048	0.0054	0.9827	0.0075	0.0077	0.8838	0.0258	0.0292	1.0764	0.0536	0.0498	0.9978	0.018	0.0181	0.8213	0.061	0.0743
SEMG2	0.5395	0.0081	0.0151	1.8032	0.0109	0.0061	0.9225	0.0086	0.0093	0.6897	0.0145	0.0211	0.8705	0.0275	0.0315	1.9518	0.0627	0.0321
SEPP1	1.1821	0.0038	0.0032	0.5786	0.0038	0.0065				0.7347	0.0096	0.0131	0.5119	0.0135	0.0264	0.8735	0.0257	0.0295
SERPINA1	0.1287	0.0011	0.0087	0.2425	0.0023	0.0093	1.0652	0.0068	0.0064	0.17	0.0068	0.0402	0.5669	0.0131	0.0231	0.5016	0.0254	0.0506
SERPINA3	0.2922	0.0047	0.0162	0.8876	0.0066	0.0075	0.3216	0.006	0.0186	0.6779	0.0191	0.0282	1.0926	0.044	0.0403	0.7329	0.0443	0.0604
SERPINA4	999	0.003	0	0	0	0.0134	0.3735	0.0032	0.0086	0.6378	0.0069	0.0109	0.5154	0.0183	0.0355	0.1706	0.0125	0.0732
SERPINA5	0.1572	0.0032	0.0202	0.4342	0.0114	0.0262	0.394	0.0032	0.008	0.1679	0.0076	0.0452	0.1232	0.0064	0.0519	0.2354	0.0204	0.0867
SERPINA6	11.4808	0.0049	0.0004	0.2968	0.003	0.01	0.231	0.0031	0.0134	0.2542	0.0034	0.0135	0.3482	0.0105	0.0301	0.315	0.0211	0.0668
SERPINB5	0.2145	0.0025	0.0118	0	0	0.0039	0.1386	0.0025	0.0183	0.3541	0.0025	0.0072	0.3686	0.0038	0.0103	0.1527	0.0038	0.0249
SERPINB6	0	0	0	0.3938	0.0103	0.026	0.1722	0.0183	0.1063	0	0	0.02	0.108	0.0035	0.0327	0.0837	0.0083	0.0987
SERPINC1	0	0	0.0116	0.3368	0.002	0.0058	0.2232	0.002	0.0092	0.0948	0.0019	0.0205	0.1672	0.0039	0.0234	0.6596	0.0515	0.0781
SERPINF1	0.1852	0.0032	0.0173	0.0766	0.0011	0.0139	0.3039	0.0053	0.0175	0.1882	0.0085	0.0454	0.1171	0.0075	0.064	0.1193	0.0163	0.137
SERPING1	0.4806	0.0047	0.0099	152.4405	0.0009	0				0.3004	0.0057	0.0191	0.2564	0.0061	0.0239	0.37	0.0297	0.0802
SERPINI1	0.4124	0.0024	0.0057	0.4155	0.0012	0.0028	0.8154	0.0024	0.0029	0.2575	0.0024	0.0092	0.1991	0.0036	0.0179	0.4246	0.0107	0.0253
sez6L2	0.1711	0.001	0.0057	0.2133	0.0025	0.0115	0	0	0.0113	0.4607	0.007	0.0152	0.0671	0.0014	0.0211	0.0428	0.002	0.0475
SFN	0	0	0.0204	0	0	0	0	0	0.0101	0.0401	0.0016	0.0395	0	0	0.0237	0.0097	0.0016	0.1642
SH3BGRL2	0	0	0	0	0	0.0125	0.3374	0.0042	0.0126	0	0	0.0125	0	0	0	0	0	0.0383
SI	0.1024	0.001	0.0093	0.1832	0.0017	0.0091	0.1875	0.0033	0.0174	0.2405	0.0055	0.023				0.3978	0.0201	0.0504
SIL1	0.2289	0.002	0.0087	0.1681	0.002	0.0119	0.2577	0.003	0.0116	0.3535	0.0123	0.0347	0.3353	0.0158	0.047	0.1687	0.0091	0.0537
SLC15A2	0.2921	0.0013	0.0046	0.1092	0.0007	0.0061	999	0.0013	0	0.1305	0.002	0.0155	0.4392	0.0047	0.0108	0.3605	0.0095	0.0264
SLC1A1	0.1008	0.0009	0.0091	1.6249	0.0037	0.0023	0.4055	0.0018	0.0045	0.0325	0.0009	0.0281	0.045	0.0021	0.0458	0.1378	0.0052	0.0381
SLC35F2	0.1767	0.0013	0.0075	0.4488	0.0015	0.0032	0.2239	0.0029	0.013	0.433	0.0066	0.0153	0.2124	0.0026	0.0124	0.1324	0.0093	0.0703
SLC44A4	0.1771	0.0018	0.0101	0.121	0.0007	0.0061	0.1636	0.002	0.0122	0.2447	0.0045	0.0183	0.1378	0.0056	0.0408	0.1316	0.0085	0.0647
SLIT2	0	0	0.0096	0.1361	0.0012	0.0089	0.51	0.0028	0.0054	0.0387	0.0009	0.0238	0.2291	0.0055	0.024	0.0651	0.0035	0.0531
SLPI	0	0	0	0.3873	0.0072	0.0185	1.1906	0.0109	0.0092	0.0947	0.0036	0.0376	0.8633	0.018	0.0209	0.5355	0.0368	0.0688
SMOC2	0.1086	0.002	0.0184	0.0733	0.001	0.0141	0.2945	0.002	0.0068				0.0001	0	0.0251	0.1341	0.0072	0.0539
SMPD1	0.1276	0.0015	0.012	0.2775	0.0031	0.0111	0	0	0.0075	0.2005	0.0031	0.0153	0.3646	0.0104	0.0284	0.1745	0.0079	0.0455
smpdl3A	0.8616	0.0021	0.0025	999	0.0043	0	0.87	0.0026	0.003	0.151	0.0032	0.0213	0.3808	0.0076	0.0198	0.2956	0.0152	0.0513
SMPDL3B	0.3705	0.001	0.0028	0.1472	0.0021	0.014	0.1234	0.0021	0.0167	0.4978	0.0083	0.0167	0.2276	0.008	0.0352	0.6621	0.0486	0.0734
SMS	0	0	0.0067	6.0914	0.0012	0.0002	0.2246	0.0107	0.0477	0.1224	0.0013	0.0104	0.5884	0.0209	0.0355	0.0723	0.0026	0.0356
SOD1	0	0	0	0	0	0.0073	0.2129	0.0031	0.0147	0.5039	0.015	0.0298	0.5715	0.0097	0.0169	0.374	0.0194	0.0519
SOD3	0	0	0	0	0	0	0	0	0.0251	0.1661	0.0061	0.0369	0.0226	0.0031	0.1358	0.0906	0.019	0.2102
SORD	0.469	0.003	0.0064	0.797	0.0051	0.0064	0.3587	0.0088	0.0245	0.2114	0.0062	0.0291	0.1525	0.0059	0.039	0.1936	0.0133	0.0688
SORL1	0.1985	0.0021	0.0105	0.0638	0.0008	0.0132	0.1607	0.0023	0.0143	0.0921	0.0017	0.0186	0.1443	0.0028	0.0195	0.0815	0.0041	0.0501
SORT1	0.3965	0.0012	0.0029	0.1386	0.0012	0.0083	0	0	0.0099	0.3842	0.004	0.0105	0.171	0.003	0.0178	0.101	0.004	0.0399
SPACA3	0	0	0	1.0634	0.0065	0.0061	0	0	0.0307	1.2497	0.0152	0.0121	0.5291	0.0129	0.0245	0.8348	0.0371	0.0444
SPINK2	999	0.0056	0	999	0.0057	0	0	0	0	0.3816	0.0068	0.0177	0.3806	0.0119	0.0314	1.7	0.1354	0.0796
SPINT1	0	0	0.0172	0	0	0.0034	354.8307	0.0047	0	0.4218	0.0156	0.037	0.6253	0.0071	0.0113	0.1506	0.0139	0.0923
SPINT3	999	0.011	0	999	0.011	0	0	0	0.0265	0.1358	0.0055	0.0402	0.4141	0.0056	0.0134	5.0794	0.0689	0.0136
SPOCK3	0.0001	0	0.0065	0.3079	0.003	0.0097				0.1363	0.003	0.0219	0.1097	0.003	0.0273	0.0619	0.002	0.0321
SPON2	0.1821	0.0036	0.02	0.0001	0	0.0067				0.1809	0.0049	0.0268	0.0582	0.0036	0.0621	0.1084	0.0098	0.0907
ST14	0.0386	0.0009	0.0245	0.1009	0.0024	0.0237	0.1345	0.0032	0.0237	0.0359	0.0018	0.0507	0.1258	0.0077	0.0613	0.0745	0.0079	0.1065
STEAP2	0.2641	0.002	0.0074	0.2707	0.002	0.0072	0	0	0.0054	0.1021	0.001	0.0096	0.257	0.0029	0.0115	0.0792	0.0024	0.0304
STXBP2	0.1281	0.0014	0.011	0.0553	0.0014	0.0255	0.3088	0.0035	0.0114	0.0352	0.0021	0.0596	0.0531	0.0024	0.0443	0.0458	0.0035	0.0775
SYT1	0	0	0.0075	0	0	0.0049	0.0936	0.0012	0.0126	0.0942	0.0012	0.0125	0	0	0.0177	0	0	0.028
SYT7	0	0	0.0097	1.0649	0.0051	0.0048	0	0	0.0224	0.0576	0.0017	0.0293	0.0737	0.0025	0.0336	0.0389	0.0026	0.0667
TAGLN2	0	0	0.0067	0	0	0.0134	0	0	0	0	0	0.0274	0.2616	0.0071	0.0271	0	0	0.0638
TALDO1	0	0	0.004	0.2267	0.0027	0.012	0.1699	0.0014	0.008	0.148	0.0027	0.0237	0.149	0.0051	0.034	0.0556	0.0027	0.0487
TCP1	0	0	0.0075	0	0	0	0	0	0.0076	0.0349	0.0008	0.0229	0.063	0.0008	0.0127	0.0223	0.0008	0.036
TEX101	999	0.0045	0	0.8606	0.0068	0.0079	0.2542	0.003	0.0119	1.8166	0.0149	0.0082	0.5542	0.0135	0.0244	1.9287	0.035	0.0182
TF	0.1799	0.0013	0.0074	0.3006	0.002	0.0066	0	0	0.0062	0.3787	0.0109	0.0288	0.7706	0.0227	0.0294	0.4881	0.0299	0.0613
TFPI2	0.1243	0.0019	0.0154	0	0	0	0.3774	0.0039	0.0102	0.9439	0.0096	0.0102	0.3675	0.006	0.0162	0.6871	0.0254	0.037
TFRC	0	0	0	0.8377	0.0025	0.003	0.0411	0.0006	0.0153	0.292	0.0044	0.015	0.2897	0.008	0.0274	0.1681	0.0214	0.1273
TGFB1	0	0	0.0087	0	0	0	0	0	0.0087	0	0	0.0267	0.0484	0.0022	0.0447	0	0	0.0837
TGFB3	0	0	0.0034	0	0	0.0034	0	0	0.0102	0	0	0.0146	0	0	0.0182	0.0648	0.0011	0.0167
TGFBR3	0.0548	0.0006	0.0105	0.4406	0.0029	0.0065	0.1102	0.0006	0.0052	0.1973	0.0029	0.0146	0.1726	0.0023	0.0134	0.216	0.0088	0.0407
TGM4	1.1356	0.004	0.0035	999	0.003	0	0.4906	0.0068	0.0139	0.0827	0.0033	0.0394	0.3465	0.0076	0.022	0.6471	0.0214	0.0331
THBS1	0.0702	0.0004	0.0055	0.2146	0.0008	0.0036	0	0	0.0129	0.0767	0.0012	0.0151	0.048	0.0012	0.0242	0.0271	0.0019	0.0714
THBS2	0	0	0.0102	0.1318	0.0012	0.0091	0.0481	0.0008	0.016	0.0647	0.0031	0.0473	0.1403	0.0084	0.06	0.0494	0.0053	0.1082
THBS4	0.1475	0.001	0.0065	0.3689	0.0039	0.0105	0.2771	0.0014	0.0052	0.0495	0.001	0.0207	0.0916	0.0025	0.0274	0.158	0.0075	0.0476
TIMP1	0.5104	0.0064	0.0125	1.2018	0.005	0.0041				0.9599	0.0143	0.0149				1.7404	0.0267	0.0153
TIMP2	0	0	0.0095	0.1972	0.0038	0.0193	0	0	0.0218	0	0	0.0391	0.0481	0.0038	0.0784	0	0	0.0786
TIMP3	0	0	0.0412	0	0	0	0	0	0.0102	0	0	0.0422	999	0.0039	0	0	0	0.0638
TKT	0.056	0.0007	0.0123	0.0463	0.0007	0.0149	999	0.0007	0	0.0236	0.0007	0.029	0.0204	0.0007	0.0352	0.0232	0.0021	0.0897
TMC5	0.8635	0.0048	0.0055	0.4817	0.0044	0.0091	0.3152	0.003	0.0095	0.1757	0.0048	0.0271	0.6704	0.0145	0.0216	0.4052	0.0197	0.0485
TMEFF2	0	0	0	0	0	0.0029	0	0	0.0034	0.1348	0.0027	0.0197	0.1404	0.0013	0.0095	0.0964	0.0013	0.0138
TMEM8	0.1434	0.0034	0.0235	0.0518	0.0011	0.0215				0.0671	0.003	0.0454	0.1618	0.0112	0.0689	0.1239	0.0171	0.1378
tmpRSS2	2.1237	0.0052	0.0025	1.2384	0.0061	0.005	0.156	0.0028	0.0178	0.4689	0.0122	0.026	0.4426	0.0138	0.0311	0.4906	0.0449	0.0916
TNFSF10	0.1391	0.0017	0.0123	0.8375	0.0034	0.0041	0	0	0	0.2737	0.0036	0.013	0.6946	0.0086	0.0124	0.2856	0.0137	0.0478
TOLLIP	0	0	0	0.1031	0.0019	0.0184	0.4166	0.0128	0.0308	0	0	0.0666	0	0	0.0388	0.0084	0.0014	0.1724
tor1B	0	0	0.0078	0.3498	0.0014	0.0039	0	0	0	0	0	0.0277	0.1484	0.0041	0.0276	0.0929	0.0041	0.044
TPS3I3	0.2165	0.0015	0.0068	0.4262	0.0015	0.0034	0	0	0.0069	0.0263	0.0007	0.0273	0.1076	0.0022	0.0207	0.3888	0.0159	0.0409
TPI1	0	0	0.01	0	0	0.0101	0.7428	0.0038	0.0051	0	0	0.0146	0	0	0.0219	0.1377	0.0095	0.0692
TPP2	0	0	0.0058	0.1437	0.0014	0.01	0	0	0.0079	0	0	0.027	0.1909	0.0032	0.0169	0.229	0.0139	0.0608
TPT1	0	0	0	0	0	0	0	0	0	0	0	0	0.7448	0.0204	0.0274	0	0	0.0243
TSG101	0	0	0.0033	0	0	0	0	0	0	0.1223	0.0024	0.0193	0	0	0.0203	0	0	0.0259
TSN	0	0	0.0049	0.3519	0	0	0	0	0.0049	0	0	0.0049	0.1389	0	0.01	0.1022	0	0.015
TSNAX	0	0	0	0	0.0016	0.0045	0	0	0.0045	0	0	0.0045	0	0.0032	0.0228	0	0.0048	0.0466
TSTA3	0.0876	0.0013	0.0152	1.0489	0.0053	0.0051	0.7907	0.004	0.0051	0.0598	0.0027	0.0451	0.0272	0.0014	0.0498	0.0738	0.004	0.0548
TTR	0.877	0.0067	0.0077	0.2907	0.0068	0.0232	0.8806	0.0068	0.0077	1.2446	0.0094	0.0075	0.9772	0.0075	0.0077	0.7448	0.0231	0.0311
TUBB1	0.3361	0.002	0.006	0	0	0.006	0.1116	0.001	0.009	0.0586	0.002	0.0346	0.1366	0.004	0.0295	0.0366	0.003	0.0831
TWSG1	999	0.002	0	0	0	0	0	0	0.006	0	0	0.0182	0	0	0.0061	0	0	0.037
TXN	0	0	0	0	0	0.0096	0	0	0	0	0	0.0096	0	0	0.0295	2.131	0.0203	0.0095
UBE2L3	0	0	0.0219	0	0	0	0	0	0.0145	0	0	0.0122	0.4665	0.0127	0.0271	0	0	0.0168
UBE2N	0.0001	0	0	0.0001	0	0				0.0001	0	0	0.0001	0	0.0094	0.0001	0	0.0188
UGCGL1	0.2341	0.0009	0.004	0.2898	0.0006	0.0021				0.1989	0.0029	0.0146	0.113	0.0016	0.0139	0.1293	0.0072	0.0559
UGDH	0	0	0.0052	0	0	0.0025	0.1198	0.0009	0.0078	0	0	0.0128	0	0	0.0053	0.0349	0.0019	0.0537
USP14	0	0	0.0074	0	0	0.0025	1.1674	0.0029	0.0025	0.1935	0.0029	0.0148	0	0	0.0135	0	0	0.0151
VAMP2	0	0	0.0119	0	0	0	0	0	0.0119	0	0	0	0	0	0.0123	0	0	0.0121
VAMP8	0	0	0.0237	0	0	0	0	0	0.0238	0	0	0.0236	0	0	0.0121	0	0	0.0366
VAT1	1.2852	0.0046	0.0036	0.9618	0.0034	0.0036	0.1593	0.0011	0.0071	0.1595	0.0035	0.0217	0.0893	0.0023	0.0257	0.0985	0.0115	0.1168
VCL	0	0	0.0038	0	0	0.0019	0	0	0.0058	0	0	0.0249	0	0	0.025	0	0	0.0517
VCP	0	0	0.009	0	0	0.0151	0	0	0.0045	0	0	0.0117	0.11	0.0018	0.016	0.0173	0.0006	0.0337
VPS28	0	0	0.0333	0.2058	0.0018	0.0086	0.1379	0.0037	0.0267	0.0844	0.0091	0.1075	0.073	0.0072	0.0983	0.0255	0.0053	0.2079
VTN	0.2411	0.0028	0.0117	0	0	0.0059	0.4053	0.005	0.0122	0.553	0.0082	0.0148	0.4484	0.0152	0.0339	0.4723	0.0311	0.0659
VWA1	0.1108	0.007	0.0635										0.136	0.0051	0.0378	389.7548	0.0127	0
VWF	0.1486	0.0017	0.0116	0.2431	0.0027	0.0111				0.17	0.0045	0.0266				0.1548	0.0131	0.0848
WFDC2	0	0	0.0138	0	0	0	0	0	0	0.493	0.0139	0.0281	0.1269	0.0035	0.0278	0.1947	0.0245	0.1257
WFDC8	0.3673	0.0038	0.0104	0.4881	0.0077	0.0158	0.7377	0.0038	0.0052	0.3598	0.0071	0.0197	0.285	0.0104

Gene	HC_ω	HC_*Ka*	HC_*Ks*	GO_ω	GO_*Ka*	GO_*Ks*	Ogi_ω	Ogi_*Ka*	Ogi_*Ks*
RAB1A	0	0	0	0	0	0.0143	0	0	0.0071
RAB1B	0	0	0	0	0	0.0184	0	0	0
RAB27A	0	0	0	0	0	0.005	0.4941	0.0022	0.0045
RAB27B	0	0	0.0056	999	0.0043	0	0	0	0.005
RAB2A	0.0001	0	0.0202				0.0612	0	0
RAB3B	0	0	0.0057	0	0	0.0245	0	0	0
RAB3D	0.2432	0.0019	0.008	0	0	0.0307	999	0.0019	0
RAB5B	0	0	0	0	0	0.0199	0	0	0
RAB5C	0	0	0	0	0	0.0045	0	0	0
RAC1	0	0	0	0	0	0	0	0	0
RAD23B	0	0	0.0115	0	0	0.003	0.2665	0.0024	0.0089
RALA	0	0	0.0261	0	0	0	0	0	0
RALB	0	0	0.0057	0.165	0.002	0.0122	0	0	0.0058
RAP1B	0	0	0	0	0	0.0069	0	0	0.0144
RBP4	0.0001	0	0	0.0001	0	0.0645			
RDX	0	0	0.0071	0	0	0.0027	3.3545	0.0007	0.0002
RELN	0.0449	0.0001	0.0031	0.0801	0.0007	0.0089	0.0803	0.0003	0.0034
RHOA	0	0	0	0	0	0	0	0	0.0052
RNASE1	999	0.0028	0	0	0	0.0207	0.5612	0.0056	0.0099
RNASE4	0	0	0	0.3067	0.003	0.0099	0.2902	0.003	0.0102
RNASET2	0	0	0.0154	0.2232	0.0018	0.008	999	0.0035	0
RPLP0	0	0	0.0039	0	0	0	0	0	0.0036
RRBP1	32.817	0.0005	0	0.0574	0.0005	0.0093	0.1644	0.0011	0.0066
RTN4RL1	0	0	0.016	0.0576	0.0027	0.0473	0.0554	0.0027	0.0483
RUVBL1	0	0	0	0	0	0.0139	0	0	0.0043
RUVBL2	0	0	0	0	0	0.0336	0	0	0.0192
s100A11	0	0	0	0	0	0	0	0	0
SCGB2A1	999	0.0107	0	999	0.0134	0	0	0	0
SCPEP1	999	0.0011	0	0.2121	0.0011	0.0052	0.6379	0.0032	0.0051
SDC1	0	0	0	0.4984	0.0073	0.0146	999	0.0046	0
SDCBP	0.5719	0	0	999	0.0015	0.0073	0	0	0.0039
SDCBP2	0	0.0029	0.005	0.2081	0.0015	0	0	0	0
SDK2	0.0001	0	0.0034	0.0314	0.0008	0.0242			
SELENBP1	0	0	0.0078	0.0404	0.0009	0.0218	50.7503	0.0009	0
SEMA3C	0.3909	0.0006	0.0016	0.0338	0.0002	0.0064	0.2326	0.0006	0.0026
SEMA3F	0.0673	0.0006	0.0084	0.1016	0.0011	0.0112	0	0	0.0128
SEMA7A	0.1193	0.0008	0.007	0	0	0.0288	0.0817	0.0011	0.0133
SEMG1	0	0	0.0048	1.6941	0.0067	0.004	0.7718	0.0101	0.0131
SEMG2	0	0	0	0.5551	0.0104	0.0188	2.2016	0.0078	0.0036
SEPP1	0.6684	0.0044	0.0065				0.7122	0.0025	0.0036
SERPINA1	0.3756	0.0023	0.006	1.7488	0.0102	0.0058	0.6837	0.0045	0.0066
SERPINA3	999	0.0009	0	1.2569	0.0103	0.0082	0.1344	0.0018	0.013
SERPINA4	0	0	0.0027	0.3979	0.0032	0.0081	0	0	0.0002
SERPINA5	999	0.0011	0	0.1329	0.0021	0.0158	0.2726	0.0031	0.0115
SERPINA6	0	0	0	0.2897	0.006	0.0207	26.6083	0.0011	0
SERPINB5	0	0	0.0031	0	0	0.0097	0	0	0.006
SERPINB6	0	0	0	0.1608	0.0024	0.0146	0.315	0.0047	0.015
SERPINC1	0.2526	0.001	0.0039	0	0	0.0077	0	0	0
SERPINF1	0	0	0	0	0	0.0122	0.1562	0.0011	0.0069
SERPING1	0.1978	0.0047	0.0237				232.5427	0.0019	0
SERPINI1	0	0	0.0028	0	0	0.0256	0	0	0
sez6L2	0.3124	0.0005	0.0016	0.0354	0.0005	0.0155	0	0	0.0045
SFN	0	0	0	0	0	0.0115	0	0	0.0217
SH3BGRL2	0	0	0	0	0	0	0	0	0
SI	168.0285	0.0003	0	0.1752	0.0032	0.0185			
SIL1	0.3519	0.001	0.0028	0.2339	0.003	0.0127	0	0	0.0235
SLC15A2	0	0	0.0015	0.3287	0.002	0.0061	0.1352	0.0007	0.0049
SLC1A1	0	0	0	0	0	0.0159	1.3122	0.0021	0.0016
SLC35F2	0	0	0	0	0	0.0076	0	0	0.0027
SLC44A4	0	0	0.0034	0.3864	0.0037	0.0096	0.4768	0.0019	0.004
SLIT2	0	0	0.0011	0	0	0.0071	0	0	0.002
SLPI	999	0.0035	0	0.9033	0.0183	0.0203	0.4359	0.0036	0.0082
SMOC2	0.0001	0	0.0026						
SMPD1	0.3959	0.0008	0.0019	0.1543	0.0015	0.0099	1.3236	0.003	0.0023
smpd3A	308.805	0.0011	0	0.6543	0.0032	0.0049	0	0	0.0092
SMPDL3B	999	0.0031	0	999	0.001	0	0.2129	0.0035	0.0164
SMS	0	0	0.0101	0	0	0.0032	0	0	0.0028
SOD1	0	0	0	1.0055	0.0074	0.0073	999	0.0223	0
SOD3	999	0.0015	0	0	0	0.037	999	0.0015	0
SORD	0.6137	0.0028	0.0046	0.5735	0.0049	0.0085	1.4414	0.0028	0.002
SORL1	0	0	0.0011	0.0197	0.0002	0.0126	0.0929	0.0009	0.0093
SORT1	0	0	0	0.0747	0.0006	0.0077	0	0	0.001
SPACA3	0	0	0	0.7141	0.0131	0.0183	999	0.0045	0
SPINK2	0	0	0	999	0.0057	0	0	0	0
SPINT1	205.1624	0.0016	0	1.0433	0.0026	0.0025	0.3318	0.0023	0.007
SPINT3	0	0	0	0	0	0	999	0.0053	0
SPOCK3	0.0932	0.001	0.0107				0.1543	0.001	0.0064
SPON2	0.0883	0.0024	0.0274				139.8	0.0012	0
ST14	0.0932	0.0005	0.0057	0.1539	0.0034	0.0218	0.3137	0.0028	0.0091
STEAP2	0	0	0	0	0	0.0123	0	0	0.0057
STXBP2	0	0	0.0116	0	0	0.0273	0.2289	0.004	0.0173
SYT1	0	0	0	0	0	0.0075	0	0	0
SYT7	0	0	0.012	0	0	0.013	0	0	0.0051
TAGLN2	0	0	0	0	0	0	0	0	0
TALDO1	0	0	0	0.6031	0.0027	0.0045	0	0	0
TCP1	0	0	0.0024	0.045	0.0008	0.0178	0	0	0
TEX101	0	0	0	0.3706	0.0029	0.0078	0	0	0.0276
TF	0	0	0.0034	1.6397	0.0161	0.0098	0.7333	0.0047	0.0065
TFPI2	999	0.0019	0	999	0.0039	0	0	0	0.0049
TFRC	0.6354	0.0019	0.003	0.3233	0.0026	0.0081	0.5608	0.0018	0.0032
TGFB1	0	0	0.0044	0.0392	0.0011	0.0273	0	0	0
TGFB3	0	0	0	0	0	0.0094	0	0	0.0033
TGFBR3	0	0	0	0.0873	0.0006	0.0066	0.1796	0.0011	0.0064
TGM4	0.3374	0.0014	0.0041	0.2435	0.0039	0.0161	0.3726	0.0027	0.0074
THBS1	0.3562	0.0004	0.0011	0	0	0.0138	0.3055	0.0008	0.0025
THBS2	2.3708	0.0005	0.0002	0.0245	0.0007	0.0296	0	0	0.0049
THBS4	0	0	0.0013	0.0424	0.0005	0.0114	0	0	0.0036
TIMP1	0.1738	0.0036	0.0208						
TIMP2	0	0	0	0	0	0.0108	0	0	0.0123
TIMP3	0	0	0	0	0	0.0205	0	0	0
TKT	0.0551	0.0007	0.0125	0.0218	0.0007	0.0314	0	0	0.0065
TMC5	0.2666	0.0005	0.0018	0.3038	0.002	0.0066	0.3278	0.002	0.006
TMEFF2	0	0	0	0	0	0.0124	0	0	0
TMEM8	0.103	0.0049	0.0474				0.1278	0.0013	0.0102
tmprSS2	0.2656	0.0033	0.0126	0.9885	0.0113	0.0114	0.4629	0.004	0.0087
TNFSF10	0	0	0	0.41	0.0035	0.0084	0.9797	0.0039	0.0039
TOLLIP	0	0	0	0	0	0.0335	0	0	0.0579
tor1B	0	0	0	0	0	0.0039	0	0	0
TP53I3	0	0	0	0.7467	0.0052	0.0069	0	0	0.0035
TPI1	0	0	0.0051	0	0	0.0057	0	0	0.0046
TPP2	0	0	0.0042	0	0	0.0075	0	0	0.0023
TPT1	0	0	0	0	0	0	0	0	0.0078
TSG101	0	0	0	0	0	0.0071	0	0	0
TSN	0	0	0	0	0	0.02	0	0	0.0049
TSNAX	0	0	0.0045	0	0	0.009	0	0	0
TSTA3	0	0	0	0.1852	0.0054	0.0289	0	0	0.0038
TTR	0	0	0	0.2655	0.0041	0.0155	0	0	0.0078
TUBB1	0	0	0	0.0844	0.001	0.0119	0	0	0.0075
TWSG1	0	0	0	0	0	0.006	0	0	0.006
TXN	0	0	0	0	0	0	0	0	0
UBE2L3	0	0	0	0	0	0.0095	0	0	0
UBE2N	0.0001	0	0.0094				0.0001	0	0
UGCGL1	0.0896	0.0009	0.0105				0.105	0.0003	0.0029
UGDH	0	0	0	0	0	0.0026	999	0.0009	0
USP14	0	0	0	0	0	0.0075	0	0	0
VAMP2	0	0	0	0	0	0.0242	0	0	0.0123
VAMP8	0	0	0	0	0	0	0	0	0.0117
VAT1	0	0	0	0.207	0.0023	0.011	534.8138	0.0023	0
VCL	0	0	0.0027	0	0	0.0049	0	0	0.0021
VCP	0	0	0.0015	0	0	0.0049	0	0	0.0009
VPS28	0	0	0.0462	0.0933	0.0018	0.0188	0	0	0.0045
VTN	151.7758	0.0019	0	0.4937	0.0057	0.0116	11.9216	0.0024	0.0002
VWA1									
VWF	0.1574	0.0028	0.0179						
WFDC2	0	0	0.0138	999	0.0068	0	0	0	0.0286
WFDC8	0	0	0	871.6779	0.0101	0	586.3912	0.0067	0
WFDC9	0	0	0	0	0	0	0.4142	0.0055	0.0132
XPNPEP1	0	0	0.0017	0.2003	0.0008	0.0038	0	0	0.0015
YWHAB	0	0	0	0	0	0.0257	0	0	0
YWHAE	0	0	0	0	0	0	0	0	0
YWHAG	0	0	0	0	0	0.0235	0	0	0.0122
YWHAQ	0	0	0	0	0	0.009	0	0	0
YWHAZ	0	0	0	0	0	0	0	0	0
ZPBP	0	0	0	0.4048	0.0033	0.0082	1.0249	0.0034	0.0033

Seminal Branch Estimate – LRT

Human

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPG2	&2087.49423	&2125.08739	75.186328	0.12357	4.28323E&18	
MYH9	&8818.523976	&8849.010846	60.97374	0	5.78412E&15	
FCGBP	&26823.49122	&26849.94823	52.914026	0.2529	3.48472E&13	
PTPRS	&9652.446204	&9676.81043	48.728452	0.0243	2.93971E&12	
LAMA5	&19256.74154	&19277.85595	42.22881	0.135	8.1195E&11	
SDK2	&10118.71621	&10138.77084	40.109256	0.05912	2.40148E&10	
FLNB	&12658.44468	&12677.75522	38.621072	0.09018	5.14603E&10	
PLXNB2	&9382.96125	&9401.501	37.0795	0.04453	1.1341E&09	
FASN	&13845.64696	&13863.46785	35.641768	0.10855	2.37148E&09	
PFKP	&4126.722019	&4144.051695	34.659352	0.01941	3.92747E&09	
col12A1	&14644.82095	&14661.64921	33.65652	0.05979	6.57541E&09	
RELN	&16739.84453	&16756.51848	33.3479	0.06098	7.7061E&09	
IGF2R	&12687.98749	&12703.84934	31.723712	0.08515	1.77739E&08	
SLIT2	&7465.783352	&7481.262092	30.95748	0	2.63744E&08	
PYGB	&4724.613067	&4739.12928	29.032426	0	7.11769E&08	
LDLR	&4411.874898	&4425.985503	28.22121	0.0763	1.08212E&07	
PTPRF	&9059.890874	&9073.914206	28.046664	0.05915	1.18425E&07	
ACTN4	&4157.334568	&4171.240275	27.811414	0	1.33735E&07	
EEF2	&4122.159908	&4136.034187	27.748558	0	1.38151E&07	
COL6A2	&6171.00574	&6184.708925	27.40637	0.03886	1.64887E&07	
OLFM1	&2196.869188	&2210.008641	26.278906	0	2.95499E&07	
VWF	&13693.87454	&13706.98751	26.225948	0.15127	3.03714E&07	
CNTNAP2	&7123.048131	&7135.951755	25.807248	0.04948	3.77269E&07	
CPZ	&2997.996352	&3010.880769	25.768834	0.06131	3.84853E&07	
ST14	&4409.488042	&4422.070432	25.16478	0.03884	5.26347E&07	
ODZ2	&12811.04083	&12823.58775	25.093832	0.05218	5.46072E&07	
CDH1	&4608.21349	&4620.167219	23.907458	0	1.01079E&06	
AGT	&2690.679286	&2702.397664	23.436756	0.05588	1.29088E&06	
THBS2	&5837.851362	&5848.96977	22.236816	0	2.41008E&06	
FN1	&12062.91609	&12073.7392	21.646228	0.12835	3.27854E&06	
PTPRD	&9072.339032	&9083.034021	21.389978	0.06159	3.74725E&06	
AGRN	&10949.45022	&10959.27345	19.646478	0.12711	9.31749E&06	
LAP3	&3055.436611	&3065.250408	19.627594	0	9.41003E&06	
ATRN	&7589.239589	&7598.696969	18.91476	0.06378	1.36691E&05	
MUC5B	&33208.11735	&33217.44014	18.645572	0.49053	1.57412E&05	
GAA	&4986.309909	&4995.608687	18.597556	0.13423	1.61427E&05	
PLOD3	&3731.582662	&3740.791197	18.41707	0	1.77461E&05	
SI	&9015.471222	&9024.429702	17.91696	0.10295	2.30756E&05	
MMP2	&3195.116172	&3204.034573	17.836802	0.0358	2.40683E&05	
CAPN1	&3437.698369	&3446.475288	17.553838	0.05596	2.79286E&05	
COL6A1	&5766.135173	&5774.854458	17.43857	0.0839	2.96743E&05	
SORL1	&10868.65421	&10877.29747	17.286518	0.19729	3.2146E&05	
KRT5	&2977.926487	&2986.52389	17.194806	0.08145	3.37357E&05	
PGM2	&3780.252677	&3788.791259	17.077164	0.03651	3.58913E&05	
CLTC	&7273.694507	&7282.196449	17.003884	0	3.73034E&05	
ACE	&6850.208897	&6858.676103	16.934412	0.10081	3.86937E&05	
SPINT1	&2725.853552	&2734.273738	16.840372	0	4.06591E&05	
MGAM	&9728.830581	&9737.235425	16.809688	0.21455	4.13218E&05	
ACO1	&4247.295061	&4255.511948	16.433774	0	5.03796E&05	
COL18A1	&9614.416243	&9622.598148	16.36381	0.28816	5.22739E&05	
FBLN2	&5916.814427	&5924.942254	16.255654	0.15615	5.53442E&05	
PSMD2	&4157.472539	&4165.497334	16.04959	0	6.1705E&05	
GFRA2	&2075.949553	&2083.952925	16.006744	0	6.31172E&05	
HSPA8	&3010.867894	&3018.757539	15.77929	0	7.11774E&05	
ADAMTS1	&4874.019994	&4881.76208	15.484172	0	8.3199E&05	
C3	&8544.024886	&8551.753293	15.456814	0.16778	8.44121E&05	
CST3	&695.994144	&703.722279	15.45627	0	8.44364E&05	
PRKCSH	&2723.845462	&2731.50908	15.327236	0.03943	9.04037E&05	
VCP	&3670.541624	&3678.128122	15.172996	0	9.80963E&05	
GAS6	&3533.547903	&3541.124793	15.15378	0.103	9.90997E&05	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PPP5C	&2321.511042	&2328.948345	14.874606	0.03804	0.000114899	
PDCD6IP	&3899.599627	&3906.965373	14.731492	0.04782	0.000123958	
TIMP3	&904.866325	&912.169191	14.605732	0	0.000132511	
NCSTN	&3552.966309	&3560.254871	14.577124	0	0.000134538	
IQGAP1	&7510.524558	&7517.809196	14.569276	0.04864	0.000135099	
TPP2	&6055.238667	&6062.459481	14.441628	0	0.000144571	
RUVBL2	&2138.610301	&2145.444751	13.6689	0	0.000218036	
RTN4RL1	&2264.470128	&2271.284022	13.627788	0	0.000222862	
GDI2	&2124.552526	&2131.314457	13.523862	0	0.000235549	
TGFBR3	&4153.324491	&4160.016421	13.38386	0.0548	0.000253799	
ACTN1	&4234.274672	&4240.963806	13.378268	0	0.000254557	
CRTAC1	&3032.63018	&3039.260006	13.259652	0.08946	0.00027118	
ESD	&1287.092979	&1293.554079	12.9222	0	0.000324708	
GPC1	&2722.754297	&2729.211143	12.913692	0.0742	0.000326187	
GLG1	&5645.71795	&5652.076357	12.716814	0	0.000362383	
PGD	&2493.373103	&2499.674432	12.602658	0	0.000385199	
TMEM8	&4067.166956	&4073.318727	12.303542	0.137	0.0004521	
RRBP1	&4917.746832	&4923.889291	12.284918	0.1557	0.000456633	
PRKAR1A	&1752.543908	&1758.681008	12.2742	0	0.000459263	
CNTN3	&5074.751612	&5080.813673	12.124122	0.12177	0.000497738	
CPAMD8	&10032.55275	&10038.59897	12.092442	0.26805	0.000506266	
CLSTN1	&4930.415275	&4936.417589	12.004628	0.08677	0.000530686	
VPS28	&1273.80542	&1279.779834	11.948828	0	0.000546818	
RDX	&2859.262592	&2865.060953	11.596722	0	0.000660682	
A4GALT	&1745.201975	&1750.937797	11.471644	0	0.000706661	
KAL1	&3349.00017	&3354.735705	11.47107	0	0.00070688	
PTGDS	&982.12617	&987.7999	11.34746	0.04011	0.000755512	
ABP1	&4017.930488	&4023.573844	11.286712	0.16249	0.000780638	
ANPEP	&5015.761828	&5021.254413	10.98517	0.19946	0.000918439	
SERPINC1	&2497.965693	&2503.445712	10.960038	0	0.000930979	
CTSB	&1794.154208	&1799.551422	10.794428	0.0517	0.001018061	
CRYZ	&1748.544009	&1753.814287	10.540556	0.12861	0.001167833	
CD151	&1220.658224	&1225.919023	10.521598	0	0.001179874	
PGK2	&1981.509557	&1986.741033	10.462952	0	0.001217925	
MUC6	&13539.90399	&13545.06194	10.315896	0.47946	0.001318892	
FUCA2	&2249.790094	&2254.858032	10.135876	0	0.001454111	
OLFM4	&2760.106058	&2765.15029	10.088464	0	0.001492004	
KPNB1	&8991.438832	&8996.474889	10.072114	0	0.001505302	
NAGLU	&8597.216647	&8602.234933	10.036572	0.0579	0.001534625	
TKT	&8006.159168	&8011.119285	9.920234	0.05593	0.001634716	
NRCAM	&6122.158845	&6127.06873	9.81977	0.06746	0.001726459	
CANT1	&2223.057749	&2227.940896	9.766294	0.08189	0.001777404	
CPD	&6384.201195	&6389.058771	9.715152	0.13941	0.00182755	
ANXA2	&1663.214904	&1668.019143	9.608478	0	0.001936811	
DDB1	&5175.393611	&5180.187621	9.58802	0	0.00195851	
KRT1	&8124.368496	&8129.133887	9.530782	0.06962	0.00202054	
CCT7	&2534.196207	&2538.943401	9.494388	0	0.002061013	
IDE	&4640.541162	&4645.265447	9.44857	0	0.002113138	
MYO1C	&5452.622088	&5457.320256	9.396336	0.17035	0.002174195	
BAIAP2	&2717.114363	&2721.773027	9.317328	0.08856	0.002269968	
PSMA1	&1252.531792	&1257.125396	9.187208	0	0.002437124	
SMOC2	&2173.208773	&2177.771776	9.126006	0.10544	0.002520013	
MPST	&1728.967673	&1733.513064	9.090782	0.10754	0.00256901	
BGN	&1722.180789	&1726.700126	9.038674	0.04839	0.002643273	
CTSH	&1640.832201	&1645.348768	9.033134	0.06574	0.002651295	
KRT9	&8259.308925	&8263.817474	9.017098	0	0.002674657	
CD109	&7431.86144	&7436.347535	8.97219	0.18862	0.002741198	
ARSA	&2672.558234	&2677.007516	8.898564	0.06558	0.00285395	
CTSF	&2581.04679	&2585.457067	8.820554	0.116	0.002978562	
NBL1	&996.175547	&1000.533335	8.715576	0.05865	0.003155027	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CTSD	&2194.772362	&2199.086594	8.628464	0.06837	0.003309505	
GAPDH	&1562.408026	&1566.70581	8.595568	0	0.003369821	
ACLY	&5465.922146	&5470.216712	8.589132	0.07015	0.003381752	
GSN	&3874.738086	&3879.018922	8.561672	0.06337	0.00343314	
TCP1	&2481.435489	&2485.654228	8.437478	0	0.003675657	
GALNT6	&2888.734616	&2892.908719	8.348206	0	0.003860683	
HSPA5	&2989.964322	&2994.060795	8.192946	0	0.004205358	
NAPA	&1260.183833	&1264.256959	8.146252	0	0.004315025	
IGHG4	&1802.825862	&1806.890901	8.130078	0.30085	0.004353687	
GALC	&3333.311613	&3337.317362	8.011498	0.07638	0.004648127	
DPP4	&3556.675932	&3560.680161	8.008458	0.07655	0.004655937	
THBS1	&5464.4833	&5468.486879	8.007158	0.0711	0.00465928	
SFN	&1070.822025	&1074.823268	8.002486	0	0.004671317	
PSME4	&3502.570277	&3506.524355	7.908156	0.12557	0.004921241	
PHGDH	&2552.172146	&2556.093857	7.843422	0	0.005100596	
SMPD1	&3206.407269	&3210.309028	7.803518	0.12727	0.005214461	
SEMA3C	&3591.022149	&3594.840559	7.63682	0	0.005718865	
USP14	&2152.195179	&2156.012794	7.63523	0	0.005723909	
GNB1	&1523.455321	&1527.253946	7.59725	0	0.00584574	
NME3	&751.357821	&755.152521	7.5894	0	0.005871249	
P4HB	&2491.980253	&2495.774159	7.587812	0	0.005876423	
CLIC1	&1147.731847	&1151.50479	7.545886	0	0.006014724	
GSR	&2856.684528	&2860.434737	7.500418	0.12238	0.006168467	
GPD1L	&1727.389514	&1731.116301	7.453574	0	0.006331061	
APLP2	&3675.585058	&3679.296471	7.422826	0.08186	0.006440159	
PFAS	&6779.45741	&6783.149515	7.38421	0.22023	0.006579897	
LEFTY2	&2008.137462	&2011.817827	7.36073	0	0.006666372	
VCL	&5089.406436	&5093.083995	7.355118	0	0.006687212	
AKR1A1	&1503.497061	&1507.154626	7.31513	0	0.006837645	
EPHA5	&4895.278261	&4898.893674	7.230826	0.1353	0.007166223	
GOT1	&2038.824818	&2042.412265	7.174894	0	0.007393082	
MAN2A1	&5436.449344	&5440.030304	7.16192	0.07672	0.007446744	
MAN2B2	&5889.372112	&5892.950171	7.156118	0.20409	0.007470871	
IL1RAP	&3278.211444	&3281.788786	7.154684	0	0.007476847	
QPCT	&1825.880416	&1829.454779	7.148726	0	0.007501726	
XPNPEP1	&2971.432803	&2975.00185	7.138094	0.08782	0.007546332	
UBE2L3	&717.729687	&721.264441	7.069508	0	0.007840678	
SYT7	&2154.509937	&2157.963636	6.907398	0	0.008583982	
IGFBP2	&1366.735245	&1370.184042	6.897594	0	0.008631183	
NRP1	&4386.015769	&4389.429899	6.82826	0.13274	0.008972663	
A1BG	&2641.461098	&2644.854806	6.787416	0.25302	0.00918027	
LGMN	&2360.260179	&2363.641674	6.76299	0.16531	0.009306769	
SYT1	&1899.503686	&1902.884222	6.761072	0	0.009316777	
DPP7	&2587.916801	&2591.261502	6.689402	0.10363	0.009698773	
STXBP2	&3028.913609	&3032.236868	6.646518	0.07939	0.009934979	
PSMA3	&1295.403603	&1298.702573	6.59794	0	0.010209682	
YWHAG	&1078.462822	&1081.751373	6.577102	0	0.010329894	
ALDH1A1	&2396.967986	&2400.254203	6.572434	0	0.010357021	
PSCA	&648.005504	&651.281984	6.55296	0	0.010470982	
TGFB1	&1740.346885	&1743.578476	6.463182	0	0.011013226	
PRKACA	&1825.971251	&1829.199742	6.456982	0	0.01105172	
SERPINA5	&2277.696373	&2280.888391	6.384036	0.15801	0.011515128	
PACSIN2	&2694.183826	&2697.372576	6.3775	0.06935	0.011557612	
RBP4	&887.087521	&890.260114	6.345186	0	0.011770027	
CREG1	&1115.853725	&1119.023853	6.340256	0.08775	0.011802785	
CAT	&2660.416218	&2663.572663	6.31289	0.12154	0.01198633	
CNP	&1957.275256	&1960.398621	6.24673	0	0.012442279	
DDR1	&4202.239179	&4205.360606	6.242854	0	0.012469538	
ALCAM	&2705.223904	&2708.330352	6.212896	0.08925	0.012682299	
ACRBP	&3029.542428	&3032.647417	6.209978	0.18156	0.012703221	0.014040562

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PRSS8	&1905.983164	&1909.073188	6.180048	0	0.012919877	0.014118565
SCPEP1	&2263.890658	&2266.949277	6.117238	0	0.013386981	0.014196568
GNB2L1	&1451.515393	&1454.546423	6.06206	0	0.013811648	0.014274571
THBS4	&4699.192171	&4702.167261	5.95018	0.14747	0.014715783	0.014352574
C1RL	&2663.712395	&2666.636842	5.848894	0.17337	0.015586844	0.014430577
GNMT	&1451.160682	&1454.08051	5.839656	0	0.01566889	0.01450858
GP2	&2924.494699	&2927.405915	5.822432	0.14204	0.015823052	0.014586583
MME	&3524.33541	&3527.242878	5.814936	0.15016	0.015890632	0.014664587
ITIH5	&5267.277744	&5270.176193	5.796898	0.26992	0.016054474	0.01474259
PAM	&4585.460527	&4588.354043	5.787032	0.15185	0.016144824	0.014820593
ENO1	&2054.175071	&2057.065972	5.781802	0	0.016192932	
KRT8	&2765.236481	&2768.119867	5.766772	0.09428	0.016332007	
ADAM10	&3311.386429	&3314.261957	5.751056	0	0.016478748	
LPL	&2389.296785	&2392.168069	5.742568	0.09781	0.016558566	
SPOCK3	&2095.976732	&2098.821726	5.689988	0	0.017061971	
SLC1A1	&2564.786463	&2567.601943	5.63096	0.10075	0.017645965	
RAB3D	&1031.992936	&1034.789618	5.593364	0.08161	0.01802864	
CPE	&2254.705299	&2257.487434	5.56427	0	0.018330652	
CCT3	&2974.870671	&2977.650048	5.558754	0	0.018388497	
ADAMTSL1	&3529.584652	&3532.359952	5.5506	0.25075	0.018474353	0.015600624
CAPNS1	&1633.675083	&1636.449544	5.548922	0.14107	0.018492072	
LNPEP	&4993.654242	&4996.425612	5.54274	0.10188	0.018557505	
SLC44A4	&3577.24945	&3580.006173	5.513446	0.15814	0.018870831	
FUT3	&2254.110299	&2256.86129	5.501982	0.13256	0.018994933	
ALDOA	&2009.855285	&2012.595669	5.480768	0	0.01922681	
CUL3	&3336.025839	&3338.736311	5.420944	0	0.0198966	
SERPINF1	&2281.626118	&2284.331146	5.410056	0.18517	0.020021074	
tor1B	&1561.616332	&1564.31468	5.396696	0	0.020174909	
LCP1	&2872.352367	&2875.043023	5.381312	0.10293	0.020353566	
YWHAB	&1085.130045	&1087.810513	5.360936	0	0.020592718	0.016380655
PDIA3	&2417.85932	&2420.528242	5.337844	0	0.020867266	
UGDH	&2199.847556	&2202.515642	5.336172	0	0.020887291	
ALDH9A1	&2588.821007	&2591.485945	5.329876	0.10673	0.020962877	
TSTA3	&1605.816755	&1608.46667	5.29983	0.08791	0.021327506	
CCT4	&2398.373315	&2401.007789	5.268948	0	0.021709128	
PSMB5	&1222.681586	&1225.311263	5.259354	0	0.02182912	
PPP1R7	&1599.557733	&1602.155502	5.195538	0	0.022644945	
FSTL1	&1390.080515	&1392.677895	5.19476	0	0.022655083	
MDH2	&1639.450138	&1642.035627	5.170978	0	0.022967282	
ACTR1A	&1747.712288	&1750.294967	5.165358	0	0.023041708	0.017160686
CAPZA2	&1219.524308	&1222.105162	5.161708	0	0.023090179	
SMS	&1889.410218	&1891.985039	5.149642	0	0.023251166	
TPI1	&1185.403137	&1187.977561	5.148848	0	0.023261801	
NEO1	&6916.771938	&6919.275742	5.007608	0.17332	0.025236154	
DSC3	&4389.338053	&4391.830691	4.985276	0.25246	0.025563907	
AZGP1	&1710.422276	&1712.903174	4.961796	0	0.02591328	
PPP1CC	&1397.75399	&1400.211242	4.914504	0	0.026632109	
FTH1	&831.824675	&834.270536	4.891722	0	0.026985758	
PTN	&768.796034	&771.241044	4.89002	0	0.027012373	
IQGAP2	&7135.182733	&7137.622375	4.879284	0.2524	0.027180892	0.017940718
VAMP8	&450.203331	&452.621188	4.835714	0	0.027876095	
ANXA11	&4322.860205	&4325.269703	4.818996	0	0.028147736	
s100A11	&496.697541	&499.100371	4.80566	0	0.028366399	
MATN2	&4673.609483	&4676.008018	4.79707	0.24428	0.02850818	
CLU	&2586.531856	&2588.920228	4.776744	0.22678	0.028846614	
RAD23B	&1919.080939	&1921.464965	4.768052	0	0.028992613	
OS9	&3131.654935	&3134.030957	4.752044	0	0.029263515	
GANAB	&4578.973639	&4581.345158	4.743038	0	0.02941708	
ACPP	&2124.05983	&2126.375719	4.631778	0	0.031385023	
ANXA1	&1595.037094	&1597.346499	4.61881	0	0.03162317	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
ENPP5	&2241.287256	&2243.586011	4.59751	0	0.032018427	
ARF1	&802.333419	&804.630988	4.595138	0	0.032062762	
ANTXR2	&2363.356157	&2365.622751	4.533188	0.12156	0.033243634	
GGT1	&3049.802095	&3052.065341	4.526492	0.24345	0.033373963	
C19orf10	&835.144036	&837.401986	4.5159	0	0.033581214	
GAPDHS	&2136.705663	&2138.937978	4.46463	0.1367	0.034603583	
LAMP1	&2236.082324	&2238.29844	4.432232	0.22379	0.035266361	
GLO1	&898.650603	&900.853331	4.405456	0.10837	0.035824146	
HSPA1L	&3826.149966	&3828.330442	4.360952	0.22237	0.03677175	
CKB	&1605.187606	&1607.325112	4.275012	0	0.038676691	
CAB39L	&1526.349135	&1528.485095	4.27192	0	0.038747126	
COLEC12	&3646.111217	&3648.226962	4.23149	0.17617	0.039680591	
AHCY	&2344.078024	&2346.153845	4.151642	0	0.041594171	
IDUA	&3709.955698	&3712.028526	4.145656	0.20641	0.041741479	
GRHPR	&1677.470959	&1679.49994	4.057962	0.12014	0.043963528	
CYB561	&1914.255084	&1916.279674	4.04918	0.21025	0.044192806	
APP	&3791.227983	&3793.23565	4.015334	0.12154	0.045088292	
UGCGL1	&7215.944123	&7217.923222	3.958198	0.23767	0.04664361	
TFPI2	&1254.816061	&1256.772472	3.912822	0.12425	0.047919069	
TF	&4067.948494	&4069.898328	3.899668	0.19	0.048295651	
PURA	&1247.294728	&1249.242204	3.894952	0	0.048431423	
SPON2	&1579.66576	&1581.602272	3.873024	0.18166	0.049068038	0.020436817
LGALS3BP	&226.827386	&228.702761	3.75075	0.25155	0.052783822	
B4GALT4	&1755.913062	&1757.783016	3.739908	999	0.05312737	
SERPINA1	&321.433098	&323.274899	3.683602	0.12628	0.054950019	
PEBP4	&1277.014759	&1278.846617	3.663716	0.11581	0.055609476	
PLA1A	&498.460341	&500.290963	3.661244	0.1332	0.055692036	
GNS	&820.042413	&821.854497	3.624168	0.13506	0.056946039	
Park7	&840.188804	&841.98629	3.594972	0	0.057954605	
TIMP2	&997.141003	&998.934196	3.586386	0	0.058254802	
PRDX2	&981.040127	&982.814655	3.549056	0	0.059579337	
SERPINB5	&1776.858513	&1778.616942	3.516858	0.19102	0.060747508	
SLC35F2	&1867.764399	&1869.522742	3.516686	0	0.060753813	
GPRC5C	&502.652756	&504.409675	3.513838	0.20961	0.060858319	
TNFSF10	&1406.688469	&1408.436632	3.496326	0.13919	0.061505134	
CTSZ	&1650.834872	&1652.568193	3.466642	0	0.062618308	
CD81	&1099.03516	&1100.753628	3.436936	0	0.063753823	
B4GALT1	&2163.283086	&2164.984689	3.403206	0.1937	0.065069834	
VTN	&592.994109	&594.683359	3.3785	0.24196	0.066052144	
LMAN2	&1581.141915	&1582.826135	3.36844	0	0.066456656	
DDT	&576.992325	&578.64132	3.29799	0	0.069364713	
GNB2	&1551.002156	&1552.630522	3.256732	0	0.071130754	
IGHG2	&1896.958176	&1898.583011	3.24967	0.4243	0.071437839	
WFDC2	&657.612737	&659.219699	3.213924	0	0.073014182	
CFL1	&744.222664	&745.82536	3.205392	0	0.073395919	
PFN1	&647.477296	&649.061572	3.168552	0	0.075068974	
PSMB6	&1148.628899	&1150.208553	3.159308	0.15358	0.075495179	
NUCB1	&2215.699645	&2217.262866	3.126442	0	0.077031692	
SERPINA3	&2835.717619	&2837.264447	3.093656	0.29712	0.078598031	
LAMB2	&9314.598498	&9316.129271	3.061546	0.41074	0.080165362	
PPIC	&1086.588908	&1088.081997	2.986178	999	0.083978161	
RAB14	&906.933411	&908.420219	2.973616	0	0.084632486	
KIF5B	&4448.474989	&4449.946518	2.943058	0.12976	0.086247309	
NIF3L1	&1932.673131	&1934.11229	2.878318	0.15503	0.089779757	
RAB5B	&1050.227116	&1051.66271	2.871188	0	0.090178281	
GNPDA1	&1287.734882	&1289.170037	2.87031	0	0.090227489	
GCHFR	&89.89059	&91.301217	2.821254	0	0.093023702	
TGFB3	&1781.978691	&1783.389292	2.821202	0	0.093026715	
CAPZB	&2005.583436	&2006.990369	2.813866	0.13617	0.093452917	
PSMA4	&1161.979802	&1163.365399	2.771194	0	0.095974547	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
VAMP2	&492.558883	&493.942625	2.767484	0	0.096197258	
TALDO1	&1588.586529	&1589.96081	2.748562	0	0.097341939	
PPIA	&756.909113	&758.28329	2.748354	0	0.097354604	
LCN2	&1101.67401	&1103.043358	2.738696	0	0.097944662	
RAB13	&919.801983	&921.170143	2.73632	0	0.098090422	
YWHAQ	&1125.984007	&1127.344642	2.72127	0	0.099019202	
PSMB8	&1421.543407	&1422.903194	2.719574	0.14993	0.099124467	
NUTF2	&660.815506	&662.171209	2.711406	0	0.099633143	
DPEP3	&2751.192753	&2752.54743	2.709354	0.28248	0.099761383	
SDCBP	&1416.616133	&1417.969728	2.70719	0	0.099896816	
TAGLN2	&907.010258	&908.359144	2.697772	0	0.100488585	
CCT5	&2476.068201	&2477.415498	2.694594	0	0.100689134	
YWHAZ	&991.250665	&992.597404	2.693478	0	0.100759664	
LDHC	&1561.066127	&1562.405438	2.678622	0	0.1017037	
LAMC1	&7892.220723	&7893.550449	2.659452	0.39034	0.102936193	
PPP2R4	&2046.274121	&2047.599922	2.651602	0.28489	0.1034456	
GPC4	&2541.930448	&2543.255876	2.650856	0	0.103494153	
ANG	&873.05443	&874.379308	2.649756	0	0.103565792	
CCT8	&2457.211942	&2458.534959	2.646034	0	0.103808594	
TSG101	&1726.863409	&1728.18255	2.638282	0	0.104316295	
RAP1B	&777.425012	&778.741564	2.633104	0	0.104656932	
SEMA7A	&323.089	&324.404883	2.631766	0.1369	0.10474515	
ELSPBP1	&1097.907201	&1099.22167	2.628938	0.22429	0.104931878	
PGK1	&1900.315919	&1901.625951	2.620064	0	0.105520185	
CALR	&1871.92492	&1873.231547	2.613254	0	0.105974109	
PSMA5	&1038.294519	&1039.581376	2.573714	0	0.108652369	
APOA2	&561.335495	&562.617055	2.56312	0	0.109382522	
PI15	&1214.443137	&1215.719443	2.552612	0	0.110112078	
MFAP4	&1278.12974	&1279.40022	2.54096	0	0.110927323	
MPI	&1971.187958	&1972.450815	2.525714	0	0.112004073	
FDPS	&2086.324115	&2087.582345	2.51646	0	0.112663246	
LYZ	&798.967138	&800.216316	2.498356	0	0.113965209	
GNPTG	&1707.90658	&1709.148727	2.484294	0.2594	0.114987936	
ANXA5	&1412.16027	&1413.402307	2.484074	0	0.115004017	
CAMP	&1001.996419	&1003.22673	2.460622	0	0.116732549	
EEF1A1	&2041.953382	&2043.178811	2.450858	0	0.117460648	
EFEMP1	&2220.512805	&2221.73616	2.44671	0	0.117771481	
PSAT1	&1798.887629	&1800.108778	2.442298	0	0.118103095	
YWHAE	&1078.824445	&1080.040111	2.431332	0	0.118931801	
PPAP2A	&1295.419727	&1296.631275	2.423096	0	0.11955843	
RUVBL1	&2020.851407	&2022.062144	2.421474	0	0.119682268	
NPC2	&720.53438	&721.736632	2.404504	0	0.120986466	
GSTO1	&1163.972995	&1165.172278	2.398566	0.15836	0.121446531	
SDCBP2	&1524.163174	&1525.352197	2.378046	999	0.123051376	
AKR7A2	&2000.197651	&2001.385426	2.37555	0.14674	0.123248184	
IDH1	&2148.725505	&2149.911827	2.372644	0.16124	0.123477761	
ALDOC	&1676.309161	&1677.494031	2.36974	0	0.123707654	
LSAMP	&1596.918728	&1598.096066	2.354676	0	0.124907835	
RAC1	&947.407385	&948.580946	2.347122	0	0.125514542	
EDIL3	&2208.867374	&2210.039081	2.343414	0.16359	0.125813552	
SIL1	&462.22007	&463.385928	2.331716	0.23532	0.12676207	
LRG1	&1930.606951	&1931.772233	2.330564	0.24939	0.126855908	
PSAP	&462.054525	&463.210953	2.312856	0.16537	0.128308107	
BTD	&766.98554	&768.136355	2.30163	0.31258	0.129238311	
MINPP1	&559.295205	&560.425089	2.259768	0.22343	0.132773951	
CDC42	&983.318698	&984.445255	2.253114	0	0.133345826	
DCD	&648.036233	&649.159216	2.245966	0	0.133963227	
PSMB1	&1155.088201	&1156.2061	2.235798	0	0.13484699	
ALDH7A1	&2687.113791	&2688.205894	2.184206	0.17772	0.139432953	
pla2g2A	&855.046989	&856.137422	2.180866	999	0.139735815	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
AGA	&1771.146693	&1772.23082	2.168254	0.17525	0.140886113	
ARHGDIA	&1707.874565	&1708.946598	2.144066	0.17681	0.143122115	
STEAP2	&2248.974974	&2250.046219	2.14249	0.26459	0.143269184	
apoa1BP	&1426.197399	&1427.267787	2.140776	0.1769	0.143429323	
LIFR	&5259.525066	&5260.595007	2.139882	0.27437	0.14351293	
GPR56	&3511.986951	&3513.050814	2.127726	0.3688	0.144655218	
WFDC9	&482.92064	&483.964654	2.088028	999	0.148457594	
PROM2	&4693.856466	&4694.880215	2.047498	0.41648	0.152456554	
CFB	&3283.882237	&3284.905215	2.045956	0.20558	0.152611088	
RAB3B	&1023.242043	&1024.263535	2.042984	0.18368	0.152909432	
DNAJC3	&2290.716107	&2291.734722	2.03723	0.18444	0.153488928	
APOE	&1813.532668	&1814.543246	2.021156	0.325	0.15512101	
BCAN	&4543.767732	&4544.770095	2.004726	0.27577	0.156809625	
fam3B	&1383.402528	&1384.395109	1.985162	0.18914	0.158847655	
FKBP4	&2244.121549	&2245.09816	1.953222	0.19166	0.162240072	
KLK2	&1339.094122	&1340.068555	1.948866	999	0.162709102	
MMP7	&1413.736277	&1414.704216	1.935878	0.18996	0.164116794	
ACE2	&4533.747212	&4534.706438	1.918452	0.31145	0.166027411	
MDH1	&1613.209205	&1614.157294	1.896178	0.19345	0.168506747	
CNDP2	&2404.58372	&2405.520187	1.872934	0.31203	0.171139423	
SLC15A2	&3496.862702	&3497.783261	1.841118	0.29201	0.174819967	
MANBA	&4390.487582	&4391.407071	1.838978	0.29347	0.175070779	
AMBP	&1761.741828	&1762.655546	1.827436	0.20814	0.176430693	
ORM1	&1198.248359	&1199.159358	1.821998	0.31442	0.177075633	
SEMA3F	&3868.838641	&3869.739149	1.801016	0.32034	0.179589714	
BASP1	&922.686168	&923.581579	1.790822	0.20527	0.180826042	
TEX101	&1483.534616	&1484.429552	1.789872	999	0.180941759	
GALNS	&2942.482263	&2943.373823	1.78312	0.41783	0.181766675	
RPLP0	&1380.870544	&1381.758461	1.775834	0	0.18266172	
LDHA	&1655.301098	&1656.177068	1.75194	0.20924	0.185633033	
ACAT2	&2217.751984	&2218.621585	1.739202	0.20988	0.18723997	
CP	&5168.658834	&5169.527428	1.737188	0.30693	0.187495521	
NP	&1452.344245	&1453.199754	1.711018	0.21285	0.190853343	
GPR64	&4793.710739	&4794.552095	1.682712	0.30943	0.194564481	
TP53I3	&1652.212407	&1653.049813	1.674812	0.21603	0.195615244	
ANXA3	&1634.966014	&1635.780577	1.629126	0.28474	0.201823978	
MAMDC2	&3253.748475	&3254.558471	1.619992	0.22232	0.203092903	
PAICS	&2100.277384	&2101.064066	1.573364	0.34949	0.209719151	
NAGA	&2039.224643	&2039.997536	1.545786	0.27601	0.213758621	
RNASE1	&845.744234	&846.495997	1.503526	0.27992	0.220129625	
LIPI	&2582.896035	&2583.640021	1.487972	0.36399	0.222531382	
IGLV1&40	&698.67396	&699.41745	1.48698	0.42633	0.222685622	
GPR115	&4130.650143	&4131.361147	1.422008	0.42955	0.233073179	
Crisp2	&1477.15656	&1477.866905	1.42069	0.29113	0.233289866	
DSC2	&4623.208028	&4623.909198	1.40234	0.43987	0.236332171	
SPINT3	&506.037701	&506.738632	1.401862	999	0.23641206	
ANXA7	&2296.445246	&2297.145073	1.399654	999	0.236781511	
SERPINA6	&2118.228356	&2118.920967	1.385222	7.47813	0.23921365	
ECM1	&2915.529787	&2916.214479	1.369384	999	0.241917749	
IL6ST	&4249.787495	&4250.455033	1.335076	0.36962	0.247904196	
PODXL2	&2868.056976	&2868.720632	1.327312	0.26049	0.249283979	
CST1	&1079.138413	&1079.801171	1.325516	0.25793	0.249604495	
GDF15	&1712.022346	&1712.667469	1.290246	0.40562	0.256002621	
PGM1	&2774.602605	&2775.246751	1.288292	0.38308	0.256362952	
TSN	&997.593312	&998.232351	1.278078	0	0.258256705	
F11R	&1623.373303	&1624.010242	1.273878	8.26353	0.259040428	
MSMB	&700.786832	&701.423621	1.273578	999	0.259096521	
IMPA1	&1611.691257	&1612.307941	1.233368	0.31828	0.266753041	
IL1RL1	&3848.067735	&3848.641718	1.147966	0.42727	0.283975342	
SEMG2	&3578.535754	&3579.102724	1.13394	0.55491	0.286936488	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TUBB1	&2181.305667	&2181.870255	1.129176	0.3361	0.287951168	
ZPBP	&1823.908348	&1824.471194	1.125692	0.33782	0.288696112	
PDGFA	&1304.005766	&1304.566209	1.120886	0.47821	0.289727755	
PGCP	&2255.01461	&2255.575043	1.120866	0.41384	0.289732058	
IGFBP5	&1175.342421	&1175.901411	1.11798	0.19398	0.290353828	
ANXA6	&3526.868789	&3527.427587	1.117596	0.36517	0.290436687	
SERPING1	&2615.248552	&2615.804056	1.111008	0.48326	0.291862937	
PPT1	&1496.430765	&1496.986071	1.110612	999	0.291948952	
ENPP3	&4424.167527	&4424.721235	1.107416	0.34352	0.292644343	
DNASE1	&1527.822394	&1528.354201	1.063614	999	0.30239236	
COPB2	&4071.625854	&4072.144294	1.03688	999	0.308548213	
Hyou1	&4705.860764	&4706.374839	1.02815	0.42983	0.310593576	
DNASE2	&1919.868759	&1920.382271	1.027024	999	0.310858671	
SERPINA4	&2415.284224	&2415.795289	1.02213	95.81563	0.312014299	
CYB5R2	&1467.799713	&1468.299664	0.999902	0.46677	0.317334222	
WFDC8	&1414.980553	&1415.46041	0.959714	0.36656	0.327258946	
HEXA	&2619.506936	&2619.986623	0.959374	0.36677	0.327344648	
NUCB2	&2066.448174	&2066.925857	0.955366	0.23605	0.328357179	
ORM2	&1234.524698	&1234.988159	0.926922	0.628	0.335664021	
INHBB	&1720.871633	&1721.308959	0.874652	0.25346	0.34967065	
CLN5	&2182.534046	&2182.966569	0.865046	0.53756	0.352330446	
PGC	&1949.980945	&1950.406339	0.850788	0.2563	0.356329512	
GSTP1	&1061.683051	&1062.098582	0.831062	0.26269	0.36196562	
IGKC	&593.489526	&593.895865	0.812678	999	0.367329682	
SORT1	&3973.61433	&3974.014119	0.799578	0.40232	0.371219571	
PRSS22	&1602.877859	&1603.263541	0.771364	0.43331	0.379795419	
AGR2	&793.962319	&794.347898	0.771158	999	0.379859054	
BPIL1	&2382.601686	&2382.98163	0.759888	999	0.383363575	
ANXA4	&1493.945976	&1494.325311	0.75867	93.17268	0.383745063	
SERPINI1	&1936.587418	&1936.964931	0.755026	0.41226	0.38488962	
GLB1L	&3242.416033	&3242.790282	0.748498	0.41061	0.38695219	
FAM12A	&791.976746	&792.3461	0.738708	999	0.390075066	
EGF	&6295.433976	&6295.794697	0.721442	0.63945	0.395671314	
ACR	&2431.69584	&2432.052992	0.714304	0.51625	0.39801868	
CRISP1	&1448.289577	&1448.645003	0.710852	0	0.399161114	
LDHB	&1500.35107	&1500.706281	0.710422	0	0.399303754	
GUSB	&3812.187765	&3812.542845	0.71016	0.43925	0.399390701	
FOLH1	&3750.608205	&3750.962675	0.70894	0.50067	0.399795931	
PSMB7	&1341.970416	&1342.324431	0.70803	86.93101	0.400098581	
CA2	&1300.296137	&1300.636794	0.681314	999	0.40913462	
MLPH	&3876.647997	&3876.987943	0.679892	0.62194	0.409623916	
PCMT1	&1288.499778	&1288.837021	0.674486	10.71224	0.411491942	
GALNT7	&2933.648478	&2933.982636	0.668316	0.30632	0.413639343	
RAB5C	&1146.424777	&1146.757813	0.666072	912.90738	0.414424448	
FAM12B	&709.389244	&709.722031	0.665574	0.30178	0.414598981	
HEBP2	&1010.496999	&1010.828544	0.66309	9.65516	0.415471172	
APEH	&359.65869	&359.987602	0.657824	999	0.417329206	
GSTZ1	&1095.357708	&1095.686037	0.656658	999	0.41774228	
SPINK2	&513.429828	&513.758096	0.656536	999	0.417785536	
MARCKS	&1424.665248	&1424.990435	0.650374	0.31344	0.419978997	
ALAD	&1834.701649	&1835.02677	0.650242	0.43863	0.420026172	
KRT10	&3013.453205	&3013.77355	0.64069	0.54365	0.423461049	
TIMP1	&1322.175402	&1322.49512	0.639436	0.51888	0.423915104	
APOB	&23797.17226	&23797.47741	0.610292	0.79527	0.434677888	
RNASET2	&1452.103108	&1452.40362	0.601024	999	0.43818759	
CAPG	&1646.520444	&1646.817622	0.594356	0.32622	0.440739607	
PROS1	&325.615954	&325.910648	0.589388	999	0.442655873	
DBI	&658.285162	&658.579246	0.588168	0.32804	0.443128417	
tmpRSS2	&227.181277	&227.470743	0.578932	2.16049	0.446731248	
PDCD6	&1147.238223	&1147.527252	0.578058	0.27657	0.447074531	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PLOD2	&3513.501869	&3513.787214	0.57069	255.56801	0.449984859	
CTBS	&1986.929064	&1987.212094	0.56606	999	0.451828829	
FH	&2428.095732	&2428.377557	0.56365	0.33587	0.452793329	
MMP14	&2638.181304	&2638.459149	0.55569	999	0.456002038	
RNASE4	&748.804549	&749.073929	0.53876	999	0.462947077	
PLA2G7	&2164.415048	&2164.678421	0.526746	0.34979	0.467978131	
ACP5	&1619.035714	&1619.297998	0.524568	0.50447	0.468899581	
CA4	&1907.908822	&1908.16905	0.520456	999	0.47064723	
EXTL2	&1508.181437	&1508.43884	0.514806	5.79159	0.473065744	
AKR1B1	&1485.497445	&1485.75475	0.51461	15.36762	0.473150003	
DAG1	&4327.281002	&4327.53242	0.502836	2.05784	0.478256652	
ADAM7	&4045.738207	&4045.989082	0.50175	2.05232	0.478732195	
LIPG	&2620.914516	&2621.163756	0.49848	999	0.480168759	
KLK3	&1482.145711	&1482.391504	0.491586	0.51369	0.483220678	
SORD	&1998.981267	&1999.226446	0.490358	0.49046	0.483767652	
HPX	&2735.849989	&2736.094841	0.489704	0.36198	0.484059373	
APOH	&1788.791377	&1789.03465	0.486546	0.36502	0.485472114	
PGLS	&1263.245363	&1263.488174	0.485622	0.35207	0.485886757	
EEF1G	&2358.806651	&2359.048139	0.482976	0.36637	0.487077394	
SMPDL3B	&2537.022934	&2537.25647	0.467072	0.371	0.494337278	
CTSO	&1609.317649	&1609.54848	0.461662	0.37468	0.496848258	
PAEP	&996.709766	&996.939056	0.45858	0.41339	0.498288361	
LCN1	&1024.278108	&1024.505965	0.455714	999	0.499633883	
GGH	&1666.89638	&1667.123673	0.454586	0.37758	0.500165143	
SELENBP1	&2612.026861	&2612.246221	0.43872	999	0.507740905	
GC	&2487.206436	&2487.42517	0.437468	0.38423	0.508347082	
CD38	&1612.218766	&1612.437312	0.437092	0.38486	0.508529373	
ALB	&215.48079	&215.697481	0.433382	0.53772	0.510334101	
HEXB	&2927.663292	&2927.877347	0.42811	0.60543	0.512917803	
TWSG1	&986.848184	&987.059827	0.423286	4.12342	0.515301932	
CD47	&1467.484985	&1467.689409	0.408848	0.3981	0.522554795	
CPO	&2176.49604	&2176.696247	0.400414	0.32023	0.526875527	
PSMA7	&1180.269516	&1180.465684	0.392336	0.40545	0.53107405	
IGJ	&899.262587	&899.454414	0.383654	0.40954	0.535654136	
ASRGL1	&1617.847685	&1618.031477	0.367584	0.41063	0.544324149	
HSPA4	&3745.022608	&3745.204855	0.364494	2.73528	0.546020915	
GSTM3	&1076.082113	&1076.26132	0.358414	3.23394	0.549388381	
IDS	&2682.715812	&2682.892843	0.354062	0.42364	0.551822688	
HRSP12	&647.5161	&647.686079	0.339958	0.4322	0.559853466	
GSS	&2204.596807	&2204.761651	0.329688	0.43862	0.565842863	
MAN2B1	&5061.787645	&5061.947447	0.319604	0.59972	0.571845724	
LGALS3	&1334.458758	&1334.603802	0.290088	0.46211	0.590164143	
PIP	&979.294768	&979.439254	0.288972	0.45832	0.590880051	
IL1R1	&2817.757391	&2817.900792	0.286802	999	0.59227721	
CA6	&1743.612287	&1743.747916	0.271258	0.68256	0.602489141	
NELL1	&4125.372449	&4125.500941	0.256984	0.63516	0.6121998	
ASAH1	&201.84462	&201.965679	0.242118	1.68469	0.622680551	
LZTFL1	&1304.260669	&1304.348601	0.175864	0.54807	0.674952016	
MSLN	&3966.671794	&3966.758349	0.17311	1.37847	0.677362514	
GPI	&2904.520453	&2904.605929	0.170952	0.58895	0.679267117	
LTF	&4531.77272	&4531.83605	0.12666	0.80108	0.721920517	
PRCP	&2722.536164	&2722.595786	0.119244	0.64706	0.729855883	
SDC1	&1665.955942	&1666.010594	0.109304	1.42824	0.740937917	
PTPRJ	&7429.424269	&7429.477212	0.105886	0.74921	0.744877379	
CACNA2D1	&4978.955401	&4979.007108	0.103414	0.6622	0.74777054	
QSCN6	&3085.248077	&3085.298303	0.100452	0.755	0.751287889	
PIGR	&4428.47171	&4428.521342	0.099264	0.82879	0.752714657	
COL9A1	&4609.835318	&4609.880244	0.089852	0.75531	0.764365391	
FBP1	&1663.151457	&1663.193843	0.084772	0.69396	0.770931771	
CRISP3	&1300.688401	&1300.728561	0.08032	0.69841	0.776864224	

Gene	lnL&free	lnL&fixed	2Δ lnL	branch_w	P&value	k
GM2A	&1026.891041	&1026.920845	0.059608	0.73685	0.807116588	
CAP1	&2292.064169	&2292.093619	0.0589	1.21671	0.808243059	
KLK11	&1492.328571	&1492.355692	0.054242	1.29504	0.815839742	
VAT1	&1978.67038	&1978.696696	0.052632	1.28489	0.818545095	
TMC5	&5450.496163	&5450.521376	0.050426	0.87688	0.822323653	
FUCA1	&2440.380231	&2440.403014	0.045566	0.76634	0.830966672	
CD14	&1922.908339	&1922.923437	0.030196	0.806	0.862046251	
TGM4	&3676.961993	&3676.97698	0.029974	1.15225	0.862549237	
APCS	&1273.398436	&1273.411031	0.02519	0.82071	0.87389454	
SEPP1	&1952.645742	&1952.656023	0.020562	1.1796	0.885978579	
C9	&3134.875415	&3134.884234	0.017638	1.16237	0.894345123	
APOD	&1108.896272	&1108.904963	0.017382	0.84798	0.895110204	
smpdl3A	&2309.340125	&2309.347263	0.014276	0.86229	0.904893328	
LAMP2	&1922.272963	&1922.279328	0.01273	1.13829	0.910167473	
TTR	&787.183756	&787.189256	0.011	0.87706	0.916470327	
RAB27A	&1046.24318	&1046.248421	0.010482	0.88091	0.918453757	
ACRV1	&1556.787377	&1556.792242	0.00973	0.91888	0.921423504	
CD44	&3892.799573	&3892.804154	0.009162	1.0852	0.923744277	
IDI1	&1551.20617	&1551.208981	0.005622	0.91068	0.940230627	
PRDX5	&1042.430969	&1042.43367	0.005402	0.91331	0.941409597	
LIPA	&2212.580665	&2212.581869	0.002408	0.95995	0.960862414	
HDHD2	&1220.73774	&1220.73831	0.00114	0.95928	0.973065434	
TFRC	&4085.701457	&4085.701982	0.00105	0	0.974150109	
LTA4H	&2793.565998	&2793.566434	0.000872	0	0.976442175	
TOLLIP	&1331.187386	&1331.187802	0.000832	0	0.976988681	
CD9	&1042.243243	&1042.243558	0.00063	0	0.979975359	
GRN	&3084.093744	&3084.093953	0.000418	0.97642	0.983688348	
PGAM2	&1125.984092	&1125.984282	0.00038	0	0.984447352	
DCXR	&1304.064176	&1304.06431	0.000268	0.98686	0.98693865	
SLPI	&797.47996	&797.480077	0.000234	0	0.987795189	
CD59	&866.471003	&866.471094	0.000182	0	0.989236275	
SERPINB6	&2140.822394	&2140.822454	0.00012	0	0.991259787	
PRKAR2A	&2023.127507	&2023.127562	0.00011	0	0.99163187	
DNAJB9	&1082.190472	&1082.190505	6.6E&05	0	0.993518026	
PSMA6	&1114.32582	&1114.325853	6.6E&05	0	0.993518026	
UBE2N	&635.71498	&635.715011	6.2E&05	0	0.993717516	
TSNAX	&1310.494078	&1310.494106	5.6E&05	0	0.994029234	
PFN2	&782.864766	&782.864791	5E&05	0	0.994358151	
HINT1	&580.02349	&580.023512	4.4E&05	0	0.994707471	
FAM3C	&978.945772	&978.94579	3.6E&05	0	0.995212721	
PPP2CA	&1404.950926	&1404.950944	3.6E&05	0	0.995212721	
DEFB129	&916.675774	&916.675791	3.4E&05	0	0.9953476	
CST6	&707.924409	&707.924425	3.2E&05	0	0.995486507	
CAPZA1	&1243.865903	&1243.865917	2.8E&05	0	0.995778011	
SH3BGRL2	&468.874796	&468.87481	2.8E&05	0	0.995778011	
GNG12	&817.92306	&817.923074	2.8E&05	0	0.995778011	
CAB39	&1447.437031	&1447.437044	2.6E&05	0	0.995931589	
RALA	&1071.344698	&1071.344711	2.6E&05	0	0.995931589	
PRDX4	&1292.397739	&1292.39775	2.2E&05	0	0.996257603	
PSMA2	&1089.873197	&1089.873207	2E&05	0	0.996431764	
CD63	&1057.698315	&1057.698325	2E&05	0	0.996431764	
DDAH1	&1302.501755	&1302.501765	2E&05	0	0.996431764	
RAB10	&817.552669	&817.552679	2E&05	0	0.996431764	
SCGB2A1	&560.015029	&560.015039	2E&05	0	0.996431764	
PKM2	&2962.122587	&2962.122596	1.8E&05	0.99525	0.996614873	
GSTT1	&1142.872232	&1142.872241	1.8E&05	0	0.996614873	
PSMB4	&1249.978421	&1249.97843	1.8E&05	0	0.996614873	
TXN	&469.042743	&469.04275	1.4E&05	0	0.997014596	
BPNT1	&1443.223404	&1443.223411	1.4E&05	0	0.997014596	
HIST2H2BE	&531.300027	&531.300033	1.2E&05	0	0.997236052	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
RAB11B	&959.630224	&959.63023	1.2E&05	0	0.997236052	
SOD1	&861.691876	&861.691882	1.2E&05	0	0.997236052	
PSMB2	&1082.810415	&1082.81042	1E&05	0	0.997476872	
FMOD	&1738.229098	&1738.229103	1E&05	0	0.997476872	
ARF6	&713.214285	&713.214289	8E&06	0	0.997743245	
B2M	&642.341008	&642.341012	8E&06	0	0.997743245	
PRDX1	&898.432196	&898.4322	8E&06	0	0.997743245	
TMEFF2	&1662.603647	&1662.603651	8E&06	0	0.997743245	
HSPB1	&964.723393	&964.723395	4E&06	0	0.998404232	
GBA	&3379.453008	&3379.453009	2E&06	1.00182	0.998871621	
SPACA3	&1235.813869	&1235.81387	2E&06	0	0.998871621	
CPVL	&2495.053699	&2495.053699	0	0.9999	1	
PRDX6	&1048.738405	&1048.738405	0	0	1	
RALB	&1037.37655	&1037.37655	0	0	1	
ACYP1	&477.581395	&477.581384	&2.2E&05	0	#NUM!	
CACYBP	&1005.809009	&1005.809006	&6E&06	0	#NUM!	
CCT2	&2334.160658	&2334.160634	&4.8E&05	0	#NUM!	
COMP	&3823.413356	&3818.562857	&9.700998	252.68745	#NUM!	
CPM	&2176.88372	&2171.793532	&10.180376	415.88677	#NUM!	
EFHD2	&1219.582355	&1219.582284	&0.000142	0	#NUM!	
GLA	&2065.806609	&2065.806581	&5.6E&05	0	#NUM!	
GLB1	&3855.168435	&3848.530484	&13.275902	132.78404	#NUM!	
GMPPA	&2235.588647	&2235.52086	&0.135574	0	#NUM!	
GNAI3	&1543.818885	&1543.818884	&2E&06	0	#NUM!	
GPX3	&1102.627374	&1102.627372	&4E&06	0	#NUM!	
HPRT1	&1071.034443	&1071.034308	&0.00027	0	#NUM!	
NEU1	&2052.725114	&2052.725103	&2.2E&05	0	#NUM!	
NPEPPS	&4279.765415	&4005.713507	&548.103816	0	#NUM!	
PITPNA	&1222.815444	&1222.815423	&4.2E&05	0	#NUM!	
PPIB	&977.200603	&977.200599	&8E&06	0	#NUM!	
PSMD14	&1271.536859	&1271.536855	&8E&06	0	#NUM!	
Rab18	&1027.789387	&1027.789378	&1.8E&05	0	#NUM!	
RAB1A	&880.866004	&880.865392	&0.001224	0	#NUM!	
RAB1B	&984.578705	&984.578546	&0.000318	0	#NUM!	
RAB27B	&1121.141061	&1001.976286	&238.32955	0	#NUM!	
RAB2A	&862.788192	&862.788162	&6E&05	0	#NUM!	
RHOA	&812.291506	&812.291489	&3.4E&05	0	#NUM!	
SEMG1	&3121.14747	&3121.137864	&0.019212	0.94668	#NUM!	
sez6L2	&4446.747292	&4435.297776	&22.899032	105.9891	#NUM!	
SOD3	&1098.868531	&1098.868525	&1.2E&05	0	#NUM!	
TPT1	&767.03445	&767.034436	&2.8E&05	0	#NUM!	

Chimpanzee

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
FCGBP	&26824.75807	&26867.13165	84.747166	0.19957	3.39065E&20	
PTPRF	&9058.413773	&9090.239547	63.651548	0.01179	1.48492E&15	
MUC5B	&33209.62578	&33240.87341	62.495266	0.33699	2.67086E&15	
MYH9	&8816.847902	&8846.823904	59.952004	0.04022	9.7199E&15	
FASN	&13845.10332	&13873.55648	56.906318	0.08686	4.57075E&14	
COL6A2	&6166.070727	&6192.744387	53.34732	0.0123	2.79492E&13	
HSPG2	&32093.05135	&32119.67261	53.242516	0.16128	2.94809E&13	
SDK2	&10118.90768	&10144.09906	50.38276	0.03316	1.26501E&12	
ODZ2	&12810.71967	&12831.85743	42.275524	0	7.92786E&11	
LAMA5	&19256.70927	&19277.51986	41.621188	0.14525	1.10786E&10	
SORL1	&10869.71397	&10889.20808	38.988224	0.06386	4.2637E&10	
ACTN1	&4233.371138	&4250.673894	34.605512	0	4.03761E&09	
EEF2	&4120.693372	&4137.047615	32.708486	0.01681	1.07069E&08	
CPAMD8	&10032.61243	&10048.92898	32.633106	0.12627	1.11303E&08	
PFKP	&4127.428887	&4142.890257	30.92274	0.03818	2.68507E&08	
COL18A1	&9613.155131	&9627.670136	29.03001	0.16815	7.12657E&08	
FN1	&12062.76738	&12077.19635	28.857958	0.08359	7.78852E&08	
ACTN4	&4157.328171	&4171.684888	28.713434	0	8.39196E&08	
FLNB	&12658.69725	&12672.77698	28.159448	0.08318	1.11721E&07	
PYGB	&4724.844598	&4738.560221	27.431246	0	1.6278E&07	
LEFTY2	&2006.464734	&2019.835753	26.742038	0	2.32508E&07	
LDLR	&4411.825531	&4424.581675	25.512288	0.0706	4.39574E&07	
VCP	&3670.268222	&3682.889313	25.242182	0	5.05641E&07	
AGRN	&10949.03334	&10961.55183	25.036968	0.18264	5.62416E&07	
MAN2B2	&5888.099308	&5900.485559	24.772502	0.1369	6.45113E&07	
PTPRD	&9070.577895	&9082.268001	23.380212	0	1.32939E&06	
PLXNB2	&9382.104233	&9393.625476	23.042486	0.11466	1.58461E&06	
GGT1	&3049.016277	&3060.272287	22.51202	0.0274	2.08833E&06	
CNTN3	&5072.14069	&5082.840343	21.399306	0	3.72906E&06	
CNTNAP2	&7124.056747	&7134.224152	20.33481	0.09814	6.50071E&06	
KRT1	&3124.490675	&3134.21282	19.44429	0.12825	1.03577E&05	
MUC6	&13541.42797	&13550.8647	18.87346	0.35637	1.39683E&05	
BAIAP2	&2716.7264	&2726.015881	18.578962	0	1.6301E&05	
MGAM	&9728.667118	&9737.916026	18.497816	0.17008	1.70099E&05	
LIPG	&2618.439215	&2627.428586	17.978742	0	2.23386E&05	
ST14	&4410.296663	&4419.142288	17.69125	0.10004	2.59819E&05	
ABP1	&4016.755427	&4025.472459	17.434064	0.059	2.97447E&05	
VWF	&13693.15484	&13701.70771	17.10573	0.24267	3.53555E&05	
CAPN1	&3437.386388	&3445.840345	16.907914	0	3.92377E&05	
STXBP2	&3028.89203	&3037.330778	16.877496	0.07773	3.98715E&05	
PTPRS	&9650.031506	&9658.385578	16.708144	0.15704	4.35935E&05	
ALCAM	&2703.722692	&2712.070181	16.694978	0	4.3897E&05	
LAMC1	&7895.282025	&7903.517707	16.471364	0.13084	4.93905E&05	
COLEC12	&3646.536206	&3654.617339	16.162266	0.04288	5.81408E&05	
IGHG4	&1802.843556	&1810.789559	15.892006	0.09472	6.70614E&05	
CTSB	&1793.812084	&1801.737792	15.851416	0.0379	6.85152E&05	
TMEM8	&4066.640171	&4074.187029	15.093716	0.05254	0.000102303	
PFAS	&6779.449459	&6786.996048	15.093178	0.19512	0.000102332	
RELN	&16731.41197	&16738.77039	14.71683	0.31401	0.000124926	
ENO1	&2054.069159	&2061.326698	14.515078	0	0.000139042	
GPC1	&2722.709685	&2729.932782	14.446194	0.03225	0.000144221	
ACE	&6847.15404	&6854.300065	14.29205	0.25098	0.000156525	
col12A1	&14645.87961	&14652.94833	14.13744	0.13388	0.000169928	
CD81	&1098.778319	&1105.821617	14.086596	0	0.000174583	
DDR1	&4201.878344	&4208.900284	14.04388	0	0.000178594	
HSPA8	&3010.867894	&3017.835385	13.934982	0	0.000189243	
PPP5C	&2320.852059	&2327.805515	13.906912	0	0.000192091	
FUT3	&2254.026393	&2260.855124	13.657462	0.12806	0.000219368	
CLSTN1	&4930.46006	&4937.288383	13.656646	0.07965	0.000219463	
CRYZ	&1746.2643	&1753.016982	13.505364	0	0.000237882	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CTSD	&2194.691824	&2201.429385	13.475122	0.09173	0.000241747	
ANXA2	&1663.181696	&1669.911297	13.459202	0	0.000243807	
ACLY	&5462.082944	&5468.7813	13.396712	0.20104	0.000252066	
LAP3	&3057.327236	&3063.888794	13.123116	0	0.000291675	
NEU1	&2051.121989	&2057.452059	12.66014	0	0.000373534	
CACNA2D1	&4979.981644	&4986.294814	12.62634	0	0.000380349	
KPNB1	&3991.368148	&3997.659224	12.582152	0	0.000389448	
TKT	&3006.228326	&3012.496958	12.537264	0.04662	0.000398916	
SLIT2	&7468.603902	&7474.850815	12.493826	0.1409	0.000408299	
NRCAM	&6121.054104	&6127.232231	12.356254	0	0.000439512	
SI	&9016.755304	&9022.904893	12.299178	0.18361	0.000453158	
IL1RAP	&3277.910495	&3283.912628	12.004266	0	0.000530789	
PROM2	&4693.448666	&4699.448367	11.999402	0.11239	0.000532176	
FBLN2	&5916.407131	&5922.397441	11.98062	0.1989	0.000537567	
GALNS	&2944.515951	&2950.474167	11.916432	0.10532	0.000556409	
BCAN	&4542.956646	&4548.911578	11.909864	0.05843	0.000558375	
IDH1	&2147.145866	&2152.981467	11.671202	0.05341	0.00063475	
KRT5	&2978.013189	&2983.74359	11.460802	0.06406	0.000710796	
pla2g2A	&853.813364	&859.49967	11.372612	0	0.00074535	
TPP2	&6057.001511	&6062.626229	11.249436	0.14274	0.000796472	
MYO1C	&5443.114687	&5448.576979	10.924584	0.28979	0.000948965	
CUL3	&3335.828596	&3341.241188	10.825184	0	0.001001287	
GAA	&4986.215331	&4991.560487	10.690312	0.15923	0.00107698	
BGN	&1721.90576	&1727.249899	10.688278	0	0.001078165	
PGLS	&1262.634754	&1267.977561	10.685614	0	0.001079719	
NEO1	&6916.698521	&6921.961124	10.525206	0.10834	0.001177573	
SERPINA4	&2414.345188	&2419.588773	10.48717	0	0.001202064	
NRP1	&4386.00653	&4391.180685	10.34831	0.10251	0.001295933	
IGHG2	&1896.888216	&1902.016217	10.256002	0.15711	0.001362406	
DDB1	&5175.333784	&5180.42956	10.191552	0	0.001410855	
IQGAP1	&7510.008384	&7515.046092	10.075416	0	0.001502607	
LPL	&2388.453965	&2393.467935	10.02794	0	0.001541834	
GNAI3	&1543.818883	&1548.791026	9.944286	0	0.001613494	
ALDH1A1	&2396.671418	&2401.578125	9.813414	0	0.001732436	
GNB2	&1550.721142	&1555.581487	9.72069	0	0.001822051	
CNDP2	&2405.512758	&2410.326083	9.62665	0.09654	0.001917741	
FMOD	&1737.71998	&1742.458795	9.47763	0	0.002079925	
SDC1	&1663.857182	&1668.559091	9.403818	0	0.002165341	
COL6A1	&5766.58983	&5771.223478	9.267296	0.17141	0.002332819	
CAPZB	&2003.077961	&2007.701301	9.24668	0	0.002359228	
CRTAC1	&3032.148771	&3036.734848	9.172154	0.15027	0.002457252	
P4HB	&2492.668293	&2497.248544	9.160502	0.10391	0.002472947	
LCP1	&2873.006021	&2877.522155	9.032268	0	0.002652552	
MATN2	&4673.59899	&4678.089575	8.98117	0.14611	0.002727759	
MAN2B1	&5063.304708	&5067.777675	8.945934	0.13572	0.002780879	
PSMA6	&1112.988202	&1117.355984	8.735564	0	0.003120628	
CPZ	&2996.285062	&3000.58947	8.608816	0.19147	0.003345397	
CTSZ	&1649.767786	&1654.070109	8.604646	0	0.003353065	
CKB	&1604.987638	&1609.271613	8.56795	0	0.003421322	
ITIH5	&5267.367685	&5271.610474	8.485578	0.23182	0.003579728	
GALNT7	&2933.772299	&2937.969658	8.394718	0.11681	0.003763129	
CAPG	&1646.41391	&1650.580411	8.333002	0	0.003893127	
CDH1	&4612.218218	&4616.351992	8.267548	0.15391	0.004035998	
CA6	&1743.968975	&1748.092229	8.246508	0.06997	0.004083047	
HIST2H2BE	&531.300085	&535.422583	8.244996	0	0.00408645	
ALDOA	&2009.780897	&2013.890252	8.21871	0	0.004146066	
HSPA5	&2989.964983	&2994.0577	8.185434	0	0.004222807	
AHCY	&2343.318784	&2347.389116	8.140664	0	0.004328343	
C19orf10	&835.026927	&839.09477	8.135686	0	0.004340242	
RAB11B	&959.630271	&963.682503	8.104464	0	0.004415638	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
THBS2	&5839.165726	&5843.150468	7.969484	0.1337	0.00475725	
MAN2A1	&5436.33905	&5440.312231	7.946362	0.07106	0.004818414	
APP	&3790.091176	&3794.033187	7.884022	0	0.004987344	
HEXA	&2618.318503	&2622.255928	7.87485	0	0.005012703	
CTSO	&1606.92688	&1610.798745	7.74373	0	0.005389935	
CAPZA1	&1243.167115	&1246.976584	7.618938	0	0.005775849	
GALC	&3332.556898	&3336.35035	7.586904	0	0.005879383	
CLIC1	&1147.736576	&1151.501409	7.529666	0	0.006069116	
MANBA	&4390.338552	&4394.087187	7.49727	0.19262	0.006179259	
sez6L2	&4432.520239	&4436.250914	7.46135	0.21333	0.006303771	
DNASE2	&1920.198546	&1923.92217	7.447248	0.11715	0.006353352	
PLA1A	&2496.894378	&2500.617122	7.445488	0	0.006359567	
CLTC	&7273.878653	&7277.538889	7.320472	0	0.006817351	
LTA4H	&2792.403863	&2796.02789	7.248054	0	0.007097789	
ALAD	&1834.281222	&1837.897343	7.232242	0.08637	0.007160573	
ARF1	&802.333419	&805.93921	7.211582	0	0.007243462	
PSMB7	&1343.384891	&1346.984344	7.198906	0	0.007294804	
SERPINF1	&2281.546666	&2285.08835	7.083368	0.07661	0.007780264	
XPNPEP1	&2971.711823	&2975.252315	7.080984	0	0.007790622	
SMOC2	&2173.261307	&2176.766391	7.010168	0.07629	0.008104807	
SORT1	&974.157747	&977.625435	6.935376	0.13838	0.00845073	
ANXA1	&1594.878863	&1598.343527	6.929328	0	0.008479354	
ANXA4	&1494.368127	&1497.790562	6.84487	0	0.008889617	
ANPEP	&5015.769189	&5019.165952	6.793526	0.21283	0.009148903	
FOLH1	&3750.591992	&3753.975918	6.767852	0.2256	0.009281448	
RBP4	&887.080518	&890.448924	6.736812	0	0.009444325	
ORM2	&1234.039092	&1237.372472	6.66676	0.1137	0.00982276	
PLOD2	&514.779595	&518.097325	6.63546	0.08307	0.009996838	
GBA	&377.561689	&380.869866	6.616354	0.08356	0.010104649	
LAMB2	&9314.543937	&9317.848267	6.60866	0.38118	0.0101484	0.011792453
EDIL3	&2208.329078	&2211.591131	6.524106	0	0.010642203	0.011871069
ACP5	&1620.33414	&1623.559477	6.450674	0.17393	0.011091026	0.011949686
PTPRJ	&7429.060139	&7432.24671	6.373142	0.24513	0.011586028	0.012028302
RRBP1	&4917.598579	&4920.708984	6.22081	0.20111	0.012625734	0.012106918
CP	&5168.390759	&5171.449119	6.11672	0.17011	0.013390905	0.012185535
MMP2	&194.842081	&197.890444	6.096726	0	0.013543257	0.012264151
COMP	&815.126297	&818.169254	6.085914	0.3199	0.013626385	0.012342767
GPRC5C	&2503.097362	&2506.134218	6.073712	0.12302	0.013720831	0.012421384
HPRT1	&1069.557638	&1072.56334	6.011404	0	0.014213714	0.0125
SMPDL3B	&2536.051525	&2539.038834	5.974618	0.14698	0.014513225	0.012578616
SEMA3C	&591.744625	&594.676076	5.862902	0.09591	0.015463278	
PRKCSH	&2724.500282	&2727.402077	5.80359	0.13117	0.015993487	
GNB2L1	&1451.515393	&1454.379636	5.728486	0	0.016691867	
RAB3D	&1031.816994	&1034.65509	5.676192	0	0.017196652	
GSTM3	&1076.805885	&1079.640854	5.669938	0	0.017258066	
VTN	&2591.57546	&2594.394444	5.637968	0	0.017575566	
LGMN	&2359.35452	&2362.150109	5.591178	0	0.018051153	
DAG1	&4330.179823	&4332.963743	5.56784	0.10224	0.018293314	
COPB2	&4073.711014	&4076.493406	5.564784	0.15304	0.018325271	
PKM2	&2962.797536	&2965.571328	5.547584	0	0.018506214	0.01336478
GC	&2486.296217	&2489.060629	5.528824	0.10117	0.018705674	
TUBB1	&2182.124845	&2184.88115	5.51261	0	0.018879853	
CCT2	&2334.107611	&2336.848178	5.481134	0	0.019222785	
IGF2R	&12689.64748	&12692.38249	5.470028	0.34904	0.019345316	
FH	&2428.322098	&2431.029719	5.415242	0.15323	0.019961686	
TAGLN2	&906.8636	&909.560185	5.39317	0	0.020215714	
PPIA	&756.764999	&759.461072	5.392146	0	0.02022758	
CPE	&2254.856084	&2257.540787	5.369406	0	0.020492955	
PRKACA	&1817.109975	&1819.743224	5.266498	108.97906	0.021739705	
EEF1G	&2358.145829	&2360.774676	5.257694	0	0.021849951	0.014150943

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SLC15A2	&3496.368029	&3498.986521	5.236984	0.10877	0.022111575	
HPX	&2733.843516	&2736.458691	5.23035	0	0.022196066	
DNAJC3	&2290.853818	&2293.465205	5.222774	0	0.022292962	
TPI1	&1185.397187	&1188.003043	5.211712	0	0.022435232	
GSN	&3874.831886	&3877.424517	5.185262	0.09073	0.022779238	
GLG1	&5645.107139	&5647.695922	5.177566	0.1537	0.022880354	
AKR7A2	&2000.217271	&2002.803094	5.171646	0.20186	0.022958452	
ACTR1A	&1747.712288	&1750.28649	5.148404	0	0.02326775	
CTBS	&1987.308606	&1989.866231	5.11525	0.19442	0.023716449	
RALA	&1070.048654	&1072.594263	5.091218	0	0.024047297	0.014937107
GGH	&1665.484927	&1668.027828	5.085802	0	0.024122517	
DPEP3	&2749.872453	&2752.414801	5.084696	0	0.024137908	
ADAMTSL1	&3529.731457	&3532.272285	5.081656	0.23449	0.024180264	
SELENBP1	&2613.579838	&2616.113177	5.066678	0.19634	0.024390082	
MME	&3524.281457	&3526.814286	5.065658	0	0.024404439	
APEH	&360.94622	&363.477147	5.061854	0	0.02445806	
PSMB2	&1082.097464	&1084.615169	5.03541	0	0.024834208	
AZGP1	&1710.742502	&1713.24006	4.995116	0.02571	0.02541895	
PSMA7	&1180.733885	&1183.217074	4.966378	0	0.025844714	
SDCBP2	&1529.142775	&1531.617593	4.949636	0.17091	0.026096162	
FDPS	&2085.851789	&2088.324409	4.94524	0	0.026162606	
PTGDS	&982.747044	&985.204783	4.915478	0.07089	0.026617097	
DPP7	&2587.917031	&2590.336214	4.838366	0.12925	0.027833256	
PODXL2	&2867.050633	&2869.468943	4.83662	0	0.027861453	
PDCD6IP	&3899.487672	&3901.900691	4.826038	0	0.028032981	
ANXA6	&3527.075404	&3529.468962	4.787116	0.18691	0.028673398	
RAC1	&947.132513	&949.47705	4.689074	0	0.030355002	
PRDX1	&897.988325	&900.332302	4.687954	0	0.030374795	
PSMB1	&1154.824571	&1157.154782	4.660422	0	0.030865605	
PRDX6	&1048.394494	&1050.724102	4.659216	0	0.030887292	
PPIC	&1090.676738	&1093.001092	4.648708	0	0.031076929	
SIL1	&2462.148054	&2464.437777	4.579446	0.16554	0.032357675	
PSMD2	&4158.023953	&4160.285467	4.523028	0	0.033441595	
ANXA3	&1635.012063	&1637.241572	4.459018	0.21678	0.034717451	
BPIL1	&2383.595874	&2385.773787	4.355826	0.16722	0.036882569	
GUSB	&3811.486923	&3813.630343	4.28684	0	0.038408489	
SYT1	&1899.562512	&1901.668755	4.212486	0	0.040127487	
AGA	&1770.583935	&1772.677577	4.187284	0.11645	0.040728298	
LIPI	&2581.899727	&2583.97651	4.153566	0.18501	0.04154694	
ORM1	&1197.727581	&1199.78737	4.119578	0.11577	0.042389651	
APOH	&1788.477101	&1790.466994	3.979786	0.12241	0.046049413	
SMPD1	&3206.716762	&3208.699051	3.964578	0.27823	0.046467168	
FBP1	&1664.896673	&1666.85064	3.907934	0.12038	0.048058643	
GSR	&2856.991937	&2858.936958	3.890042	0.22571	0.048573209	
PSME4	&8500.073113	&8502.015255	3.884284	0.33059	0.048740041	
SLC44A4	&577.22418	&579.16021	3.87206	0.13059	0.049096227	0.017767296
IQGAP2	&7135.292955	&7137.200331	3.814752	0.19846	0.050803125	
THBS4	&4696.908682	&4698.794002	3.77064	0.36907	0.052159672	
PPT1	&1498.704195	&1500.583425	3.75846	0	0.052540948	
OLFM4	&2762.333298	&2764.207923	3.74925	0.13058	0.052831212	
MLPH	&3876.243493	&3878.105495	3.724004	0.29186	0.053635607	
SPON2	&1579.383533	&1581.20163	3.636194	0	0.056536038	
EPHA5	&4895.290008	&4897.095574	3.611132	0.13559	0.057394041	
TOLLIP	&1330.724429	&1332.528307	3.607756	0.10302	0.057510671	
MPST	&1728.971889	&1730.775545	3.607312	0.09183	0.057526028	
EGF	&6294.911842	&6296.684793	3.545902	0.34077	0.059692704	
PGD	&2494.483378	&2496.240711	3.514666	0.25013	0.060827916	
CD151	&1221.366215	&1223.11203	3.49163	0	0.061679825	
IDI1	&1551.551181	&1553.25688	3.411398	0.15478	0.064747572	
GLA	&2061.115257	&2062.80764	3.384766	999	0.065801519	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CD44	&3893.273015	&3894.963166	3.380302	0.35501	0.065979964	
APOE	&1812.560672	&1814.2495	3.377656	0.40181	0.06608598	
GSS	&2204.597877	&2206.275368	3.354982	0.1456	0.067001943	
AGT	&2693.297738	&2694.963584	3.331692	0.28914	0.067956931	
LMAN2	&1580.907637	&1582.560538	3.305802	0.11347	0.069035639	
NUCB2	&2065.442095	&2067.091045	3.2979	0	0.069368514	
ACO1	&4249.262336	&4250.906346	3.28802	0.14859	0.069787131	
SPINT1	&2729.229799	&2730.870458	3.281318	0	0.070072635	
MSLN	&3968.11794	&3969.73328	3.23068	0.3705	0.072270674	
ASAH1	&2202.519626	&2204.093746	3.14824	0.16382	0.076008905	
KIF5B	&4448.110227	&4449.678919	3.137384	0	0.076516443	
KLK3	&1482.180335	&1483.738812	3.116954	0.37947	0.077481494	
DCXR	&1305.715768	&1307.236488	3.04144	0	0.081163889	
GAS6	&3533.22639	&3534.731779	3.010778	0.20246	0.082712583	
GLB1L	&3242.312714	&3243.817085	3.008742	0.37288	0.082816542	
PGAM2	&1125.850453	&1127.354746	3.008586	0	0.082824513	
NAGLU	&3597.025024	&3598.524599	2.99915	0	0.083308213	
LAMP1	&2235.80323	&2237.300044	2.993628	0.28986	0.083592692	
TGM4	&3674.83711	&3676.323382	2.972544	999	0.084688578	
PSMB8	&1421.656079	&1423.141175	2.970192	0.21505	0.084811788	
DNASE1	&1529.829112	&1531.312494	2.966764	0.20643	0.084991711	
CD59	&865.794296	&867.25548	2.922368	999	0.087359576	
ADAM10	&3311.615426	&3313.053627	2.876402	0	0.089886662	
GAPDH	&1562.658677	&1564.096112	2.87487	0	0.08997224	
GNPDA1	&1287.735283	&1289.167813	2.86506	0	0.090522334	
smpdl3A	&2306.300391	&2307.728744	2.856706	999	0.090993661	
PFN2	&782.002061	&783.413484	2.822846	0	0.092931494	
TGFB3	&1781.978665	&1783.389831	2.822332	0	0.092961253	
THBS1	&5463.235554	&5464.64068	2.810252	0.21665	0.093663662	
RDX	&2860.643125	&2862.044634	2.803018	0	0.094087054	
GLO1	&898.313476	&899.711869	2.796786	0	0.094453471	
DBI	&657.586507	&658.983272	2.79353	0	0.094645528	
ANXA11	&4323.51954	&4324.913036	2.786992	0	0.095032461	
PSAP	&2461.802466	&2463.192742	2.780552	0	0.095415278	
TF	&4068.334634	&4069.723938	2.778608	0.26901	0.095531166	
GNMT	&1451.376256	&1452.75835	2.764188	0	0.096395589	
RAB13	&919.801983	&921.179752	2.755538	0	0.096918209	
GSTT1	&1142.309754	&1143.67974	2.739972	0	0.097866482	
BPNT1	&1442.785516	&1444.153581	2.73613	0	0.098102088	
C3	&8543.071171	&8544.435342	2.728342	0.44555	0.098581578	
SERPINB6	&2138.946948	&2140.309675	2.725454	0.39352	0.098760036	
RAB10	&817.552669	&818.91303	2.720722	0	0.099053201	
LDHB	&1500.35107	&1501.709235	2.71633	0	0.099326153	
SH3BGRL2	&468.70873	&470.065733	2.714006	0	0.099470915	
LGALS3BP	&3226.977161	&3228.331455	2.708588	0.17342	0.0998093	
NAPA	&1260.183833	&1261.534211	2.700756	0	0.100300676	
CCT5	&2476.06829	&2477.410784	2.684988	0	0.101297989	
PGM1	&2775.603929	&2776.938983	2.670108	0.20561	0.102249085	
PDIA3	&2418.221813	&2419.556016	2.668406	0	0.102358494	
FUCA1	&2440.552762	&2441.881758	2.657992	0.38102	0.103030728	
LDHC	&1561.070137	&1562.397898	2.655522	0	0.103190877	
TALDO1	&1588.693602	&1590.01174	2.636276	0.2268	0.104448116	
CCT4	&2398.484136	&2399.802018	2.635764	0	0.10448179	
MMP7	&1413.805518	&1415.122566	2.634096	0.28602	0.104591578	
HSPB1	&963.971995	&965.28265	2.62131	0.1803	0.105437363	
GM2A	&1026.187618	&1027.492618	2.61	0	0.106191762	
MSMB	&699.624511	&700.927389	2.605756	0	0.106476371	
GPR56	&512.131533	&513.430337	2.597608	0.33484	0.107025137	
GDF15	&1712.009564	&1713.305049	2.59097	0.36285	0.107474498	
GPI	&2903.021241	&2904.313511	2.58454	0.36035	0.107911754	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
RPLP0	&1380.870208	&1382.152799	2.565182	0	0.109239985	
IL6ST	&4250.065099	&4251.342088	2.553978	0.23244	0.110016937	
ADAMTS1	&4874.974475	&4876.250229	2.551508	0.08843	0.110189038	
PI15	&1214.587388	&1215.861507	2.548238	0	0.110417335	
USP14	&2152.659079	&2153.92952	2.540882	0	0.110932803	
APOA2	&559.730283	&560.99926	2.537954	999	0.111138717	
ALDH7A1	&2687.026451	&2688.288117	2.523332	0.24165	0.112173339	
LYZ	&798.957439	&800.216964	2.51905	0	0.112478328	
IL1RL1	&3847.808238	&3849.052153	2.48783	0.31722	0.114729814	
SERPINA1	&2321.884833	&2323.127583	2.4855	0.23738	0.114899828	
ANXA5	&1412.16084	&1413.401462	2.481244	0	0.115211096	
FTH1	&831.998121	&833.233695	2.471148	0	0.115953207	
ARHGDIA	&1707.929663	&1709.165044	2.470762	0.23852	0.115981684	
BASP1	&922.291922	&923.526548	2.469252	0	0.116093161	
UGDH	&2199.968466	&2201.201782	2.466632	0	0.116286864	
PRKAR1A	&1752.769903	&1753.997842	2.455878	0	0.117085683	
EEF1A1	&2041.953382	&2043.179011	2.451258	0	0.117430722	
IGFBP2	&1366.879923	&1368.10465	2.449454	0	0.117565756	
VCL	&5089.733973	&5090.955575	2.443204	0	0.118034914	
GANAB	&4579.494492	&4580.697402	2.40582	0.35118	0.120884766	
s100A11	&496.919834	&498.119283	2.398898	0	0.121420757	
A1BG	&2641.529815	&2642.725561	2.391492	0.22093	0.121997144	
HINT1	&579.814625	&581.006392	2.383534	0	0.122619874	
ACR	&2431.729722	&2432.916886	2.374328	0.4463	0.123344665	
CCT7	&2534.54211	&2535.720024	2.355828	0	0.124815597	
LSAMP	&1596.918746	&1598.095841	2.35419	0	0.12494677	
MAMDC2	&3253.666321	&3254.843149	2.353656	0	0.124989566	
RAD23B	&1918.957019	&1920.131297	2.348556	0.30837	0.125399118	
GRN	&3084.248236	&3085.421859	2.347246	0.16174	0.125504557	
NPEPPS	&4005.489201	&4006.661723	2.345044	0	0.125682013	
TIMP2	&995.3293	&996.491124	2.323648	0.19753	0.127420887	
CCT3	&2975.92638	&2977.088068	2.323376	0.16461	0.127443165	
TMEFF2	&1662.426779	&1663.580502	2.307446	0	0.128755454	
SERPINA5	&2276.779082	&2277.930585	2.303006	0.43314	0.12912389	
ADAM7	&4046.780778	&4047.925567	2.289578	0.44915	0.130245331	
DSC3	&4389.28041	&4390.418789	2.276758	0.31797	0.131326136	
CD9	&1042.121784	&1043.258248	2.272928	0.1549	0.131650967	
A4GALT	&1745.415362	&1746.539709	2.248694	0.25532	0.133727222	
SCGB2A1	&557.967609	&559.087805	2.240392	999	0.134446892	
PEBP4	&1277.559117	&1278.659185	2.200136	0.28485	0.137998562	
CPO	&2174.214331	&2175.310394	2.192126	67.11266	0.13871773	
CRISP3	&1300.438142	&1301.530845	2.185406	0.17259	0.139324321	
PSMB6	&1148.605432	&1149.693128	2.175392	0	0.14023378	
CAB39	&1447.371407	&1448.448088	2.153362	0	0.142258081	
TXN	&468.497307	&469.565744	2.136874	0	0.14379464	
HSPA4	&3746.482069	&3747.539503	2.114868	0.17898	0.145874631	
PGM2	&3783.932015	&3784.989405	2.11478	0.22513	0.145883016	
STEAP2	&2248.956014	&2249.977656	2.043284	0.27043	0.152879287	
PHGDH	&2552.621853	&2553.642765	2.041824	0.18427	0.153026058	
PPP1R7	&1599.288923	&1600.304149	2.030452	0.18364	0.154174749	
FSTL1	&1389.24914	&1390.254886	2.011492	0.18429	0.156111725	
MDH2	&1639.694266	&1640.698921	2.00931	0.18733	0.156336408	
PAEP	&996.261735	&997.234555	1.94564	0.22631	0.163057458	
SPOCK3	&2095.781874	&2096.744492	1.925236	0.30725	0.165280594	
KRT10	&3014.144553	&3015.105628	1.92215	0.35063	0.165619839	
NELL1	&4125.67885	&4126.628627	1.899554	0.41033	0.168128249	
PFN1	&645.034459	&645.983357	1.897796	999	0.168325224	
GP2	&2925.401014	&2926.349734	1.89744	0.31688	0.168365145	
TTR	&786.873183	&787.796022	1.845678	0.29078	0.174286906	
GNS	&2819.988263	&2820.898325	1.820124	0.20331	0.177298517	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TMC5	&5451.40271	&5452.31231	1.8192	0.502	0.177408532	
BTD	&2766.895297	&2767.77674	1.762886	0.20868	0.184264949	
DSC2	&4623.10196	&4623.93893	1.67394	0.48533	0.195731634	
UGCGL1	&7215.912328	&7216.745825	1.666994	0.29013	0.196661648	
NP	&1452.35239	&1453.181477	1.658174	0.21667	0.197850047	
LCN1	&1024.836282	&1025.658573	1.644582	0.26345	0.199697957	
PROS1	&3326.283202	&3327.101509	1.636614	0.34265	0.200790675	
SERPINB5	&1776.651939	&1777.466963	1.630048	0	0.20169641	
TGFBR3	&4153.36677	&4154.178648	1.623756	0.44064	0.202568861	
APOB	&23797.83492	&23798.63552	1.60119	0.69561	0.205734652	
GLB1	&3849.02452	&3849.812563	1.576086	0.31954	0.209325376	
KLK11	&1493.698715	&1494.471688	1.545946	0.27502	0.21373492	
KAL1	&3350.851954	&3351.620826	1.537744	0.2313	0.214953919	
GPR64	&4792.160075	&4792.921377	1.522604	999	0.217225855	
B4GALT4	&1758.787353	&1759.528962	1.483218	999	0.223271714	
AMBP	&1761.633542	&1762.341551	1.416018	0.2808	0.234059934	
PACSIN2	&2693.949091	&2694.655643	1.413104	0.31402	0.234541794	
SPINT3	&506.03374	&506.738587	1.409694	999	0.235107198	
ACRV1	&1555.862352	&1556.566993	1.409282	999	0.235175622	
ACAT2	&2216.823362	&2217.515392	1.38406	999	0.23941079	
PGCP	&2253.504804	&2254.19512	1.380632	999	0.239993524	
PGC	&1947.04991	&1947.726608	1.353396	999	0.2446853	
SEMA7A	&3319.666984	&3320.277854	1.22174	0.49306	0.269019446	
IMPA1	&1611.691703	&1612.301986	1.220566	0.32034	0.269249603	
ENPP3	&4424.050192	&4424.657252	1.21412	0.42578	0.270517699	
PRKAR2A	&2023.109472	&2023.715842	1.21274	0.32196	0.27079015	
PLA2G7	&2163.040539	&2163.641455	1.201832	999	0.272955828	
ECM1	&2916.591127	&2917.184099	1.185944	0.40398	0.276149229	
PRSS8	&1907.472139	&1908.062693	1.181108	0.30715	0.277130544	
CD109	&7432.303809	&7432.878319	1.14902	0.54133	0.283754392	
LNPEP	&4994.362191	&4994.935398	1.146414	0.40974	0.284301085	
INHBB	&1717.438049	&1718.001447	1.126796	0.37155	0.288459791	
SERPINC1	&2501.013953	&2501.577191	1.126476	0.33628	0.288528265	
SEMA3F	&3867.942063	&3868.498525	1.112924	0.42871	0.291447218	
GFRA2	&2075.810353	&2076.335218	1.04973	0.21926	0.305569278	
GPR115	&4130.650459	&4131.168084	1.03525	0.43246	0.308928775	
CA2	&1299.517619	&1300.022486	1.009734	4.48114	0.314966573	
CD14	&1923.020782	&1923.520026	0.998488	0.50295	0.317676644	
MINPP1	&2559.086125	&2559.58386	0.99547	0.49178	0.318409124	
GRHPR	&1677.539824	&1678.027558	0.975468	0.36417	0.323320251	
PGK2	&1983.24668	&1983.731876	0.970392	0.3636	0.324582435	
KRT8	&2764.355819	&2764.824221	0.936804	0.49118	0.333101129	
CANT1	&2221.756028	&2222.216326	0.920596	0.40663	0.337318531	
CAMP	&1002.81038	&1003.259537	0.898314	0.15276	0.343234192	
PDCD6	&1146.720922	&1147.168012	0.89418	0.38589	0.344347076	
ENPP5	&242.49843	&242.942717	0.888574	0.42004	0.345864033	
CPM	&2172.173881	&2172.613902	0.880042	0.38313	0.348190176	
LZTFL1	&1303.286348	&1303.724053	0.87541	999	0.349461933	
CD38	&1612.050019	&1612.486131	0.872224	0.38497	0.350340346	
SLPI	&797.408699	&797.837258	0.857118	0.38756	0.354546458	
WFDC8	&1415.07206	&1415.486541	0.828962	0.48714	0.362572849	
Hyou1	&4704.560491	&4704.970029	0.819076	0.53707	0.36545046	
LIPA	&2212.867048	&2213.269771	0.805446	0.43466	0.369470077	
DCD	&648.535011	&648.930728	0.791434	999	0.373666867	
RAB1B	&984.182503	&984.574836	0.784666	0.27326	0.375717899	
RNASE1	&845.775403	&846.156323	0.76184	0.27774	0.382753312	
CYB561	&1914.470997	&1914.84517	0.748346	0.28276	0.387000403	
FAM12A	&791.977485	&792.346144	0.737318	999	0.390521375	
ALDOC	&1674.718131	&1675.081784	0.727306	999	0.393757815	
PRSS22	&1603.051858	&1603.4151	0.726484	0.28842	0.39402524	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
GMPPA	&2233.769348	&2234.127094	0.715492	999	0.397626608	
PPAP2A	&1294.898757	&1295.250949	0.704384	999	0.401314516	
ALDH9A1	&2587.781222	&2588.132351	0.702258	276.10715	0.402026012	
IGJ	&899.15912	&899.504475	0.69071	999	0.405922988	
CLU	&2586.117767	&2586.458914	0.682294	0.46319	0.408797911	
RAB27B	&1000.866011	&1001.199948	0.667874	999	0.413793811	
RAB27A	&1046.134985	&1046.468591	0.667212	13.78288	0.414025323	
B2M	&641.759187	&642.089553	0.660732	999	0.416301639	
SPINK2	&513.428308	&513.758409	0.660202	999	0.416488639	
IDE	&4640.969393	&4641.292739	0.646692	0.30895	0.421297865	
fam3B	&1383.660261	&1383.982047	0.643572	999	0.422420276	
EXTL2	&1508.118085	&1508.438924	0.641678	999	0.423103822	
CRISP1	&1448.605408	&1448.92571	0.640604	0.46738	0.423492165	
GNB1	&1519.034464	&1519.352692	0.636456	29.0653	0.424997052	
SERPING1	&2614.65317	&2614.969066	0.631792	999	0.426698758	
SMS	&1889.453458	&1889.768775	0.630634	999	0.427122854	
ESD	&1287.358747	&1287.672508	0.627522	999	0.42826572	
ANG	&874.334471	&874.645306	0.62167	999	0.43042738	
IGLV1&40	&698.291257	&698.596066	0.609618	999	0.434931676	
AKR1A1	&1502.671178	&1502.974809	0.607262	9.00822	0.435820582	
apoa1BP	&1425.382303	&1425.681461	0.598316	999	0.439221271	
NUCB1	&2215.969632	&2216.264947	0.59063	0.32321	0.442175605	
SERPINA6	&2120.188969	&2120.483638	0.589338	0.43999	0.442675224	
GALNT6	&2888.375363	&2888.667907	0.585088	0.48501	0.444324869	
IGFBP5	&1174.418892	&1174.702802	0.56782	0.37035	0.451126493	
PRCP	&2722.025331	&2722.3048	0.558938	999	0.454688455	
MMP14	&2638.180386	&2638.458493	0.556214	999	0.455789714	
DNAJB9	&1082.179755	&1082.455728	0.551946	0.34002	0.457523648	
GSTO1	&1163.30226	&1163.578204	0.551888	999	0.457547283	
PPIB	&974.518287	&974.792537	0.5485	13.47723	0.458931242	
IDS	&2680.317737	&2680.591156	0.546838	2.12116	0.459612572	
FKBP4	&2242.864026	&2243.134556	0.54106	999	0.46199376	
LIFR	&5259.419401	&5259.683968	0.529134	0.39903	0.466971172	
tor1B	&1561.542787	&1561.805581	0.525588	0.34982	0.468467685	
GDI2	&2124.837879	&2125.100038	0.524318	0.34707	0.469005536	
CPD	&6383.53885	&6383.800883	0.524066	0.65493	0.469112377	
PPP2R4	&2046.207262	&2046.466913	0.519302	0.50635	0.471139581	
FAM12B	&709.059614	&709.319111	0.518994	999	0.471271129	
TSNAX	&1310.076424	&1310.335659	0.51847	0.35194	0.471495067	
CD63	&1055.961714	&1056.219803	0.516178	5.77044	0.472476608	
RNASET2	&1452.976547	&1453.233445	0.513796	0.35359	0.473500198	
GSTZ1	&1095.870881	&1096.126227	0.510692	999	0.474839448	
SEMG2	&3579.118007	&3579.370484	0.504954	1.63109	0.477331428	
NIF3L1	&1933.002393	&1933.254354	0.503922	0.36048	0.47778188	
FAM3C	&978.463957	&978.714418	0.500922	0.35888	0.479095283	
LTF	&4531.95439	&4532.20288	0.49698	0.63017	0.480830098	
HSPA1L	&3827.399846	&3827.632011	0.46433	0.37233	0.495607264	
LRG1	&1930.593017	&1930.816329	0.446624	0.3781	0.503942538	
PAM	&4585.775691	&4585.997886	0.44439	0.38173	0.505011165	
IL1R1	&2818.148063	&2818.368913	0.4417	0.38306	0.506303077	
LAMP2	&1922.642781	&1922.863336	0.44111	0.38233	0.506587192	
PSCA	&647.787845	&648.001583	0.427476	999	0.513230043	
DDAH1	&1301.864447	&1302.077256	0.425618	0.39011	0.514147	
KLK2	&1341.131052	&1341.340192	0.41828	0.38829	0.517796541	
SERPINI1	&1936.66285	&1936.849009	0.372318	0.41431	0.541743463	
ANXA7	&2298.579717	&2298.763456	0.367478	0.41839	0.544382194	
LDHA	&1654.953584	&1655.136212	0.365256	0.41912	0.545601579	
PSMB4	&1249.322354	&1249.502238	0.359768	0.42206	0.548635111	
APOD	&1108.56805	&1108.746107	0.356114	0.42371	0.550672382	
TP53I3	&1652.112869	&1652.287133	0.348528	0.4282	0.554947579	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
LGALS3	&1333.798643	&1333.96993	0.342574	1.85749	0.558347215	
CST6	&707.084396	&707.25272	0.336648	999	0.56177048	
SEPP1	&1952.727224	&1952.895091	0.335734	0.57964	0.56230205	
CTSF	&2580.715269	&2580.882988	0.335438	0.65887	0.562474406	
C9	&3135.211995	&3135.378806	0.333622	0.58742	0.563534067	
RAB5C	&1146.864907	&1147.030057	0.3303	0.438	0.565482491	
ALB	&3215.396237	&3215.558852	0.32523	0.60557	0.568481429	
SLC35F2	&1867.849083	&1868.004957	0.311748	0.44879	0.576609518	
ACPP	&2125.625672	&2125.777253	0.303162	1.55687	0.581906888	
HEXB	&2926.748045	&2926.898274	0.300458	1.78109	0.583595438	
HEBP2	&1011.545621	&1011.693652	0.296062	0.45765	0.586361791	
CAT	&2660.665647	&2660.806635	0.281976	0.47147	0.595408992	
ATRN	&7570.665325	&7570.805539	0.280428	0.87501	0.596420828	
CPVL	&2494.131627	&2494.271189	0.279124	1.60321	0.597275954	
KRT9	&3261.918396	&3262.052911	0.26903	0.56867	0.6039832	
GNPTG	&1707.579975	&1707.711502	0.263054	0.51461	0.608029737	
PSAT1	&1797.68051	&1797.801043	0.241066	0.63182	0.623437251	
EFHD2	&1218.281548	&1218.400321	0.237546	999	0.625984168	
QPCT	&1826.682658	&1826.789518	0.21372	0.64822	0.6438672	
ASRGL1	&1616.207111	&1616.310983	0.207744	1.64008	0.648541409	
SLC1A1	&2560.76934	&2560.871897	0.205114	1.62434	0.650624257	
CYB5R2	&1467.886393	&1467.983991	0.195196	0.57112	0.658626764	
PIP	&979.851121	&979.945372	0.188502	1.60428	0.664166325	
PIGR	&4428.8969	&4428.990454	0.187108	0.67717	0.665334583	
MARCKS	&1423.921642	&1424.006229	0.169174	0.59828	0.680846946	
IDUA	&3704.77725	&3704.858095	0.16169	1.24348	0.687605317	
PRDX4	&1291.841611	&1291.912921	0.14262	0.71585	0.705690146	
PDGFA	&1304.179299	&1304.245821	0.133044	0.61584	0.71529656	
ANTXR2	&2362.753408	&2362.819331	0.131846	0.62507	0.716525669	
LCN2	&1102.420757	&1102.483712	0.12591	0.63813	0.722710965	
AKR1B1	&1485.7033	&1485.763591	0.120582	0.6451	0.728404119	
CFB	&3283.287423	&3283.344683	0.11452	0.77887	0.735055718	
SERPINA3	&2836.545766	&2836.601606	0.11168	0.76868	0.738239527	
ELSPBP1	&1097.148957	&1097.20234	0.106766	0.66002	0.743856473	
OLFM1	&2196.888901	&2196.937149	0.096496	0.29854	0.756075795	
tmpRSS2	&3227.646988	&3227.68812	0.082264	1.2577	0.774252434	
PAICS	&2099.991284	&2100.029355	0.076142	0.7046	0.78259538	
ACE2	&4534.164159	&4534.199005	0.069692	0.79755	0.791785756	
ACRBP	&3030.209544	&3030.241027	0.062966	0.72929	0.801868022	
CLN5	&2182.491813	&2182.522478	0.06133	0.72974	0.804406037	
SCPEP1	&2263.091498	&2263.121976	0.060956	1.22281	0.804991274	
COL9A1	&4609.342727	&4609.373183	0.060912	0.83335	0.805060251	
CAPZA2	&1215.853444	&1215.880561	0.054234	0.7462	0.815853079	
SORD	&1998.316141	&1998.34154	0.050798	0.81743	0.821680467	
NCSTN	&3554.942349	&3554.965801	0.046904	0.76311	0.828540885	
CD47	&1466.428651	&1466.450321	0.04334	0.77145	0.835086385	
GAPDHS	&2135.293417	&2135.314791	0.042748	1.263	0.836200503	
DPP4	&3557.244474	&3557.265139	0.04133	0.77512	0.838902266	
TFRC	&4084.340304	&4084.360789	0.04097	0.83744	0.839595841	
APCS	&1273.40008	&1273.414214	0.028268	0.81126	0.8664803	
PLOD3	&3731.322346	&3731.334695	0.024698	1.28407	0.875121925	
OS9	&3130.839312	&3130.851536	0.024448	0.82103	0.875750398	
APLP2	&3673.368538	&3673.379995	0.022914	1.1892	0.879680927	
TNFSF10	&1406.91302	&1406.923259	0.020478	0.83718	0.886210129	
C1RL	&2663.39449	&2663.401186	0.013392	0.87262	0.907871436	
TEX101	&1484.655799	&1484.662317	0.013036	0.90322	0.909098829	
TIMP1	&1322.314268	&1322.320247	0.011958	1.14032	0.912922796	
SEMG1	&3121.137686	&3121.142213	0.009054	0.92915	0.924193691	
CAPNS1	&1630.710032	&1630.714272	0.00848	0.89818	0.926628984	
QSCN6	&3085.118554	&3085.122685	0.008262	1.11002	0.927575591	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CA4	&1908.241912	&1908.245236	0.006648	0.90917	0.935016278	
ZPBP	&1823.263122	&1823.266083	0.005922	0.92544	0.938659716	
CCT8	&2453.544538	&2453.547222	0.005368	1.0878	0.941593941	
SPACA3	&1235.71218	&1235.713641	0.002922	1.06423	0.956890925	
B4GALT1	&2161.605818	&2161.60702	0.002404	0.9607	0.960894908	
SYT7	&2148.506476	&2148.507622	0.002292	1.05382	0.961815994	
TSTA3	&1603.016648	&1603.017513	0.00173	1.04752	0.966822939	
ARSA	&2668.342185	&2668.342832	0.001294	0.98003	0.971304517	
VAT1	&1979.5769	&1979.577474	0.001148	0.96145	0.972971128	
CAP1	&2295.682322	&2295.682892	0.00114	0	0.973065434	
MDH1	&1613.269829	&1613.27037	0.001082	0	0.973759302	
FUCA2	&2251.739029	&2251.739282	0.000506	0	0.982053544	
TSN	&997.593312	&997.593491	0.000358	0	0.984904216	
CST1	&1078.738418	&1078.73858	0.000324	1.01633	0.985638853	
TCP1	&2481.710388	&2481.710547	0.000318	0	0.985772434	
PPP2CA	&1397.859642	&1397.859761	0.000238	0.98228	0.987691325	
PSMA3	&1296.800332	&1296.800429	0.000194	0	0.988887113	
SOD3	&1098.868449	&1098.868525	0.000152	0	0.990163268	
RAB3B	&1024.365537	&1024.3656	0.000126	0	0.991043956	
CREG1	&1115.995425	&1115.995487	0.000124	0	0.991115317	
SFN	&1070.961115	&1070.96117	0.00011	0	0.99163187	
PSMA1	&1253.110847	&1253.110897	0.0001	0	0.992021287	
Crisp2	&1477.307305	&1477.307348	8.6E&05	0	0.992600829	
RAB14	&906.933411	&906.933453	8.4E&05	0	0.99268737	
TPT1	&767.034396	&767.034438	8.4E&05	0	0.99268737	
CFL1	&744.260391	&744.260432	8.2E&05	0	0.992774947	
EFEMP1	&2220.761515	&2220.761555	8E&05	0	0.992863599	
PGK1	&1900.768993	&1900.769026	6.6E&05	0	0.993518026	
PSMA5	&1038.294519	&1038.29455	6.2E&05	0	0.993717516	
UBE2N	&635.71498	&635.715011	6.2E&05	0	0.993717516	
TSG101	&1726.947063	&1726.947091	5.6E&05	0	0.994029234	
CTSH	&1641.380935	&1641.380961	5.2E&05	0	0.994246422	
WFDC9	&484.053815	&484.05384	5E&05	0	0.994358151	
NUTF2	&661.35881	&661.358834	4.8E&05	0	0.994472138	
RUVBL1	&2020.851331	&2020.851352	4.2E&05	0	0.994829153	
PCMT1	&1290.088827	&1290.088847	4E&05	0	0.994953769	
SDCBP	&1416.988043	&1416.988061	3.6E&05	0	0.995212721	
WFDC2	&658.224877	&658.224893	3.2E&05	0	0.995486507	
PTN	&769.043881	&769.043896	3E&05	0	0.995629828	
GNG12	&817.92306	&817.923074	2.8E&05	0	0.995778011	
PSMA4	&1162.065778	&1162.06579	2.4E&05	0	0.996091196	
RAB5B	&1050.846222	&1050.846234	2.4E&05	0	0.996091196	
PSMA2	&1089.873197	&1089.873207	2E&05	0	0.996431764	
NAGA	&2039.417346	&2039.417356	2E&05	0	0.996431764	
DEFB129	&916.675782	&916.675791	1.8E&05	0	0.996614873	
GOT1	&2039.486906	&2039.486915	1.8E&05	0	0.996614873	
RTN4RL1	&2262.297473	&2262.297482	1.8E&05	1.00639	0.996614873	
F11R	&1624.957832	&1624.95784	1.6E&05	0	0.99680847	
GSTP1	&1061.846917	&1061.846925	1.6E&05	0	0.99680847	
YWHAZ	&991.250665	&991.250673	1.6E&05	0	0.99680847	
CNP	&1957.911778	&1957.911785	1.4E&05	0	0.997014596	
CACYBP	&1005.809	&1005.809006	1.2E&05	0	0.997236052	
VAMP8	&450.203308	&450.203314	1.2E&05	0	0.997236052	
ACYP1	&477.581379	&477.581384	1E&05	0	0.997476872	
NPC2	&720.695596	&720.695601	1E&05	0	0.997476872	
TGFB1	&1740.483058	&1740.483063	1E&05	0	0.997476872	
AGR2	&795.1436	&795.143604	8E&06	0	0.997743245	
Rab18	&1027.789374	&1027.789378	8E&06	0	0.997743245	
TFPI2	&1255.92129	&1255.921294	8E&06	0	0.997743245	
TIMP3	&905.35898	&905.358984	8E&06	0	0.997743245	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
PPP1CC	&1397.753986	&1397.753989	6E&06	0	0.998045592	
PRDX5	&1042.862124	&1042.862127	6E&06	0	0.998045592	
DDT	&577.492789	&577.492792	6E&06	0	0.998045592	
IGKC	&593.684163	&593.684166	6E&06	0	0.998045592	
RNASE4	&749.658605	&749.658608	6E&06	0	0.998045592	
VAMP2	&492.558869	&492.558872	6E&06	0	0.998045592	
RUVBL2	&2138.776525	&2138.776528	6E&06	0	0.998045592	
HRSP12	&647.632213	&647.632215	4E&06	0	0.998404232	
NME3	&751.632491	&751.632493	4E&06	0	0.998404232	
PRDX2	&981.3774	&981.377402	4E&06	0	0.998404232	
UBE2L3	&718.559454	&718.559456	4E&06	0	0.998404232	
GCHFR	&390.366009	&390.366009	0	0	1	
ARF6	&713.214294	&713.214289	&1E&05	0	#NUM!	
CAB39L	&1526.469559	&1526.469493	&0.000132	0	#NUM!	
CALR	&2081.082968	&1872.00321	&418.159516	0	#NUM!	
CDC42	&983.518286	&983.518243	&8.6E&05	0	#NUM!	
GPC4	&2659.242314	&2542.324179	&233.83627	0	#NUM!	
GPX3	&1102.627541	&1102.627372	&0.000338	0	#NUM!	
HDHD2	&1221.468842	&1221.468813	&5.8E&05	0	#NUM!	
MPI	&1973.135445	&1971.618468	&3.033954	7.54864	#NUM!	
Park7	&841.89195	&840.185642	&3.412616	18.52626	#NUM!	
PITPNA	&1375.602982	&1222.815423	&305.575118	0	#NUM!	
PSMD14	&1271.536867	&1271.536856	&2.2E&05	0	#NUM!	
PURA	&1247.663262	&1247.663232	&6E&05	0	#NUM!	
RAB1A	&880.866004	&880.865392	&0.001224	0	#NUM!	
RAB2A	&862.788181	&862.788162	&3.8E&05	0	#NUM!	
RALB	&1037.376555	&1037.376536	&3.8E&05	0	#NUM!	
RAP1B	&777.570235	&777.425023	&0.290424	0	#NUM!	
RHOA	&812.29152	&812.291489	&6.2E&05	0	#NUM!	
SOD1	&919.347355	&862.002819	&114.689072	0	#NUM!	
TWSG1	&990.387484	&990.387471	&2.6E&05	0	#NUM!	
VPS28	&1275.703147	&1274.734447	&1.9374	260.8564	#NUM!	
YWHAB	&1085.130054	&1085.130049	&1E&05	0	#NUM!	
YWHAE	&1079.034222	&1079.034221	&2E&06	0	#NUM!	
YWHAG	&1078.462837	&1078.462834	&6E&06	0	#NUM!	
YWHAQ	&1126.692122	&1126.692116	&1.2E&05	0	#NUM!	

Gorilla

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CD59	%864.847577	%868.166036	6.636918	999	0.009988659	
MUC6	%13539.60247	%13543.64114	8.077338	0.50603	0.004482224	
CCT3	%2965.629545	%2969.441039	7.622988	0.48955	0.005762893	
CNTNAP2	%7110.930123	%7115.132941	8.405636	0.44657	0.003740595	
ARSA	%2673.087094	%2676.260887	6.347586	0.30556	0.011754114	
GSN	%3871.927353	%3875.046889	6.239072	0.29325	0.012496194	
LAMB2	%9314.87304	%9320.036276	10.326472	0.28529	0.001311356	
PTPRD	%9066.242952	%9071.968598	11.451292	0.28517	0.000714443	
CD109	%7432.418345	%7435.606832	6.376974	0.26947	0.011561038	
FCGBP	%26823.23678	%26843.86187	41.250188	0.26687	1.33939E%10	
LAMC1	%7893.267627	%7897.509919	8.484584	0.25193	0.003581685	
PTPRJ	%7428.655844	%7433.488209	9.66473	0.2324	0.001878394	
ABP1	%4017.794653	%4020.755218	5.92113	0.23129	0.014960361	0.016440678
ATRN	%7591.655404	%7594.762943	6.215078	0.23051	0.012666677	
SMS	%1890.387601	%1895.932871	11.09054	0.22192	0.000867692	
ACR	%2431.089892	%2434.921041	7.662298	0.22129	0.005638664	
GRN	%3083.98982	%3087.069771	6.159902	0.20088	0.013067845	
SEMA3F	%3869.251076	%3872.232136	5.96212	0.20088	0.014616456	0.016271186
Hyou1	%4706.779618	%4709.81159	6.063944	0.1899	0.013796922	
SI	%9016.549217	%9026.86507	20.631706	0.18851	5.56665E%06	
MGAM	%9728.776068	%9736.585775	15.619414	0.18705	7.74553E%05	
PFAS	%6779.43206	%6785.45656	12.049	0.18505	0.000518202	
GPR56	%3512.550071	%3517.805038	10.509934	0.1811	0.001187345	
NRCAM	%6121.933053	%6126.36332	8.860534	0.18087	0.002914023	
SERPINB6	%2140.691125	%2153.372528	25.362806	0.17203	4.74989E%07	
GALNS	%2944.458907	%2948.149661	7.381508	0.17123	0.006589789	
SLC44A4	%3577.254927	%3580.682361	6.854868	0.16853	0.008840009	
GNPTG	%1708.203509	%1711.48837	6.569722	0.16737	0.010372815	
AGRN	%10949.25572	%10963.35145	28.19146	0.16709	1.09888E%07	
NAGA	%2039.410715	%2042.487416	6.153402	0.16286	0.013115957	
IDH1	%2148.515236	%2152.067349	7.104226	0.16007	0.007690242	
SORL1	%10869.27802	%10883.09327	27.6305	0.15984	1.46845E%07	
C9	%3133.769581	%3137.797026	8.05489	0.15927	0.0045381	
IGF2R	%12689.76414	%12701.85828	24.188284	0.15908	8.73621E%07	
GAA	%4986.2085	%4993.477987	14.538974	0.15448	0.00013729	
CAPNS1	%1633.344887	%1637.103808	7.517842	0.15233	0.006109082	
IL1R1	%2817.51527	%2820.406583	5.782626	0.15132	0.016185343	0.016610169
FASN	%13845.557	%13860.75766	30.401324	0.14777	3.51288E%08	
tmpRSS2	%3226.658097	%3230.681882	8.04757	0.14269	0.004556473	
MANBA	%4390.147191	%4393.573179	6.851976	0.14267	0.008854329	
PIGR	%4426.517836	%4432.408835	11.781998	0.13735	0.000598063	
FN1	%12062.85742	%12076.36159	27.008346	0.13583	2.02579E%07	
BPIL1	%2383.243273	%2388.276513	10.06648	0.13507	0.001509912	
ST14	%4410.07443	%4416.730038	13.311216	0.13375	0.000263823	
GPRC5C	%2503.034962	%2506.988942	7.90796	0.13325	0.004921774	
GLG1	%5644.863577	%5650.016437	10.30572	0.12995	0.001326185	
IL1RAP	%3278.287389	%3282.169006	7.763234	0.12804	0.00533204	
SMPDL3B	%2535.6632	%2539.382958	7.439516	0.12643	0.006380705	
ZPBP	%1822.381268	%1828.050955	11.339374	0.12491	0.000758809	
MYO1C	%5453.650394	%5459.230959	11.16113	0.12468	0.00083529	
SERPINB5	%1776.825666	%1780.427555	7.203778	0.12311	0.007275027	
LGALS3BP	%3226.845738	%3230.359549	7.027622	0.12156	0.008026186	
EEF1G	%2358.812397	%2362.860612	8.09643	0.11963	0.004435253	
ACE	%6850.206177	%6859.777378	19.142402	0.11885	1.21319E%05	
DAG1	%4330.09254	%4334.359576	8.534072	0.11683	0.00348559	
KRT5	%2977.703332	%2982.349364	9.292064	0.11403	0.002301487	
COLEC12	%3646.478903	%3650.791843	8.62588	0.11286	0.003314203	
CRTAC1	%3032.705724	%3036.157509	6.90357	0.11193	0.00860238	
ACO1	%4249.219287	%4254.35991	10.281246	0.11077	0.001343892	
CNTN3	%5074.713242	%5081.792561	14.158638	0.10993	0.000168024	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
FBLN2	%5916.844736	%5930.184466	26.67946	0.1085	2.40161E%07	
IQGAP1	%7510.175276	%7515.347011	10.34347	0.10571	0.001299335	
B4GALT1	%2162.595226	%2167.330958	9.471464	0.10481	0.002086928	
HSPG2	%32087.6425	%32121.29001	67.295022	0.10294	2.33771E%16	
col12A1	%14645.74191	%14656.39764	21.311454	0.10285	3.90392E%06	
PYGB	%4728.36601	%4745.397426	34.062832	0.09415	5.33608E%09	
SYT1	%1898.988325	%1902.318087	6.659524	0.09351	0.009862726	
ANXA4	%1495.139089	%1498.535405	6.792632	0.09249	0.009153486	
FUT3	%2253.69987	%2260.741522	14.083304	0.0914	0.000174889	
PDCD6IP	%3899.328618	%3902.54372	6.430204	0.08691	0.011219569	
GMPPA	%2235.512367	%2239.230443	7.436152	0.08332	0.006392643	
KRT10	%3013.447006	%3021.151188	15.408364	0.07985	8.66041E%05	
FLNB	%12658.72561	%12676.25355	35.055882	0.07871	3.20378E%09	
APEH	%3361.355942	%3365.328694	7.945504	0.07768	0.004820699	
MMP14	%2639.789127	%2643.262344	6.946434	0.07762	0.008398648	
CDH1	%4611.317178	%4619.219157	15.803958	0.076	7.02554E%05	
FH	%2428.390353	%2432.313419	7.846132	0.07453	0.005092956	
ADAMTS1	%4874.936017	%4884.505067	19.1381	0.07353	1.21593E%05	
LEFTY2	%2008.737779	%2016.349163	15.222768	0.07347	9.55445E%05	
MATN2	%4673.164494	%4677.44788	8.566772	0.07109	0.003423536	
ACTN1	%4234.609018	%4237.764247	6.310458	0.07084	0.012002783	
SDCBP2	%1528.64652	%1532.752426	8.211812	0.06685	0.004161857	
PGAM2	%1125.703395	%1128.716857	6.026924	0.0652	0.014089265	0.016101695
PSME4	%8502.478186	%8512.649463	20.342554	0.06492	6.47445E%06	
LPL	%2389.244807	%2394.22645	9.963286	0.06447	0.001596928	
ALDH7A1	%2686.587641	%2691.736886	10.29849	0.06417	0.001331391	
ADAMTSL1	%8529.160705	%8538.921119	19.520828	0.06375	9.95088E%06	
RELN	%16739.85479	%16756.19117	32.672762	0.0614	1.09055E%08	
NEO1	%6915.783393	%6927.511793	23.4568	0.05943	1.2775E%06	
HSPA4	%3746.754207	%3752.160578	10.812742	0.05911	0.001008039	
PTPRF	%9059.9008	%9074.065034	28.328468	0.05805	1.02379E%07	
NRP1	%4385.712413	%4391.544622	11.664418	0.056	0.000637069	
PPP5C	%2321.447784	%2325.990636	9.085704	0.05561	0.002576153	
THBS2	%5839.528508	%5848.764703	18.47239	0.05428	1.72384E%05	
BAIAP2	%2717.564077	%2722.186735	9.245316	0.05354	0.002360986	
SDK2	%10118.82453	%10150.22165	62.794258	0.05182	2.29467E%15	
CLSTN1	%4930.52088	%4942.813013	24.584266	0.04997	7.11301E%07	
CPZ	%2997.538589	%3020.980975	46.884772	0.04909	7.52854E%12	
MPST	%1728.484928	%1732.796429	8.623002	0.0468	0.003319443	
COL6A2	%6170.668897	%6187.643427	33.94906	0.04527	5.6574E%09	
ANXA6	%3525.588233	%3532.264551	13.352636	0.04364	0.00025806	
PTGDS	%982.220861	%987.353151	10.26458	0.04224	0.001356086	
TFRC	%4083.689567	%4092.855029	18.330924	0.0413	1.85669E%05	
ALDOA	%2009.898648	%2017.892698	15.9881	0.04082	6.37419E%05	
PTPRS	%9653.038028	%9670.769073	35.46209	0.04021	2.60063E%09	
RRBP1	%4916.734474	%4925.422839	17.37673	0.03868	3.06556E%05	
ODZ2	%12811.386	%12830.43929	38.106588	0.03702	6.69836E%10	
GPC1	%2722.666362	%2730.148059	14.963394	0.02984	0.000109617	
RTN4RL1	%2265.3058	%2274.518043	18.424486	0.02429	1.76772E%05	
CANT1	%2221.230092	%2234.474069	26.487954	0.02113	2.65187E%07	
CAPN1	%3437.942741	%3452.691745	29.498008	0.01993	5.59742E%08	
PLXNB2	%9380.462842	%9411.641902	62.35812	0.01508	2.86348E%15	
DSC3	%4386.141545	%4395.592437	18.901784	0.00761	1.37624E%05	
MYH9	%8818.536176	%8849.679202	62.286052	0	2.97021E%15	
EEF2	%4122.121142	%4145.416612	46.59094	0	8.74637E%12	
PFKP	%4124.928678	%4142.94168	36.026004	0	1.94702E%09	
CACNA2D1	%4978.582154	%4994.240161	31.316014	0	2.19264E%08	
COL6A1	%5761.744387	%5777.075167	30.66156	0	3.07191E%08	
DDB1	%5174.827907	%5190.107502	30.55919	0	3.23834E%08	
THBS1	%5463.151179	%5478.094967	29.887576	0	4.57837E%08	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CTSD	%2192.602569	%2205.874172	26.543206	0	2.57709E%07	
ACTN4	%4157.303221	%4170.305285	26.004128	0	3.40688E%07	
P4HB	%2490.394901	%2502.688373	24.586944	0	7.10314E%07	
RUVBL2	%2138.479223	%2150.410249	23.862052	0	1.03492E%06	
AHCY	%2340.161859	%2351.849172	23.374626	0	1.33326E%06	
MME	%3522.878945	%3533.973729	22.189568	0	2.47012E%06	
CA6	%1740.260637	%1750.955032	21.38879	0	3.74957E%06	
HSPA8	%3010.867894	%3021.392673	21.049558	0	4.47556E%06	
MMP2	%3193.967974	%3204.131556	20.327164	0	6.52674E%06	
KPNB1	%3991.148957	%4001.199523	20.101132	0	7.34532E%06	
sez6L2	%4431.050758	%4441.016801	19.932086	0	8.02423E%06	
TPP2	%6054.539062	%6064.399851	19.721578	0	8.95841E%06	
CCT8	%2456.02255	%2465.284269	18.523438	0	1.67828E%05	
SDC1	%1661.020135	%1670.078641	18.117012	0	2.07737E%05	
CPM	%2168.62841	%2177.556546	17.856272	0	2.38233E%05	
SORT1	%3971.954171	%3980.620756	17.33317	0	3.13664E%05	
LAP3	%3056.138209	%3064.745408	17.214398	0	3.33896E%05	
EFHD2	%1218.290983	%1226.832154	17.082342	0	3.57936E%05	
SYT7	%2153.578766	%2162.118026	17.07852	0	3.58657E%05	
PLOD2	%3512.836044	%3521.286822	16.901556	0	3.93693E%05	
EDIL3	%2207.284382	%2215.730747	16.89273	0	3.95528E%05	
XPNPEP1	%2971.435489	%2979.72791	16.584842	0	4.65214E%05	
RAB1A	%880.866004	%888.981319	16.23063	0	5.608E%05	
CFL1	%744.051345	%752.025456	15.948222	0	6.50989E%05	
PRKACA	%1824.043229	%1831.867099	15.64774	0	7.63037E%05	
RAB11B	%959.630271	%967.43856	15.616578	0	7.75715E%05	
LNPEP	%4990.709558	%4998.379324	15.339532	0	8.98172E%05	
ENO1	%2054.068678	%2061.338961	14.540566	0	0.000137174	
CTSB	%1792.738924	%1799.842762	14.207676	0	0.000163701	
CCT5	%2475.93397	%2482.6485	13.42906	0	0.000247756	
SPACA3	%1230.161728	%1236.857595	13.391734	0	0.000252736	
FMOD	%1737.548635	%1743.830972	12.564674	0	0.000393107	
GPI	%2904.58126	%2910.649517	12.136514	0	0.000494441	
GOT1	%2038.3305	%2044.395946	12.130892	0	0.000495934	
KRT1	%3123.240183	%3129.273944	12.067522	0	0.000513079	
OLFM1	%2197.4029	%2203.38073	11.95566	0	0.000544816	
HSPA1L	%3827.998622	%3833.921868	11.846492	0	0.000577701	
CCT7	%2534.079317	%2539.99707	11.835506	0	0.000581119	
GNB2	%1550.583602	%1556.331886	11.496568	0	0.000697248	
ANXA2	%1663.205633	%1668.64382	10.876374	0	0.000973987	
DNASE1	%1528.297593	%1533.33952	10.083854	0	0.001495742	
LMAN2	%1580.816571	%1585.843262	10.053382	0	0.001520685	
VCL	%5089.229061	%5094.174765	9.891408	0	0.001660523	
SMPD1	%3204.904606	%3209.794841	9.78047	0	0.001763752	
LTA4H	%2792.000385	%2796.812558	9.624346	0	0.001920148	
GAPDH	%1562.380512	%1566.801118	8.841212	0	0.002945035	
PGC	%1948.658724	%1953.045768	8.774088	0	0.003055399	
PPT1	%1498.131963	%1502.452275	8.640624	0	0.003287488	
TGFB3	%1781.886939	%1786.119914	8.46595	0	0.003618562	
TCP1	%2481.43078	%2485.651992	8.442424	0	0.003665673	
TF	%4065.714511	%4069.895014	8.361006	0	0.003833583	
PSAP	%2461.189866	%2465.351169	8.322606	0	0.003915471	
ANXA3	%1633.463293	%1637.614485	8.302384	0	0.003959307	
HSPA5	%2989.966287	%2994.092816	8.253058	0	0.004068341	
NAPA	%1260.183833	%1264.246241	8.124816	0	0.004366342	
ARF1	%802.333419	%806.310983	7.955128	0	0.004795132	
A4GALT	%1745.617219	%1749.521414	7.80839	0	0.005200422	
NEU1	%2051.780282	%2055.584312	7.60806	0	0.005810797	
VCP	%3670.73514	%3674.519485	7.56869	0	0.005939094	
HSPB1	%964.171163	%967.917	7.491674	0	0.006198491	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
GNAI3	%1543.818883	%1547.557124	7.476482	0	0.006251009	
GNS	%2819.156194	%2822.87032	7.428252	0	0.006420768	
KLK3	%1479.97554	%1483.685741	7.420402	0	0.006448841	
PPAP2A	%1294.327225	%1297.945796	7.237142	0	0.007141056	
TIMP2	%996.98763	%1000.595488	7.215716	0	0.007226798	
RAB27A	%1046.568145	%1050.125963	7.115636	0	0.007641449	
CD81	%1098.954482	%1102.432992	6.95702	0	0.008349098	
HEBP2	%1010.760934	%1014.230012	6.938156	0	0.008437605	
YWHAG	%1078.462822	%1081.744555	6.563466	0	0.010409343	
ALCAM	%2704.64226	%2707.894882	6.505244	0	0.01075568	
ARF6	%713.214321	%716.33875	6.248858	0	0.01242734	
KIF5B	%4447.74537	%4450.792889	6.095038	0	0.013556201	
TGFB1	%1740.346902	%1743.376214	6.058624	0	0.013838547	
MFAP4	%1277.996078	%1281.005903	6.01965	0	0.014147452	0.016186441
RAB14	%906.933411	%909.899003	5.931184	0	0.014875244	0.016355932
ALDH1A1	%2397.039547	%2399.983267	5.88744	0	0.015249253	0.016525424
SCPEP1	%2264.087184	%2266.968268	5.762168	0	0.016374855	0.016694915
PRCP	%2720.952429	%2723.769593	5.634328	0	0.017612095	0.016779661
LCN1	%1024.192378	%1027.007652	5.630548	0.12938	0.017650113	0.016864407
PROM2	%4694.157883	%4696.967966	5.620166	0.307	0.017754967	0.016949153
MAN2A1	%5436.932531	%5439.733897	5.602732	0.16969	0.017932493	
PPP2CA	%1404.699377	%1407.488276	5.577798	0	0.018189579	
LAMP1	%2236.03805	%2238.819952	5.563804	0.22546	0.018335531	
KAL1	%3350.644745	%3353.423384	5.557278	0.10293	0.018404008	
COL18A1	%9608.522659	%9611.299941	5.554564	0.57104	0.018432563	
GNMT	%1451.152204	%1453.898804	5.4932	0	0.019090571	
CCT2	%2334.107607	%2336.848335	5.481456	0	0.019219244	
RAB13	%919.801983	%922.530601	5.457236	0	0.019487449	
NUCB1	%2216.066359	%2218.791018	5.449318	0.17565	0.019575967	
GPX3	%1101.773382	%1104.481101	5.415438	0	0.019959445	0.01779661
PPIB	%977.00439	%979.709319	5.409858	0	0.020023345	
RAP1B	%777.425012	%780.050684	5.251344	0	0.021929826	
GSS	%2204.396814	%2207.019166	5.244704	0.10852	0.022013673	
HEXA	%2618.786177	%2621.407696	5.243038	0	0.022034763	
NCSTN	%3554.635265	%3557.253454	5.236378	0	0.022119279	
PPP1R7	%1599.55625	%1602.166781	5.221062	0	0.022314919	
DNAJC3	%2290.854672	%2293.461716	5.214088	0	0.022404595	
LDHB	%1500.35107	%1502.956547	5.210954	0	0.022445016	
RAB3B	%1024.215781	%1026.813703	5.195844	0	0.022640958	
TGFBR3	%4154.186935	%4156.777814	5.181758	0.11025	0.022825218	0.018644068
MAMDC2	%3253.894214	%3256.483175	5.177922	0.10984	0.022875666	
CAPZA2	%1219.525125	%1222.102109	5.153968	0	0.023193315	
ACTR1A	%1747.712288	%1750.270859	5.117142	0	0.023690603	
DCXR	%1305.942912	%1308.501456	5.117088	0.09253	0.02369134	
A1BG	%2641.17146	%2643.709052	5.075184	0.15514	0.024270696	
MMP7	%1412.652395	%1415.184372	5.063954	0	0.024428443	
SOD3	%1098.261663	%1100.776054	5.028782	0	0.024929424	
RAB27B	%1001.058172	%1003.568855	5.021366	0	0.025036411	
STEAP2	%2248.86765	%2251.35636	4.97742	0	0.025680253	
PSAT1	%1798.570204	%1801.03227	4.924132	0	0.026484103	0.019491525
SPINT3	%503.859841	%506.311902	4.904122	0	0.026792669	
EEF1A1	%2041.953382	%2044.403076	4.899388	0	0.026866215	
PTN	%768.795314	%771.244296	4.897964	0	0.026888379	
PPP1CC	%1397.753986	%1400.199715	4.891458	0	0.026989884	
GSR	%2856.974442	%2859.417541	4.886198	0.19473	0.027072241	
VAMP8	%450.203331	%452.642837	4.879012	0	0.027185176	
IDS	%2681.653924	%2684.079348	4.850848	0	0.027632544	
CLTC	%7273.924187	%7276.345818	4.843262	0	0.027754348	
RUVBL1	%2020.851407	%2023.271064	4.839314	0	0.027817959	
YWHAE	%1078.587663	%1081.003998	4.83267	0	0.027925352	0.020338983

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TP53I3	%1651.332225	%1653.744579	4.824708	0	0.028054617	
DDR1	%4202.253856	%4204.66156	4.815408	0.09978	0.028206394	
ALDOC	%1676.10391	%1678.474471	4.741122	0	0.029449859	
UBE2L3	%718.030044	%720.389071	4.718054	0	0.029847503	
RAC1	%947.128828	%949.48256	4.707464	0	0.030031923	
LSAMP	%1596.811789	%1599.165264	4.70695	0	0.030040904	
F11R	%1623.75109	%1626.096545	4.69091	0	0.030322584	
PRDX6	%1048.395558	%1050.720657	4.650198	0	0.031049966	
PDGFA	%1303.929706	%1306.24552	4.631628	0.10103	0.031387767	
PRKCSH	%2724.028428	%2726.335322	4.613788	0.21809	0.031715901	
PKM2	%2963.629451	%2965.930381	4.60186	0.16523	0.031937289	
SDCBP	%1416.836076	%1419.136962	4.601772	0.08856	0.031938928	
IQGAP2	%7135.291949	%7137.592162	4.600426	0.17782	0.031964013	
PSMB6	%1148.424874	%1150.705419	4.56109	0	0.032706252	
GPD1L	%1726.767611	%1729.029231	4.52324	0.25264	0.033437452	
GDI2	%2125.377341	%2127.607317	4.459952	0.11239	0.034698473	
CAPG	%1646.995472	%1649.214232	4.43752	0.10852	0.035157282	
PACSIN2	%2694.382489	%2696.587594	4.41021	0.14068	0.035724443	
OLFM4	%2762.649422	%2764.832412	4.36598	0.2597	0.036663389	
TMC5	%5451.346351	%5453.523087	4.353472	0.30394	0.036933577	
TUBB1	%2182.43051	%2184.607109	4.353198	0.11164	0.036939519	
CAB39L	%1526.347386	%1528.489256	4.28374	0	0.038478593	
NELL1	%4125.439247	%4127.571425	4.264356	0.37464	0.038919999	
SEMA7A	%3321.665877	%3323.788999	4.246244	0.2931	0.03933724	
QPCT	%1826.427524	%1828.528655	4.202262	0	0.040370096	
CKB	%1605.195855	%1607.291839	4.191968	0	0.040615922	
HIST2H2BE	%531.300085	%533.369079	4.137988	0	0.04193098	
UGDH	%2199.674047	%2201.709707	4.07132	0.11984	0.043617177	
CAB39	%1447.299331	%1449.330424	4.062186	0	0.043853695	
PLOD3	%3733.168793	%3735.188797	4.040008	0.20758	0.044433611	
MAN2B1	%5062.76113	%5064.780229	4.038198	0.27141	0.044481294	
SFN	%1070.893461	%1072.888879	3.990836	0	0.04574836	
LIPG	%2616.641107	%2618.636401	3.990588	0.49505	0.045755094	
GPR115	%4130.478291	%4132.473012	3.989442	0.28243	0.045786225	
GALNT7	%2933.265186	%2935.209582	3.888792	0	0.048609375	
CNDP2	%2405.035238	%2406.941862	3.813248	0.21666	0.050848757	0.023389831
MDH1	%1613.269972	%1615.149083	3.758222	0.12883	0.052548428	
APLP2	%3675.689076	%3677.529199	3.680246	0.13179	0.055060726	
FDPS	%2086.479498	%2088.319574	3.680152	0.35318	0.05506383	
TIMP3	%905.247432	%907.080395	3.665926	0	0.055535775	
BGN	%1721.504186	%1723.305475	3.602578	0.11894	0.057690044	
MAN2B2	%5889.212125	%5891.003294	3.582338	0.36651	0.058396908	
EFEMP1	%2220.748728	%2222.523946	3.550436	0.13727	0.059529806	
BCAN	%4543.837208	%4545.601492	3.528568	0.2069	0.060319864	
LDLR	%4412.274986	%4414.032356	3.51474	0.25214	0.0608252	
CD151	%1221.364101	%1223.120019	3.511836	0	0.060931896	
VPS28	%1274.085649	%1275.840684	3.51007	0.14064	0.060996878	
GFRA2	%2076.223482	%2077.969014	3.491064	0.10719	0.061700916	
MINPP1	%2558.699332	%2560.400286	3.401908	0	0.065121052	
RBP4	%887.185987	%888.875629	3.379284	0	0.06602073	
SERPINF1	%2280.885348	%2282.547018	3.32334	0.30404	0.068302934	
FOLH1	%3743.240992	%3744.890589	3.299194	4.57467	0.069313886	
NUCB2	%2065.443233	%2067.090679	3.294892	0	0.069495678	
GNB2L1	%1451.515393	%1453.161136	3.291486	0	0.069639969	
SERPINA3	%2835.711973	%2837.354577	3.285208	0.32391	0.06990677	
SLC35F2	%1868.021245	%1869.620459	3.198428	0.22392	0.073709088	
GBA	%3362.428461	%3364.013917	3.170912	1.55361	0.074960578	
STXBP2	%3026.810416	%3028.359004	3.097176	0.27349	0.078428233	
CLU	%2586.537377	%2588.074611	3.074468	0.20767	0.07953061	
CRISP3	%1300.215716	%1301.749587	3.067742	0.14141	0.079860325	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SIL1	%2462.209732	%2463.74278	3.066096	0.25415	0.079941237	
PSMA1	%1252.92673	%1254.456988	3.060516	0	0.080216192	
SERPINA6	%2120.056982	%2121.574224	3.034484	0.22365	0.081512462	
SORD	%1999.027573	%2000.504689	2.954232	0.36452	0.085652991	
PSMA6	%1113.91006	%1115.367713	2.915306	0	0.087742768	
LIFR	%5259.376173	%5260.808079	2.863812	0.31406	0.090592577	
CTSZ	%1651.585616	%1653.013235	2.855238	0.22013	0.091076759	
CPO	%2176.068827	%2177.496224	2.854794	0.21356	0.091101909	
GP2	%2925.395088	%2926.813645	2.837114	0.33677	0.092109514	
CAPZB	%2005.580648	%2006.992484	2.823672	0.13579	0.092883691	
LRG1	%1930.615229	%1932.015981	2.801504	0.27499	0.094175929	
GLO1	%898.313748	%899.711571	2.795646	0	0.094520666	
FKBP4	%2243.079506	%2244.47652	2.794028	0.43093	0.094616126	
PSMA4	%1161.978523	%1163.373561	2.790076	0	0.094849729	
ACP5	%1620.248203	%1621.642995	2.789584	0	0.094878855	
THBS4	%4698.742022	%4700.13509	2.786136	0.27677	0.095083248	
DBI	%657.589398	%658.98191	2.785024	0	0.095149268	
NME3	%749.358883	%750.740322	2.762878	0.1708	0.09647454	
VAMP2	%492.558883	%493.939866	2.761966	0	0.096529545	
PPP2R4	%2045.601511	%2046.972536	2.74205	0	0.097739308	
BPNT1	%1442.785652	%1444.153431	2.735558	0	0.098137218	
AKR7A2	%2000.177374	%2001.544427	2.734106	0.13388	0.098226456	
ANXA11	%4323.965707	%4325.331413	2.731412	0.25141	0.09839226	
TWSG1	%990.312247	%991.675208	2.725922	0	0.098731093	
YWHAQ	%1125.984073	%1127.344469	2.720792	0	0.099048858	
LCP1	%2873.140966	%2874.498666	2.7154	0	0.099384055	
SERPINC1	%2500.849436	%2502.204292	2.709712	0.22283	0.099738996	
AGT	%2692.831387	%2694.181466	2.700158	0	0.100338302	
YWHAB	%1085.130045	%1086.479082	2.698074	0	0.10046955	
LCN2	%1101.665981	%1103.011378	2.690794	0	0.100929509	
TSNAX	%1310.24195	%1311.577422	2.670944	0	0.102195391	
PLA2G7	%2164.260605	%2165.59472	2.66823	0.2254	0.102369815	
FAM3C	%978.693898	%980.026592	2.665388	0	0.102552814	
RNASET2	%1452.493037	%1453.822167	2.65826	0	0.103013368	
KLK11	%1493.135677	%1494.449962	2.62857	0	0.104956203	
GC	%2486.491013	%2487.799668	2.61731	0	0.105703497	
FSTL1	%1390.16813	%1391.470685	2.60511	0	0.106519766	
APOA2	%561.33124	%562.618031	2.573582	0	0.108661434	
CAPZA1	%1243.651326	%1244.934194	2.565736	0	0.109201724	
CST6	%707.902238	%709.180773	2.55707	0.17752	0.109801914	
GNB1	%1523.517106	%1524.794	2.553788	0	0.110030165	
MPI	%1971.186827	%1972.45226	2.530866	0	0.111638931	
CD47	%1467.59172	%1468.853595	2.52375	0	0.112143615	
Rab18	%1027.655075	%1028.908465	2.50678	0	0.11335734	
SPINT1	%2726.277042	%2727.518518	2.482952	999	0.115086068	
PSMA7	%1180.896274	%1182.13659	2.480632	0	0.115255932	
PIP	%979.296477	%980.536762	2.48057	999	0.115260475	
LDHA	%1655.327526	%1656.544652	2.434252	0	0.118710509	
CPVL	%2495.044469	%2496.256051	2.423164	0.28592	0.119553241	
VAT1	%1981.047747	%1982.252009	2.408524	0.1593	0.1206761	
PSMB4	%1249.795445	%1250.990368	2.389846	0	0.122125659	
TSN	%997.593312	%998.78391	2.381196	0	0.122803497	
MDH2	%1639.224865	%1640.394185	2.33864	0.24902	0.126199689	
TMEFF2	%1662.426611	%1663.580821	2.30842	0	0.128674787	
IGKC	%593.117795	%594.262765	2.28994	999	0.130214957	
CALR	%1869.494421	%1870.63431	2.279778	0.24607	0.131070634	
B4GALT4	%1760.542622	%1761.681509	2.277774	0.35884	0.131240117	
PRKAR2A	%2023.088263	%2024.218256	2.259986	0.15988	0.132755261	
CD38	%1611.412662	%1612.534655	2.243986	0.25548	0.134134811	
SEMA3C	%3591.245554	%3592.357437	2.223766	0.25733	0.1359012	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PITPNA	%1222.646354	%1223.74628	2.199852	0	0.138023989	
ANXA1	%1595.120444	%1596.21223	2.183572	0.15308	0.139490386	
IDE	%4640.580901	%4641.66182	2.161838	0.27061	0.141475374	
PGLS	%1263.532772	%1264.599688	2.133832	0.17577	0.144080168	
TALDO1	%1588.881252	%1589.943168	2.123832	0.17007	0.145023296	
CAP1	%2295.614501	%2296.668442	2.107882	0.26664	0.146542017	
CAT	%2660.765019	%2661.808515	2.086992	0.27049	0.148558324	
GRHPR	%1677.633002	%1678.670805	2.075606	0.18142	0.149670484	
DNASE2	%1921.139752	%1922.177519	2.075534	0.29667	0.149677547	
FUCA2	%2251.710213	%2252.739285	2.058144	0.16855	0.151394473	
EXTL2	%1509.142673	%1510.13815	1.990954	0.18797	0.158241166	
TEX101	%1484.025	%1485.002487	1.954974	0.25284	0.162051862	
PGD	%2494.823886	%2495.799995	1.952218	0.19155	0.16234804	
PSMB7	%1342.871295	%1343.832889	1.923188	0.284	0.165505643	
PLA1A	%2498.997078	%2499.954817	1.915478	0.38183	0.166356021	
PSMA2	%1076.264497	%1077.218695	1.908396	3.48093	0.167141542	
PHGDH	%2550.513306	%2551.461869	1.897126	0.36853	0.168400364	
TGM4	%3677.852258	%3678.783615	1.862714	0.49927	0.172311892	
PGM2	%3759.071656	%3759.985968	1.828624	0.75949	0.176290158	
ANXA5	%1412.482085	%1413.39243	1.82069	0.20241	0.177231166	
ALB	%3215.514409	%3216.4215	1.814182	0.30603	0.178007373	
CTBS	%1987.621777	%1988.512289	1.781024	0.32574	0.182023635	
APOB	%23797.39623	%23798.28396	1.775466	0.71688	0.182707063	
APP	%3791.278282	%3792.162935	1.769306	0.19239	0.18346799	
SOD1	%861.276965	%862.134958	1.715986	0.21254	0.190210556	
ORM1	%1198.227971	%1199.085918	1.715894	0.39667	0.190222436	
COPB2	%4073.061103	%4073.913652	1.705098	0.30816	0.191622617	
LGALS3	%1334.171135	%1335.022028	1.701786	0.30661	0.192054573	
INHBB	%1721.278946	%1722.125616	1.69334	0.10342	0.193161268	
RAB5C	%1147.217284	%1148.052424	1.67028	0.21728	0.196221035	
SERPINA4	%2416.814712	%2417.646708	1.663992	0.34485	0.197065193	
VTN	%2593.364592	%2594.178239	1.627294	0.40947	0.202077735	
PGM1	%2773.990203	%2774.79882	1.617234	0.39641	0.203477899	
GUSB	%3809.960101	%3810.751807	1.583412	0.59472	0.208269906	
ACPP	%2125.513619	%2126.296456	1.565674	0.22844	0.210836368	
ENPP3	%4424.179766	%4424.962379	1.565226	0.28439	0.210901671	
HEXB	%2927.679117	%2928.452513	1.546792	0.33539	0.213609654	
ECM1	%2916.571953	%2917.34016	1.536414	0.40801	0.215152364	
C1RL	%2663.718486	%2664.485029	1.533086	0.4329	0.215649881	
ALDH9A1	%2588.331933	%2589.079202	1.494538	0.41147	0.221513696	
SMOC2	%2172.431505	%2173.173769	1.484528	0.28681	0.223067416	
PRSS8	%1907.407432	%1908.13158	1.448296	0.37908	0.228801571	
SLC15A2	%3495.003329	%3495.726186	1.445714	999	0.229216924	
APOD	%1108.675256	%1109.379146	1.40778	104.8521	0.235425276	
CPE	%2254.551033	%2255.244976	1.387886	0.29761	0.238762428	
ACAT2	%2216.828868	%2217.517405	1.377074	999	0.240600181	
ITIH5	%5262.707813	%5263.377523	1.33942	0.62307	0.247136278	
RDX	%2840.116048	%2840.784203	1.33631	0.65841	0.247685757	
TOLLIP	%1321.484566	%1322.151512	1.333892	0.41664	0.248114005	
FUCA1	%2440.699342	%2441.362744	1.326804	0.38246	0.249374586	
pla2g2A	%857.200848	%857.856449	1.311202	0.02992	0.252177142	
SLIT2	%7464.045534	%7464.697512	1.303956	0.5141	0.253491877	
KRT9	%3261.609998	%3262.249363	1.27873	0.6049	0.258135304	
LTF	%4531.978341	%4532.616231	1.27578	0.55889	0.25868515	
CD44	%3893.379465	%3894.015149	1.271368	0.49708	0.259510201	
CAMP	%1002.812326	%1003.440493	1.256334	127.76828	0.262346157	
GLB1	%3849.04849	%3849.673126	1.249272	0.34625	0.263691567	
ADAM10	%3308.937533	%3309.548402	1.221738	0.41525	0.269019838	
RALA	%1061.054445	%1061.662033	1.215176	0.67171	0.270309446	
CA2	%1301.100012	%1301.697248	1.194472	0.39997	0.274429353	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
DPP7	%2585.55367	%2586.132839	1.158338	0.45292	0.281810491	
GALNT6	%2886.972589	%2887.514893	1.084608	23.72288	0.297668997	
ENPP5	%2242.521318	%2243.062675	1.082714	0.25878	0.298091208	
ARHGDIA	%1707.906486	%1708.438258	1.063544	0.34578	0.30240827	
KRT8	%2765.505252	%2766.035247	1.05999	0.25067	0.303217466	
GGT1	%3045.52569	%3046.054746	1.058112	0.55234	0.303646189	
GPC4	%2542.026105	%2542.521026	0.989842	0.36054	0.319780994	
PSMB5	%1222.571193	%1223.051504	0.960622	0.24994	0.327030215	
SERPINA5	%2277.584056	%2278.048046	0.92798	0.39478	0.335388371	
APOE	%1813.363042	%1813.815922	0.90576	0.42035	0.341241924	
RPLP0	%1378.123478	%1378.571181	0.895406	0.37951	0.344016525	
NIF3L1	%1933.000673	%1933.411166	0.820986	0.39749	0.36489204	
GDF15	%1711.958998	%1712.353997	0.789998	0.50916	0.37410073	
SLC1A1	%2564.037353	%2564.430462	0.786218	0.40545	0.375246175	
GSTP1	%1061.675953	%1062.063597	0.775288	0.26896	0.378586122	
AGR2	%793.96209	%794.347793	0.771406	999	0.379782446	
NAGLU	%3595.854592	%3596.238701	0.768218	0.41348	0.380768893	
RNASE1	%845.776901	%846.15246	0.751118	0.28012	0.386122496	
PPIC	%1090.355127	%1090.727937	0.74562	999	0.387866518	
Crisp2	%1477.234218	%1477.592076	0.715716	0.29061	0.397552744	
CA4	%1908.27441	%1908.631885	0.71495	0.52331	0.397805413	
GAPDHS	%2136.526937	%2136.875323	0.696772	0.44144	0.403870479	
DSC2	%4622.962745	%4623.309845	0.6942	0.58106	0.404739468	
PRKAR1A	%1749.537188	%1749.8799	0.685424	118.28303	0.407725223	
CRISP1	%1448.597549	%1448.937321	0.679544	0.45613	0.40974379	
HPRT1	%1070.30601	%1070.639297	0.666574	0.55883	0.414248623	
GANAB	%4579.51931	%4579.847709	0.656798	0.43935	0.417692651	
RNASE4	%749.641886	%749.968283	0.652794	0.30761	0.419115519	
GNPDA1	%1286.835468	%1287.156324	0.641712	0.31086	0.423091536	
MSMB	%701.028439	%701.344079	0.63128	999	0.42688619	
GSTM3	%1077.112108	%1077.425595	0.626974	0.31364	0.428467448	
GSTO1	%1164.085867	%1164.396593	0.621452	0.31698	0.430508225	
RAB3D	%1031.382483	%1031.691781	0.618596	0.27149	0.4315695	
PRDX5	%1042.796966	%1043.103083	0.612234	0.45167	0.433947907	
ANG	%874.339817	%874.645278	0.610922	65.6673	0.434440872	
LDHC	%1560.408692	%1560.712587	0.60779	999	0.43562113	
EGF	%6295.442287	%6295.739455	0.594336	0.60793	0.440747296	
RAB1B	%972.002635	%972.299495	0.59372	2.12348	0.440984212	
GLA	%2065.081879	%2065.369172	0.574586	999	0.448442295	
CTSH	%1640.684164	%1640.965993	0.563658	0.49068	0.452790122	
DNAJB9	%1082.179005	%1082.458393	0.558776	0.33769	0.454753832	
ELSPBP1	%1097.852382	%1098.128849	0.552934	0.33462	0.457121335	
DEFB129	%916.267563	%916.543734	0.552342	5.45191	0.45736233	
SH3BGRL2	%467.389171	%467.661613	0.544884	0.33741	0.460415657	
AMBP	%1760.10476	%1760.376689	0.543858	999	0.460838229	
CUL3	%3334.969036	%3335.239294	0.540516	0.34462	0.462218958	
DDAH1	%1300.690871	%1300.960033	0.538324	6.3397	0.463128146	
RALB	%1036.863013	%1037.124445	0.522864	0.34774	0.469622532	
APOH	%1788.794352	%1789.049607	0.51051	0.35566	0.474918164	
ACLY	%5465.244074	%5465.493144	0.49814	0.35192	0.480318532	
CCT4	%2397.488749	%2397.737151	0.496804	0.36111	0.480907793	
GM2A	%1026.978878	%1027.215952	0.474148	0.3697	0.491085058	
TKT	%3003.971755	%3004.208171	0.472832	999	0.491687193	
AGA	%1771.514252	%1771.75049	0.472476	0.52335	0.491850293	
GSTT1	%1142.057316	%1142.289941	0.46525	5.56338	0.495180545	
apoa1BP	%1425.897928	%1426.125945	0.456034	0.52672	0.499483345	
fam3B	%1383.982694	%1384.208302	0.451216	0.37928	0.50175806	
CREG1	%1114.829002	%1115.04758	0.437156	3.90862	0.508498337	
PSCA	%647.787645	%648.001909	0.428528	999	0.512712122	
PRDX4	%1292.389491	%1292.597492	0.416002	0.39396	0.51893874	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CLIC1	%1149.099745	%1149.305999	0.412508	0.39579	0.520699281	
SELENBP1	%2612.729511	%2612.93395	0.408878	999	0.522539538	
PSMB2	%1082.6038	%1082.807058	0.406516	0.3972	0.523743164	
ACRBP	%3030.272675	%3030.473306	0.401262	0.54967	0.526438226	
CD14	%1923.045293	%1923.245317	0.400048	0.4025	0.527064469	
CTSF	%2581.298032	%2581.487238	0.378412	0.57083	0.538454335	
TFPI2	%1255.921255	%1256.107082	0.371654	0.56324	0.542104074	
PSMA3	%1282.511835	%1282.694898	0.366126	0.7521	0.54512354	
PAM	%4585.4901	%4585.669944	0.359688	0.57007	0.548679563	
AKR1A1	%1503.796904	%1503.976226	0.358644	0.42252	0.549260289	
BASP1	%922.532851	%922.703716	0.34173	0.41962	0.558832331	
IDUA	%3708.640316	%3708.810188	0.339744	0.69842	0.559977027	
PRDX1	%897.837287	%897.99813	0.321686	0.44147	0.570596178	
MSLN	%3967.536931	%3967.687188	0.300514	0.73432	0.583560368	
PCMT1	%1289.649409	%1289.798049	0.29728	0.45738	0.585592663	
PSMB8	%1421.91061	%1422.047765	0.27431	0.52813	0.600455132	
CP	%5167.475595	%5167.610228	0.269266	0.71669	0.603824571	
NBL1	%995.170386	%995.30369	0.266608	999	0.605616284	
CRYZ	%1748.329966	%1748.45809	0.256248	0.75413	0.612709627	
CNP	%1956.795693	%1956.918818	0.24625	0.5303	0.619728034	
ASAH1	%2201.85069	%2201.970276	0.239172	1.68034	0.624804781	
BTD	%2765.758085	%2765.874771	0.233372	1.67452	0.629034735	
PEBP4	%1277.35778	%1277.467989	0.220418	999	0.638721608	
LGMN	%2347.67787	%2347.787166	0.218592	0.82718	0.640114844	
MLPH	%3876.575456	%3876.6777	0.204488	0.72598	0.651122391	
ALAD	%1834.233856	%1834.335082	0.202452	0.65579	0.6527489	
PI15	%1214.586348	%1214.685603	0.19851	0	0.655926229	
ANTXR2	%2358.445028	%2358.531467	0.172878	1.47504	0.677566602	
LZTFL1	%1304.259184	%1304.34509	0.171812	0.55124	0.678506421	
CTSO	%1608.451004	%1608.523114	0.14422	1.50729	0.704121288	
SEMG1	%3121.127412	%3121.197857	0.14089	0.8555	0.70739783	
GPR64	%4793.247794	%4793.304764	0.11394	0.77874	0.73570233	
IDI1	%1551.505997	%1551.56153	0.111066	0.64133	0.738933759	
CACYBP	%1001.495336	%1001.550618	0.110564	1.42894	0.739502941	
PSMD2	%4153.925727	%4153.976108	0.100762	0.73666	0.750917113	
SEMG2	%3579.206234	%3579.255709	0.09895	0.82027	0.753093332	
PPIA	%752.94522	%752.994604	0.098768	0.67185	0.753313121	
CYB5R2	%1466.517861	%1466.567088	0.098454	1.39406	0.753692842	
COL9A1	%4606.118681	%4606.166876	0.09639	1.17394	0.756205554	
PDIA3	%2406.898919	%2406.94703	0.096222	1.20139	0.756411371	
CLN5	%2181.953732	%2181.998822	0.09018	1.38602	0.763948448	
smpdl3A	%2309.128045	%2309.172107	0.088124	1.96196	0.766575787	
IL1RL1	%3848.026295	%3848.060324	0.068058	0.80022	0.794185602	
PRSS22	%1600.647335	%1600.679484	0.064298	3.00156	0.799827387	
WFDC8	%1415.12548	%1415.155443	0.059926	0.73619	0.806612939	
TPI1	%1184.066493	%1184.094718	0.05645	0.74304	0.812197488	
GGH	%1666.73125	%1666.758471	0.054442	0.74703	0.815506644	
HPX	%2733.459138	%2733.483752	0.049228	1.06648	0.824412097	
ACRV1	%1556.890356	%1556.913972	0.047232	0.83134	0.827951769	
LAMP2	%1922.554068	%1922.574982	0.041828	0.77306	0.837947987	
TSTA3	%1604.061608	%1604.08178	0.040344	0.78873	0.840809485	
ADAM7	%4046.343974	%4046.362525	0.037102	0.88976	0.847257525	
LYZ	%800.071222	%800.089086	0.035728	0.78967	0.850078303	
DPP4	%3555.596936	%3555.613212	0.032552	1.15788	0.856821498	
DPEP3	%2750.176207	%2750.192041	0.031668	1.15574	0.858758277	
SERPINI1	%1936.18868	%1936.203198	0.029036	0.80839	0.864695941	
SLPI	%797.205812	%797.220178	0.028732	1.21582	0.865399312	
NUTF2	%661.345412	%661.358909	0.026994	0	0.869496156	
IGJ	%899.473601	%899.485266	0.02333	0.82701	0.878602044	
CFB	%3282.818122	%3282.829768	0.023292	0.90137	0.878700185	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
APCS	%1273.39612	%1273.406799	0.021358	0.83347	0.883807898	
ANXA7	%2297.980323	%2297.99059	0.020534	0.8373	0.886055708	
PODXL2	%2867.608614	%2867.618687	0.020146	0.83292	0.88713008	
USP14	%2149.285199	%2149.294333	0.018268	1.16741	0.892486032	
ANPEP	%5012.760846	%5012.769153	0.016614	0.90876	0.897440491	
AZGP1	%1711.443015	%1711.449743	0.013456	1.14337	0.907652542	
GSTZ1	%1095.917315	%1095.923769	0.012908	0.88607	0.909544281	
SERPINA1	%2321.497957	%2321.504092	0.01227	1.09533	0.91179871	
TTR	%787.182373	%787.187499	0.010252	0.88102	0.919350291	
PROS1	%3325.437492	%3325.441354	0.007724	0.93017	0.929967053	
SCGB2A1	%559.887878	%559.89134	0.006924	0.90141	0.933684103	
PAICS	%2099.455499	%2099.456493	0.001988	1.05288	0.96443651	
NPC2	%720.695517	%720.695902	0.00077	0	0.977862443	
HDHD2	%1220.72636	%1220.726616	0.000512	0.97249	0.981947474	
YWHAZ	%991.250665	%991.25081	0.00029	0	0.986413172	
LIPA	%2212.725158	%2212.725293	0.00027	0.98104	0.986890009	
TNFSF10	%1407.152971	%1407.153056	0.00017	0	0.989597153	
PSMA5	%1038.294519	%1038.294553	6.8E%05	0	0.99342055	
PSMD14	%1271.537039	%1271.537069	6E%05	0	0.993819675	
WFDC2	%658.224871	%658.224899	5.6E%05	0	0.994029234	
WFDC9	%484.053815	%484.05384	5E%05	0	0.994358151	
PFN2	%782.864767	%782.864791	4.8E%05	0	0.994472138	
HINT1	%580.02349	%580.023511	4.2E%05	0	0.994829153	
CD63	%1057.698313	%1057.698331	3.6E%05	0	0.995212721	
CD9	%1042.243327	%1042.243341	2.8E%05	0	0.995778011	
RAB5B	%1050.846223	%1050.846234	2.2E%05	0	0.996257603	
CYB561	%1914.481332	%1914.481342	2E%05	0	0.996431764	
RAD23B	%1919.641356	%1919.641366	2E%05	0	0.996431764	
s100A11	%497.122244	%497.122251	1.4E%05	0	0.997014596	
TXN	%469.042743	%469.042748	1E%05	0	0.997476872	
GNG12	%817.923069	%817.923074	1E%05	0	0.997476872	
HRSP12	%647.632213	%647.632215	4E%06	0	0.998404232	
PFN1	%648.281839	%648.28184	2E%06	0	0.998871621	
SPINK2	%513.689213	%513.689214	2E%06	0	0.998871621	
TAGLN2	%907.149041	%907.149042	2E%06	0	0.998871621	
ACYP1	%477.58139	%477.581387	%6E%06	0	#NUM!	
AKR1B1	%1486.811167	%1486.811156	%2.2E%05	0	#NUM!	
B2M	%642.341013	%642.341012	%2E%06	0	#NUM!	
DCD	%649.029897	%649.029896	%2E%06	0	#NUM!	
EPHA5	%4886.089616	%4885.957635	%0.263962	0.67722	#NUM!	
FBP1	%1925.91591	%1667.032877	%517.766066	0	#NUM!	
GCHFR	%390.36601	%390.366008	%4E%06	0	#NUM!	
PGK1	%1900.76904	%1900.769027	%2.6E%05	0	#NUM!	
PRDX2	%981.383701	%981.377656	%0.01209	0	#NUM!	
PURA	%1247.663256	%1247.663255	%2E%06	0	#NUM!	
RAB10	%817.552681	%817.552679	%4E%06	0	#NUM!	
RHOA	%812.291506	%812.291489	%3.4E%05	0	#NUM!	
tor1B	%1562.057248	%1562.057244	%8E%06	0	#NUM!	
TPT1	%819.794478	%767.034436	%105.520084	0	#NUM!	
TSG101	%1830.004102	%1726.947091	%206.114022	0	#NUM!	

Orangutan

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPG2	&32047.29965	&32160.7028	226.806294	0.0647	2.96386E&51	
FCGBP	&26823.89729	&26887.80657	127.818562	0.15756	1.22988E&29	
PLXNB2	&9381.207848	&9442.830071	123.244446	0.03331	1.23285E&28	
ODZ2	&12811.56765	&12860.81734	98.499384	0.01609	3.25126E&23	
LAMA5	&19256.10133	&19303.43252	94.662382	0.16316	2.25789E&22	
PTPRS	&9651.392565	&9693.221472	83.657814	0.02013	5.88273E&20	
MYH9	&8816.860455	&8856.612381	79.503852	0.03416	4.81286E&19	
AGRN	&10949.43482	&10988.49372	78.11781	0.12931	9.70747E&19	
FASN	&13844.76182	&13883.18371	76.843782	0.15938	1.8503E&18	
ACE	&6849.465468	&6887.535489	76.140042	0.07718	2.64244E&18	
COL6A2	&6163.217242	&6200.605184	74.775884	0.01644	5.27299E&18	
EEF2	&4122.002285	&4159.194498	74.384426	0	6.42942E&18	
MUC5B	&33209.60656	&33245.94661	72.680094	0.40042	1.52464E&17	
ACTN4	&4157.607179	&4192.249359	69.28436	0.00655	8.52429E&17	
TPP2	&6048.160146	&6081.539583	66.758874	0	3.06833E&16	
PTPRF	&9059.558323	&9092.530444	65.944242	0.06514	4.63862E&16	
SDK2	&10118.68238	&10151.20899	65.053214	0.0546	7.29026E&16	
FLNB	&12657.81322	&12688.0511	60.475766	0.09537	7.44899E&15	
RELN	&16740.01313	&16769.05679	58.087318	0.10619	2.50738E&14	
THBS2	&5839.556634	&5868.332983	57.552698	0.06372	3.29044E&14	
col12A1	&14644.71156	&14673.41178	57.400432	0.07591	3.55529E&14	
MYO1C	&5453.717634	&5481.907106	56.378944	0.03804	5.9767E&14	
ACTN1	&4232.279953	&4260.18059	55.801274	0.06757	8.01796E&14	
SLIT2	&7466.940528	&7494.701609	55.522162	0.03828	9.24113E&14	
KIF5B	&4443.082623	&4470.256233	54.34722	0.01275	1.68016E&13	
IGF2R	&12688.13164	&12714.71962	53.175976	0.12974	3.04966E&13	
VWF	&13693.88683	&13720.05604	52.338432	0.16995	4.67142E&13	
MUC6	&13540.07698	&13565.62238	51.090808	0.25339	8.81903E&13	
FN1	&12062.5336	&12088.05985	51.052498	0.08014	8.99284E&13	
RRBP1	&4914.669946	&4939.908438	50.476984	0.04029	1.20571E&12	
ST14	&4408.582942	&4433.482632	49.79938	0.03759	1.70298E&12	
BAIAP2	&2717.368937	&2741.990094	49.242314	0.02362	2.26218E&12	
GAA	&4985.882435	&5010.452158	49.139446	0.09214	2.38398E&12	
STXBP2	&3028.276511	&3051.64	46.726978	0.03492	8.15979E&12	
CAPN1	&3437.549794	&3460.668486	46.237384	0.01266	1.04759E&11	
SORL1	&10870.05716	&10892.64673	45.17914	0.08637	1.7981E&11	
LDLR	&4409.829539	&4432.253464	44.84785	0.05011	2.12955E&11	
CPZ	&2997.693611	&3018.7911	42.194978	0.05205	8.26119E&11	
LAMC1	&7895.483377	&7916.227027	41.4873	0.09261	1.18639E&10	
CPAMD8	&10033.09711	&10053.45575	40.717272	0.19522	1.75925E&10	
PTPRD	&9069.072772	&9088.851353	39.557162	0	3.18596E&10	
FBLN2	&5916.630463	&5936.226864	39.192802	0.0975	3.83953E&10	
CTSD	&2193.781115	&2212.832907	38.103584	0.03092	6.70868E&10	
ENO1	&2053.718668	&2072.572171	37.707006	0	8.22088E&10	
PLOD3	&3732.318559	&3750.752007	36.866896	0.04428	1.26475E&09	
AHCY	&2339.028451	&2356.711403	35.365904	0.0175	2.73228E&09	
CLTC	&7273.290129	&7290.953941	35.327624	0	2.78652E&09	
CLSTN1	&4928.781768	&4946.215222	34.866908	0.11555	3.5303E&09	
ACLY	&5465.709435	&5483.071809	34.724748	0.03976	3.79773E&09	
GGT1	&3050.111755	&3066.704665	33.18582	0.08305	8.37591E&09	
CACNA2D1	&4978.446051	&4994.967658	33.043214	0	9.01331E&09	
TGM4	&3671.007737	&3687.047735	32.079996	0.07399	1.47953E&08	
TMEM8	&4066.507046	&4082.361935	31.709778	0.06714	1.79019E&08	
ADAMTS1	&4872.977378	&4888.830637	31.706518	0.16078	1.79319E&08	
LEFTY2	&2008.711791	&2023.947236	30.47089	0.05433	3.38914E&08	
APP	&3786.371888	&3801.451063	30.15835	0	3.98169E&08	
IQGAP1	&7509.331157	&7524.330069	29.997824	0.10407	4.32531E&08	
GLG1	&5645.828069	&5660.766423	29.876708	0.04814	4.60411E&08	
EFHD2	&1217.291631	&1231.659142	28.735022	0.09363	8.29893E&08	
PRKCSH	&2723.286172	&2737.646478	28.720612	0.04173	8.36091E&08	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
ITIH5	&5266.790173	&5281.136621	28.692896	0.14531	8.48143E&08	
TOLLIP	&1329.851544	&1343.812778	27.922468	0	1.26275E&07	
PGM2	&3777.350848	&3791.279728	27.85776	0.02433	1.30569E&07	
PYGB	&4728.067676	&4741.938684	27.742016	0.14697	1.38619E&07	
GALNS	&2944.539181	&2958.198636	27.31891	0.1182	1.72516E&07	
XPNPEP1	&2971.084602	&2984.741715	27.314226	0	1.72934E&07	
CDH1	&4612.268089	&4625.920444	27.30471	0.18563	1.73788E&07	
SELENBP1	&2613.120035	&2626.71502	27.18997	0.06273	1.84413E&07	
PSMD2	&4158.226517	&4171.701354	26.949674	0.05447	2.08822E&07	
THBS4	&4697.947335	&4711.419012	26.943354	0.04893	2.09506E&07	
TKT	&3006.27538	&3019.479059	26.407358	0.02351	2.76485E&07	
C3	&8544.18871	&8557.388178	26.398936	0.24586	2.77693E&07	
GAS6	&3533.526662	&3546.267331	25.481338	0.09956	4.46683E&07	
KRT5	&2977.93607	&2990.533082	25.194024	0.0462	5.18426E&07	
PFKP	&4127.679961	&4140.26701	25.174098	0.05512	5.2381E&07	
CCT2	&2333.886575	&2346.348176	24.923202	0	5.96601E&07	
FMOD	&1738.131144	&1750.588435	24.914582	0.03176	5.99274E&07	
P4HB	&2492.56425	&2504.933215	24.73793	0.06663	6.56788E&07	
ADAMTSL1	&8529.18816	&8541.51407	24.65182	0.21453	6.86799E&07	
GPRC5C	&2502.367602	&2514.688486	24.641768	0.04255	6.9039E&07	
GBA	&3371.491965	&3383.809405	24.63488	0.08477	6.92862E&07	
GPC1	&2722.804499	&2735.071068	24.533138	0.04576	7.30427E&07	
LMAN2	&1581.167807	&1593.402872	24.47013	0.02432	7.54708E&07	
HSPA8	&3010.867894	&3022.981405	24.227022	0	8.56225E&07	
CNTNAP2	&7123.474656	&7135.559164	24.169016	0.20217	8.82405E&07	
PROM2	&4693.198277	&4705.264265	24.131976	0.14677	8.99542E&07	
GALNT6	&2888.163068	&2900.140009	23.953882	0.02912	9.86711E&07	
SLC1A1	&2563.464669	&2575.323499	23.71766	0.03168	1.11554E&06	
CAPNS1	&1632.085678	&1643.893725	23.616094	0	1.176E&06	
NRCAM	&6122.24742	&6133.940404	23.385968	0.12383	1.32542E&06	
CCT4	&2397.488011	&2409.146061	23.3161	0	1.37445E&06	
LGALS3BP	&3226.71449	&3238.322634	23.216288	0.21344	1.44766E&06	
ANPEP	&5015.599791	&5027.152045	23.104508	0.17469	1.53431E&06	
RAB1B	&982.252669	&993.755074	23.00481	0	1.61597E&06	
GFRA2	&2076.386575	&2087.700101	22.627052	0.04905	1.96696E&06	
ABP1	&4017.499935	&4028.611329	22.222788	0.11455	2.42775E&06	
CANT1	&222.370923	&233.323137	21.904428	0.04806	2.86572E&06	
TMC5	&5448.570682	&5459.500415	21.859466	0.17277	2.93366E&06	
LCP1	&2872.699843	&2883.623893	21.8481	0	2.95109E&06	
PACSIN2	&2690.953903	&2701.861558	21.81531	0	3.00195E&06	
RBP4	&886.445502	&897.307042	21.72308	0	3.14979E&06	
SEMA7A	&322.700127	&333.520537	21.64082	0.06971	3.2878E&06	
NAGLU	&597.270338	&608.060476	21.580276	0.07552	3.39324E&06	
GNPTG	&1708.081497	&1718.796133	21.429272	0.09212	3.67123E&06	
RUVBL2	&138.374796	&149.040579	21.331566	0.02417	3.86318E&06	
THBS1	&5464.497728	&5475.15442	21.313384	0.05856	3.89999E&06	
APOB	&23797.7951	&23808.36426	21.138314	0.40176	4.27299E&06	
SI	&9016.969272	&9027.416662	20.89478	0.23417	4.85215E&06	
DDR1	&4202.417343	&4212.796529	20.758372	0.05732	5.21033E&06	
GNB1	&1523.250802	&1533.536821	20.572038	0	5.74288E&06	
MMP2	&195.199881	&205.366487	20.333212	0.05392	6.50614E&06	
OLFM1	&197.643863	&207.786663	20.2856	0.03985	6.67007E&06	
VPS28	&1274.108395	&1284.234729	20.252668	0.08539	6.78588E&06	
ANTXR2	&360.316115	&370.428714	20.225198	0	6.88402E&06	
CNDP2	&405.005293	&415.069302	20.128018	0.0482	7.24279E&06	
HSPA5	&2989.2934	&2999.30097	20.01514	0	7.68314E&06	
PSME4	&502.550172	&512.507467	19.91459	0.11662	8.098E&06	
C1RL	&662.107901	&672.034609	19.853416	0.12285	8.36132E&06	
MAN2B1	&5062.952347	&5072.755887	19.60708	0.19129	9.51161E&06	
TCP1	&481.697572	&491.402782	19.41042	0.03491	1.0543E&05	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
VCP	&670.424352	&680.028376	19.208048	0	1.17218E&05	
DPP7	&2587.917231	&2597.487506	19.14055	0.10909	1.21437E&05	
FH	&2427.732075	&2437.207009	18.949868	0.0372	1.34199E&05	
TGFB1	&1740.045475	&1749.494265	18.89758	0	1.37928E&05	
tor1B	&1560.357462	&1569.764378	18.813832	0	1.44118E&05	
NME3	&750.842345	&760.136153	18.587616	0	1.62271E&05	
KRT8	&2764.376034	&2773.502369	18.25267	0.087	1.93455E&05	
LGMN	&2359.398519	&2368.503243	18.209448	0.08382	1.97895E&05	
RUVBL1	&2020.851407	&2029.915904	18.128994	0	2.06434E&05	
COL18A1	&9614.013667	&9623.026974	18.026614	0.34486	2.17838E&05	
ACTR1A	&1747.712288	&1756.653566	17.882556	0	2.34965E&05	
PRKAR1A	&1752.385424	&1761.323641	17.876434	0	2.35722E&05	
PHGDH	&2552.46231	&2561.333983	17.743346	0.04027	2.528E&05	
TUBB1	&2182.488028	&2191.237105	17.498154	0.0606	2.87587E&05	
HSPA1L	&3828.475093	&3837.183396	17.416606	0.03603	3.00192E&05	
ENPP5	&2237.921904	&2246.615716	17.387624	0	3.04804E&05	
LAMP1	&2235.430048	&2244.099398	17.3387	0.07036	3.12752E&05	
EPHA5	&4894.917496	&4903.58363	17.332268	0.09671	3.13813E&05	
RTN4RL1	&2265.835812	&2274.462656	17.253688	0.05062	3.27062E&05	
IQGAP2	&7134.922788	&7143.539431	17.233286	0.12167	3.30593E&05	
ANXA6	&3525.978865	&3534.530193	17.102656	0.08536	3.54127E&05	
OS9	&3132.16896	&3140.692364	17.046808	0.11634	3.64696E&05	
PSMB7	&1342.567698	&1351.030582	16.925768	0	3.88703E&05	
TSTA3	&1605.367714	&1613.798963	16.862498	0.0596	4.01878E&05	
PSAP	&2461.328236	&2469.751898	16.847324	0.03862	4.05104E&05	
PPP2CA	&1404.10762	&1412.43749	16.65974	0	4.47201E&05	
CTSB	&1794.11097	&1802.396314	16.570688	0.0599	4.68699E&05	
MGAM	&9728.262685	&9736.523016	16.520662	0.28994	4.81228E&05	
ADAM10	&3311.558339	&3319.766784	16.41689	0.03916	5.08303E&05	
GAPDH	&1562.519883	&1570.67238	16.304994	0.06705	5.39217E&05	
MARCKS	&1424.468442	&1432.612637	16.28839	0.07389	5.43962E&05	
BGN	&1721.531992	&1729.647929	16.231874	0.06434	5.60432E&05	
PPP5C	&2321.505199	&2329.591377	16.172356	0.0336	5.7832E&05	
UGCGL1	&7215.796883	&7223.754439	15.915112	0.19793	6.62476E&05	
CD81	&1098.648305	&1106.587028	15.877446	0	6.75793E&05	
CREG1	&1114.850723	&1122.780115	15.858784	0.04304	6.8249E&05	
PGC	&1949.960749	&1957.883837	15.846176	0.12705	6.87052E&05	
CRTAC1	&3032.155969	&3040.014048	15.716158	0.12938	7.35928E&05	
GUSB	&3811.928676	&3819.771607	15.685862	0.19756	7.47811E&05	
CALR	&1871.495455	&1879.251342	15.511774	0	8.1993E&05	
LIPG	&2620.085437	&2627.838353	15.505832	0.04493	8.22511E&05	
RAB11B	&959.630271	&967.227876	15.19521	0	9.6949E&05	
RNASE4	&746.942569	&754.440164	14.99519	0.04099	0.000107786	
GAPDHS	&2135.548329	&2143.043836	14.991014	0.07446	0.000108024	
SEMA3F	&3869.851695	&3877.23247	14.76155	0.11305	0.000121998	
IDE	&4640.756862	&4648.105642	14.69756	0.14749	0.00012621	
MAN2B2	&5889.125735	&5896.45701	14.66255	0.32026	0.000128576	
PGAM2	&1125.385518	&1132.710956	14.650876	0	0.000129375	
TP53I3	&1650.106516	&1657.409777	14.606522	0.00485	0.000132455	
CCT8	&2456.270556	&2463.56379	14.586468	0	0.000133872	
GOT1	&2039.485649	&2046.721837	14.472376	0.10047	0.00014223	
GPR64	&4791.572944	&4798.717954	14.29002	0.14133	0.000156693	
CCT3	&2973.050439	&2980.19511	14.289342	0	0.00015675	
PGM1	&2774.505909	&2781.649277	14.286736	0	0.000156967	
MME	&3524.653432	&3531.75004	14.193216	0.07662	0.000164964	
CPE	&2253.54763	&2260.610577	14.125894	0	0.000170974	
TIMP3	&904.858005	&911.849915	13.98382	0	0.000184391	
DDB1	&5168.477316	&5175.411164	13.867696	0.15363	0.000196141	
LAMB2	&9314.227444	&9321.15145	13.848012	0.37364	0.000198206	
RDX	&2858.859713	&2865.778842	13.838258	0	0.000199238	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
ATRN	&7591.328622	&7598.122751	13.588258	0.18013	0.000227605	
GSN	&873.38345	&880.140403	13.513906	0.19983	0.000236802	
SYT7	&2155.096235	&2161.832506	13.472542	0.05491	0.00024208	
PPIB	&976.665985	&983.401742	13.471514	0	0.000242213	
SERPINA1	&2319.604103	&2326.329346	13.450486	0.16993	0.000244943	
NUCB1	&2216.179941	&2222.874396	13.38891	0.10492	0.000253116	
SERPINF1	&2281.46187	&2288.131727	13.339714	0.18596	0.000259844	
AKR1B1	&1486.628413	&1493.269892	13.282958	0.0792	0.00026783	
AKR7A2	&2000.209047	&2006.78462	13.151146	0.20202	0.000287343	
IL1RAP	&3278.209033	&3284.781134	13.144202	0.11575	0.00028841	
PDIA3	&2416.657177	&2423.195836	13.077318	0	0.000298893	
YWHAG	&1078.462822	&1084.9772	13.028756	0	0.000306744	
PSCA	&646.817197	&653.289359	12.944324	0	0.000320893	
EEF1A1	&2041.953382	&2048.400115	12.893466	0	0.000329731	
UGDH	&2199.496438	&2205.943085	12.893294	0	0.000329762	
CD109	&7432.286205	&7438.667382	12.762354	0.27947	0.000353666	
a4GALT	&1746.20249	&1752.500597	12.596214	0.10194	0.000386529	
PGD	&2492.685904	&2498.796727	12.221646	0.25571	0.000472382	
GLB1	&3847.048689	&3853.149271	12.201164	0.16409	0.000477597	
ALDOA	&2009.849469	&2015.904466	12.109994	0.0461	0.000501523	
PKM2	&2963.500349	&2969.53959	12.078482	0.12519	0.000510071	
SLC15A2	&3495.85653	&3501.782669	11.852278	0.13027	0.000575909	
GNB2	&1548.171255	&1554.071112	11.799714	0.11932	0.000592398	
SERPINA5	&2277.598697	&2283.498335	11.799276	0.16255	0.000592538	
HSPA4	&3746.694879	&3752.522777	11.655796	0.09108	0.000640028	
PRKACA	&1827.221927	&1833.000483	11.557112	0.23627	0.000674906	
CD9	&1042.242825	&1047.992761	11.499872	0.08781	0.00069601	
ENPP3	&4423.85628	&4429.596555	11.48055	0.20624	0.000703283	
ORM1	&1197.412189	&1203.10859	11.392802	0.20559	0.000737292	
PPP2R4	&2044.114762	&2049.790166	11.350808	0.0557	0.000754152	
CAPZB	&2002.883108	&2008.554962	11.343708	0.04747	0.00075704	
GPI	&2905.091197	&2910.745146	11.307898	0.16466	0.000771781	
PIGR	&4428.302556	&4433.914342	11.223572	0.34351	0.000807649	
ADAM7	&4044.943385	&4050.553526	11.220282	0.24768	0.000809082	
RAB5C	&1146.306692	&1151.884368	11.155352	0	0.000837896	
IDS	&2682.135287	&2687.708749	11.146924	0.17883	0.000841711	
GPR56	&512.260204	&517.829396	11.138384	0.25	0.000845595	
ALB	&3214.455015	&3220.009828	11.109626	0.19752	0.000858808	
SERPINB6	&2139.844227	&2145.390766	11.093078	0	0.000866505	
GRN	&3083.405442	&3088.933794	11.056704	0.18997	0.000883671	
NRP1	&4385.732857	&4391.25838	11.051046	0.17579	0.000886372	
SERPINC1	&2499.094428	&2504.575537	10.962218	0.09467	0.000929884	
AGT	&2693.333514	&2698.799196	10.931364	0.21792	0.000945499	
FBP1	&1664.022059	&1669.479766	10.915414	0	0.000953674	
TAGLN2	&906.53363	&911.967324	10.867388	0	0.000978725	
FUT3	&2254.105106	&2259.530645	10.851078	0.18793	0.000987383	
ANXA1	&1595.330216	&1600.74122	10.822008	0.0644	0.001003006	
CFB	&3282.992367	&3288.394255	10.803776	0.16784	0.001012933	
DSC2	&4622.523202	&4627.901418	10.756432	0.21605	0.001039175	
GPC4	&2541.622682	&2546.992559	10.739754	0.0593	0.001048583	
Hyou1	&4706.732854	&4712.083614	10.70152	0.17969	0.001070476	
GPX3	&1100.842869	&1106.185461	10.685184	0	0.00107997	
CRISP1	&1444.875227	&1450.211733	10.673012	0.08752	0.0010871	
ALAD	&1834.129071	&1839.430482	10.602822	0.10537	0.001129152	
GNMT	&1451.193761	&1456.477609	10.567696	0.117	0.001150811	
NBL1	&995.168183	&1000.44694	10.557514	0	0.001157167	
TGFB3	&1781.828761	&1787.090429	10.523336	0	0.001178765	
DNASE1	&1529.839594	&1535.083475	10.487762	0.18311	0.001201678	
APEH	&361.355449	&366.593763	10.476628	0.10008	0.001208942	
COMP	&818.225664	&823.46273	10.474132	0.13544	0.001210577	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
NEO1	&6915.982036	&6921.216271	10.46847	0.24869	0.001214292	
PPIA	&756.438676	&761.639962	10.402572	0	0.001258399	
GSTP1	&1061.44212	&1066.643201	10.402162	0.05012	0.001258679	
PDCD6IP	&3899.511052	&3904.585375	10.148646	0.06076	0.001444073	
RALB	&1036.399119	&1041.456188	10.114138	0	0.001471362	
DPEP3	&2750.11191	&2755.154286	10.084752	0.17293	0.001495013	
NAPA	&1260.183833	&1265.193863	10.02006	0	0.001548444	
TIMP2	&996.764015	&1001.772945	10.01786	0	0.001550295	
GNAI3	&1543.818883	&1548.788162	9.938558	0	0.001618523	
TGFBR3	&4154.319234	&4159.269739	9.90101	0.1972	0.001651881	
PODXL2	&2867.880996	&2872.830673	9.899354	0.20724	0.001653368	
GDF15	&1710.337148	&1715.252377	9.830458	0.12793	0.001716456	
LDHA	&1654.674629	&1659.540136	9.731014	0	0.001811845	
PSMA7	&1181.051929	&1185.845026	9.586194	0.06668	0.001960459	
RAB13	&919.801983	&924.581942	9.559918	0	0.00198872	
LIFR	&5259.534446	&5264.284135	9.499378	0.23848	0.002055416	
CNTN3	&5073.220995	&5077.963089	9.484188	0.26525	0.002072503	
CTSH	&1641.37632	&1646.053777	9.354914	0.18573	0.002223884	
PRDX6	&1048.011727	&1052.676061	9.328668	0	0.002255963	
COLEC12	&3644.937372	&3649.569517	9.26429	0.18853	0.00233665	
PFAS	&6778.614342	&6783.244815	9.260946	0.32544	0.002340921	
CCT5	&2472.307321	&2476.935685	9.256728	0.1017	0.002346318	
COPB2	&4073.260008	&4077.864166	9.208316	0.17483	0.002409182	
SFN	&1070.288036	&1074.880892	9.185712	0.0398	0.002439116	
BCAN	&4543.640834	&4548.231705	9.181742	0.2553	0.002444413	
ALDH7A1	&2687.090864	&2691.681702	9.181676	0.18726	0.002444501	
CTSF	&2581.514906	&2586.063741	9.09767	0.19369	0.002559353	
OLFM4	&2762.461734	&2767.001019	9.07857	0.26381	0.002586222	
ANXA11	&4321.671652	&4326.209514	9.075724	0.09729	0.00259025	
IDH1	&2148.037522	&2152.508532	8.94202	0.10663	0.002786844	
COL9A1	&4610.129033	&4614.564652	8.871238	0.23759	0.002896986	
PGLS	&1263.643264	&1268.012346	8.738164	0.10708	0.003116181	
MAN2A1	&5436.975465	&5441.285383	8.619836	0.20178	0.003325218	
CAPG	&1647.033497	&1651.338914	8.610834	0.08809	0.003341693	
PDCD6	&147.158554	&151.43213	8.547152	0.09514	0.003460632	
GSTM3	&1076.478145	&1080.729681	8.503072	0	0.003545474	
SPOCK3	&2096.570763	&2100.814461	8.487396	0.13677	0.003576153	
GSR	&2856.906129	&2861.138515	8.464772	0.26587	0.003620906	
C19orf10	&835.143401	&839.349086	8.41137	0.06031	0.003728816	
ORM2	&1234.67582	&1238.873128	8.394616	0.26154	0.00376334	
EFEMP1	&2220.650327	&2224.831252	8.36185	0.07397	0.003831803	
APLP2	&3675.662886	&3679.828768	8.331764	0.15149	0.003895781	
CNP	&1957.910537	&1962.059943	8.298812	0.10051	0.003967102	
BPNT1	&1441.840527	&1445.955595	8.230136	0	0.004120044	
CPD	&6384.848588	&6388.951776	8.206376	0.29797	0.004174344	
PPIC	&1090.80283	&1094.900439	8.195218	0.07567	0.004200095	
LDHB	&1500.35107	&1504.436061	8.169982	0	0.004258933	
TWSG1	&990.137389	&994.20777	8.140762	0	0.004328109	
CUL3	&3335.928004	&3339.991246	8.126484	0	0.004362326	
C9	&3134.640706	&3138.676994	8.072576	0.31358	0.004494018	
RAB3B	&1023.92162	&1027.95728	8.07132	0.07242	0.004497134	
B4GALT1	&2162.124778	&2166.14605	8.042544	0	0.004569132	
GNB2L1	&1451.515393	&1455.481046	7.931306	0	0.004858672	
smpdl3A	&2308.807845	&2312.772513	7.929336	0.15727	0.004863964	
PLOD2	&3513.707593	&3517.607187	7.799188	0.23808	0.005226972	
A1BG	&2641.618021	&2645.508493	7.780944	0.31639	0.00528002	
CST6	&706.575502	&710.452646	7.754288	0	0.005358516	
CAPZA2	&1219.346056	&1223.220593	7.749074	0	0.005374009	
KPNB1	&3982.328935	&3986.202422	7.746974	0.21751	0.005380262	
EXTL2	&1508.448335	&1512.300023	7.703376	0.07642	0.005511764	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TALDO1	&1588.905609	&1592.715758	7.620298	0.11814	0.005771495	
CLU	&2586.535385	&2590.323745	7.57672	0.20466	0.005912693	
CD151	&1221.610625	&1225.370512	7.519774	0.05198	0.006102534	
TSG101	&1724.44861	&1728.203981	7.510742	0.12227	0.00613321	
TMEFF2	&1662.383217	&1666.096007	7.42558	0.13457	0.00643031	
CPM	&2171.947462	&2175.654214	7.413504	0.12767	0.006473612	
TPI1	&1185.178452	&1188.873082	7.38926	0	0.006561448	
GC	&2485.199421	&2488.884208	7.369574	0	0.006633665	
ACRV1	&1555.958292	&1559.599206	7.281828	0.1374	0.006965562	
HRSP12	&646.220189	&649.829098	7.217818	0	0.00721834	
MATN2	&4673.087839	&4676.656122	7.136566	0.29739	0.007552765	
SMPD1	&3206.706687	&3210.269621	7.125868	0.19916	0.007597962	
RNASET2	&1452.805394	&1456.311428	7.012068	0.1573	0.008096211	
VAT1	&1981.046584	&1984.535605	6.978042	0.15958	0.008251584	
MMP14	&2639.343563	&2642.831924	6.976722	0.15762	0.008257672	
HEBP2	&1010.75076	&1014.23201	6.9625	0	0.008323565	
PSMB1	&1154.564715	&1158.03725	6.94507	0	0.008405055	
ARF1	&802.333419	&805.801679	6.93652	0	0.008445326	
IGFBP5	&1175.612224	&1179.080286	6.936124	0.06151	0.008447196	
LTA4H	&2793.553006	&2797.012205	6.918398	0.17312	0.008531337	
PSMA1	&1252.650124	&1256.0931	6.885952	0	0.008687579	
GMPPA	&2235.046565	&2238.48803	6.88293	0.17828	0.008702279	
SLC44A4	&3576.949427	&3580.341123	6.783392	0.25063	0.009200988	
QSCN6	&3085.774546	&3089.10267	6.656248	0.35141	0.009880874	
PSMA3	&1295.393581	&1298.707131	6.6271	0	0.010043866	
DCXR	&1306.257085	&1309.570114	6.626058	0.18601	0.010049743	
SYT1	&1898.983439	&1902.270318	6.573758	0.09413	0.01034932	
ARSA	&2673.307953	&2676.558295	6.500684	0.17304	0.0107833	
ARHGDIA	&1707.805333	&1711.046264	6.481862	0.20129	0.010898076	
SCPEP1	&2264.678981	&2267.918107	6.478252	0.13828	0.010920233	
CCT7	&2531.535254	&2534.767369	6.46423	0.21788	0.011006732	
IMPA1	&1611.040933	&1614.257924	6.433982	0.16484	0.01119573	
CD47	&1467.812509	&1471.015797	6.406576	0.08759	0.011369846	
ACPP	&2123.512101	&2126.671532	6.318862	0.15063	0.011946027	
PTGDS	&982.879388	&986.02398	6.289184	0.13575	0.012147697	
ANXA2	&1661.144698	&1664.275037	6.260678	0.07708	0.012344695	
AMBP	&1761.500365	&1764.624988	6.249246	0.07797	0.012424618	
CFL1	&744.18099	&747.299141	6.236302	0	0.012515754	
NELL1	&4126.087416	&4129.193224	6.211616	0.26882	0.012691472	
EEF1G	&2358.942757	&2362.037245	6.188976	0.18091	0.012854855	
PAM	&4585.794769	&4588.871847	6.154156	0.29406	0.013110366	
ACP5	&1620.092269	&1623.161327	6.138116	0.19829	0.01322982	
MDH2	&1639.714473	&1642.756769	6.084592	0.13954	0.013636586	
FKBP4	&2244.133415	&2247.173635	6.08044	0.24066	0.013668672	
ACO1	&4248.388344	&4251.419708	6.062728	0.26813	0.013806425	
ASRGL1	&1617.539216	&1620.567598	6.056764	0.15754	0.01385313	
APCS	&1271.229224	&1274.256223	6.053998	0.11343	0.013874846	
IGHG4	&1803.701534	&1806.728081	6.053094	0.14846	0.013881951	
HPRT1	&1069.555449	&1072.564083	6.017268	0	0.01416656	
SORD	&1999.061318	&2002.048486	5.974336	0.22472	0.014515546	
CD63	&1057.406119	&1060.37241	5.932582	0.14669	0.014863448	
CP	&5168.475036	&5171.435022	5.919972	0.36293	0.014970196	
MANBA	&4390.367616	&4393.320391	5.90555	0.32963	0.015093252	
GALC	&333.941023	&336.876693	5.87134	0.17657	0.015389333	
CLIC1	&148.778859	&151.703313	5.848908	0.0951	0.01558672	
GPD1L	&1728.075006	&1730.997192	5.844372	0.09566	0.01562695	
NCSTN	&555.3041	&558.211819	5.815438	0.29396	0.015886097	
RAB5B	&1049.557979	&1052.454581	5.793204	0	0.016088242	
NUCB2	&2064.947088	&2067.843138	5.7921	0.07817	0.016098348	
GNS	&2819.465657	&2822.35195	5.772586	0.24263	0.016278064	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
RAB1A	&880.359053	&883.238762	5.759418	0	0.016400503	
YWHAB	&1085.130045	&1088.003344	5.746598	0	0.01652062	
ALCAM	&2704.996956	&2707.844522	5.695132	0.15336	0.017012033	
USP14	&2152.128578	&2154.967384	5.677612	0.19324	0.017182739	
RAP1B	&777.425012	&780.252429	5.654834	0	0.017407322	
KAL1	&3350.585424	&3353.40991	5.648972	0.28821	0.017465608	
Rab18	&1025.985561	&1028.803136	5.63515	0.15258	0.017603839	
NP	&1451.920801	&1454.737892	5.634182	0.19648	0.017613562	
IDUA	&3709.897325	&3712.714329	5.634008	0.34609	0.01761531	
TF	&4068.381661	&4071.160553	5.557784	0.40065	0.018398689	0.029133858
KLK11	&1493.694468	&1496.466956	5.544976	0.28462	0.018533811	
GDI2	&2125.405055	&2128.153211	5.496312	0.10279	0.019056623	
STEAP2	&2249.38369	&2252.123153	5.478926	0.10176	0.019247081	
SIL1	&2461.545717	&2464.277871	5.464308	0.35301	0.019408738	
SLPI	&795.791313	&798.503998	5.42537	0.09567	0.01984623	
NUTF2	&660.240091	&662.948093	5.416004	0	0.019952975	
TFRC	&4085.470005	&4088.172842	5.405674	0.30423	0.020071397	
PTN	&768.748447	&771.450778	5.404662	0	0.020083037	
KLK3	&1482.078765	&1484.774338	5.391146	0.32869	0.020239175	
BTD	&2766.999487	&2769.677876	5.356778	0.34657	0.020641877	0.02992126
NPEPPS	&4005.494404	&4008.151187	5.313566	0.18675	0.021160002	
FAM3C	&978.423591	&981.06866	5.290138	0	0.02144652	
MPST	&1728.020997	&1730.633336	5.224678	0.26564	0.022268569	
MSLN	&3968.138667	&3970.739395	5.201456	0.42395	0.022567977	
PSMB2	&1082.713309	&1085.306272	5.185926	0.10382	0.022770535	
FUCA2	&2251.628399	&2254.205673	5.154548	0.15917	0.02318557	
ALDOC	&1675.031777	&1677.601713	5.139872	0.23913	0.023382372	
LDHC	&1561.435596	&1563.998545	5.125898	0.13955	0.023571371	
CD44	&893.225908	&895.768432	5.085048	0.36336	0.024133009	
SPON2	&1579.591492	&1582.108038	5.033092	0.18162	0.024867465	0.030708661
GALNT7	&2933.51301	&2936.026383	5.026746	0	0.024958749	0.030787402
FOLH1	&3750.759544	&3753.268267	5.017446	0.35159	0.025093155	0.030866142
MFAP4	&1277.911591	&1280.402044	4.980906	0.08812	0.025628558	0.030944882
NEU1	&2052.439538	&2054.920222	4.961368	0.22851	0.025919694	0.031023622
MAMDC2	&3253.04085	&3255.497387	4.913074	0.25111	0.026654165	0.031102362
PSMB6	&1148.723331	&1151.17327	4.899878	0.11628	0.026858593	0.031181102
VAMP8	&450.203331	&452.618297	4.829932	0	0.027969734	0.031259843
HSPB1	&960.09795	&962.508528	4.821156	0.22095	0.028112485	0.031338583
ACAT2	&2217.207418	&2219.597264	4.779692	0.2161	0.028797271	0.031417323
PRDX1	&897.989074	&900.330444	4.68274	0	0.030467116	0.031496063
YWHAQ	&1125.381984	&1127.709465	4.654962	0	0.030963918	0.031574803
IDI1	&1551.497719	&1553.816301	4.637164	0.16411	0.031286664	0.031653543
PRSS22	&1602.907281	&1605.211389	4.608216	0.17413	0.031819119	0.031732283
PSMA6	&1113.464912	&1115.765316	4.600808	0	0.031956892	0.031811024
SDCBP	&1416.984773	&1419.241301	4.513056	0.13731	0.033637091	0.031889764
DAG1	&4328.274302	&4330.498503	4.448402	0.43619	0.034933922	0.031968504
CAB39L	&1526.34404	&1528.519753	4.351426	0	0.036977972	0.032047244
RHOA	&812.291506	&814.453832	4.324652	0	0.037564095	0.032125984
LAP3	&3060.648692	&3062.788545	4.279706	0.17	0.038570019	0.032204724
IL1R1	&2818.095947	&2820.224653	4.257412	0.3014	0.039079415	
UBE2L3	&718.059477	&720.185112	4.25127	0	0.03922099	
SERPING1	&2615.33457	&2617.439942	4.210744	0.302	0.040168715	
PPT1	&1498.793316	&1500.881749	4.176866	0.13995	0.040979413	
PLA1A	&2498.937023	&2501.021533	4.16902	0.33691	0.041169606	
LTF	&4531.806992	&4533.878536	4.143088	0.43995	0.041804842	
LCN2	&1102.033629	&1104.100991	4.134724	0.21176	0.042011918	
HIST2H2BE	&531.300085	&533.364503	4.128836	0	0.042158339	
PRDX2	&981.605162	&983.645358	4.080392	0.07641	0.043383593	
KRT1	&3123.101206	&3125.126827	4.051242	0.30416	0.044138859	
CAB39	&1447.30121	&1449.321368	4.040316	0	0.044425502	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HEXA	&2619.568545	&2621.579149	4.021208	0.12057	0.04493152	
GSTT1	&1142.720997	&1144.726696	4.011398	0.32031	0.045193663	
FUCA1	&2440.818758	&2442.821844	4.006172	0.27989	0.045333969	
SMS	&1890.208739	&1892.210296	4.003114	0.12176	0.045416282	
ALDH1A1	&2396.733306	&2398.689792	3.912972	0.24026	0.047914793	
DDT	&577.20069	&579.151494	3.901608	0.23067	0.048239915	0.033543307
ESD	&1288.768099	&1290.676233	3.816268	0.12637	0.050757173	
HINT1	&579.626665	&581.530457	3.807584	0	0.051020994	
CAPZA1	&1243.801855	&1245.700588	3.797466	0.1257	0.05133021	
ALDH9A1	&2588.782617	&2590.653075	3.740916	0.27811	0.05309533	
KLK2	&1341.068075	&1342.929464	3.722778	0.35721	0.053674999	
AKR1A1	&1503.478354	&1505.335135	3.713562	0.24825	0.053972096	
MSMB	&699.821203	&701.654483	3.66656	999	0.055514651	
SPINT1	&2729.278155	&2731.102674	3.649038	0.43041	0.056101607	
PRSS8	&1907.43229	&1909.235095	3.60561	0.33474	0.057584939	
SPINT3	&504.257921	&506.036198	3.556554	0.13571	0.059310747	
PEBP4	&1277.365473	&1279.140098	3.54925	0.22436	0.059572371	
FDPS	&2086.806715	&2088.567386	3.521342	0.24158	0.060583374	
IL6ST	&4249.957834	&4251.672775	3.429882	0.2748	0.064026676	
GSS	&2204.688018	&2206.388878	3.40172	0.20989	0.065128474	
NIF3L1	&1932.738782	&1934.394874	3.312184	0.20543	0.068768042	
LNPEP	&4993.971399	&4995.612031	3.281264	0.47377	0.070074941	
sez6L2	&4426.183442	&4427.821501	3.276118	0.44613	0.070295016	
BPIL1	&2383.490895	&2385.127538	3.273286	0.33979	0.070416446	
ANXA3	&1634.987756	&1636.618745	3.261978	0.25168	0.070903551	
HEXB	&2927.663241	&2929.259255	3.192028	0.37094	0.073998159	
CST3	&697.20898	&698.804431	3.190902	0	0.074049143	
SOD3	&1098.357124	&1099.947621	3.180994	0.15798	0.074499397	
ANXA4	&1495.326088	&1496.890736	3.129296	0.15471	0.076896941	
CACYBP	&1005.334264	&1006.850106	3.031684	0	0.081653229	
SORT1	&972.124978	&973.606629	2.963302	0.38625	0.085173838	
SDCBP2	&1529.141374	&1530.612985	2.943222	0.18036	0.086238554	
PI15	&1213.527875	&1214.990973	2.926196	0.28573	0.087152623	
AZGP1	&1711.567307	&1713.009205	2.883796	0.21526	0.089474867	
GNPDA1	&1287.735094	&1289.154089	2.83799	0	0.092059306	
GCHFR	&889.891619	&891.300167	2.817096	0	0.093265002	
PSMB5	&1222.849873	&1224.25008	2.800414	0	0.09423997	
CD14	&1922.930747	&1924.330745	2.799996	0.32221	0.094264542	
RAB3D	&1031.836668	&1033.20824	2.743144	0.11685	0.097672427	
KRT10	&3013.949446	&3015.316117	2.733342	0.3618	0.098273446	
RAB10	&817.552669	&818.913767	2.722196	0	0.09896178	
apoa1BP	&1426.118867	&1427.479827	2.72192	0.14401	0.098978891	
SH3BGRL2	&468.708437	&470.066866	2.716858	0	0.099293296	
YWHAZ	&991.250812	&992.595968	2.690312	0	0.100960044	
TSNAX	&1310.242201	&1311.583395	2.682388	0	0.101463475	
CA6	&1743.344316	&1744.681128	2.673624	0.4728	0.102023472	
PPP1R7	&1599.452453	&1600.785422	2.665938	0.14282	0.102517371	
ELSPBP1	&1097.927978	&1099.232124	2.608292	0.21642	0.106306203	
GRHPR	&1677.652524	&1678.952603	2.600158	0.22803	0.106853062	
PSMA2	&1089.441853	&1090.730319	2.576932	0	0.108431642	
PSMA5	&1038.294519	&1039.581656	2.574274	0	0.108613923	
DNAJC3	&2289.953428	&2291.227029	2.547202	0.23212	0.110489773	
PSMD14	&1271.537248	&1272.789226	2.503956	0	0.113560718	
GPR115	&4130.648608	&4131.891143	2.48507	0.4253	0.114931235	
PIP	&979.299111	&980.535704	2.473186	999	0.115802979	
PPP1CC	&1397.753986	&1398.989937	2.471902	0	0.115897602	
RAB2A	&862.788137	&864.015646	2.455018	0	0.117149826	
YWHAE	&1078.824401	&1080.040231	2.43166	0	0.118906921	
SERPINA6	&2120.154392	&2121.367216	2.425648	0.27099	0.119363874	
s100A11	&496.919133	&498.121111	2.403956	0	0.121028843	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
tmpRSS2	&3228.412956	&3229.607818	2.389724	0.4849	0.12213519	
LSAMP	&1596.917647	&1598.102717	2.37014	0	0.12367596	
RAC1	&947.407579	&948.58056	2.345962	0	0.125607999	
TSN	&997.593312	&998.757928	2.329232	0	0.126964504	
MLPH	&3876.701122	&3877.865116	2.327988	0.53607	0.127066019	
GANAB	&4578.395161	&4579.556191	2.32206	0.46034	0.127551009	
PCMT1	&1289.842998	&1290.991775	2.297554	0	0.129577912	
GLB1L	&3242.409186	&3243.555951	2.29353	0.43417	0.129914156	
SERPINI1	&1936.733227	&1937.866019	2.265584	0.25431	0.13227634	
CTSZ	&1649.092321	&1650.222149	2.259656	0.50112	0.132783554	
CDC42	&983.318116	&984.446634	2.257036	0	0.133008419	
ECM1	&2916.506314	&2917.627873	2.243118	0.3954	0.134210109	
CPVL	&2495.25764	&2496.374706	2.234132	0.48666	0.134992413	
ACYP1	&476.969809	&478.085871	2.232124	0	0.135167922	
PITPNA	&1222.642321	&1223.747663	2.210684	0	0.13705789	
Crisp2	&1477.188403	&1478.279195	2.181584	0.3751	0.139670646	
PROS1	&3326.202951	&3327.290554	2.175206	0.43902	0.140250735	
ZPBP	&1823.885933	&1824.962771	2.153676	0.38534	0.142228999	
FAM12A	&791.327719	&792.402242	2.149046	0.23825	0.142658508	
PTPRJ	&7428.99488	&7430.062619	2.135478	0.61592	0.143925592	
TXN	&468.497868	&469.565479	2.135222	0	0.143949621	
PGK2	&1983.386616	&1984.4181	2.062968	0.2558	0.150915973	
APOD	&1108.804777	&1109.830193	2.050832	3.71291	0.152123038	
LZTFL1	&1303.890376	&1304.912898	2.045044	0	0.152702569	
APOA2	&561.950172	&562.968044	2.035744	0.30507	0.15363899	
FSTL1	&1389.255466	&1390.27101	2.031088	0.18292	0.154110249	
ASAH1	&2202.925225	&2203.934376	2.018302	0.40093	0.155412846	
TNFSF10	&1407.084505	&1408.084651	2.000292	0.27469	0.157268908	
PSAT1	&1798.912204	&1799.902936	1.981464	0.27731	0.159236262	
CAT	&2660.56427	&2661.534134	1.939728	0.37437	0.16369807	
PAEP	&996.405298	&997.336631	1.862666	0.32865	0.172317421	
APOH	&1788.512756	&1789.430768	1.836024	0.43376	0.175417675	
MINPP1	&2558.879369	&2559.795326	1.831914	0.484	0.175901641	
GSTO1	&1164.072101	&1164.986399	1.828596	0.31752	0.176293469	
CTBS	&1987.512582	&1988.415351	1.805538	0.43067	0.179044417	
LPL	&2383.244186	&2384.143064	1.797756	0.46867	0.17998402	
NAGA	&2038.666772	&2039.565202	1.79686	0.3512	0.18009257	
FTH1	&831.763117	&832.661301	1.796368	0.19988	0.180152207	
ANXA5	&1412.483574	&1413.373974	1.7808	0.20093	0.182051122	
DSC3	&4386.834907	&4387.717686	1.765558	0.56577	0.183932768	
PFN1	&648.268292	&649.125552	1.71452	0.25584	0.190399972	
MPI	&1970.858222	&1971.709332	1.70222	0.38809	0.191997905	
SLC35F2	&1866.964084	&1867.805139	1.68211	0.43243	0.194644319	
PRCP	&2722.599643	&2723.423141	1.646996	0.3612	0.199368285	
SMPDL3B	&2537.001407	&2537.816468	1.630122	0.48739	0.201686175	
IL1RL1	&848.121518	&848.931835	1.620634	0.52871	0.203003408	
LRG1	&1930.256333	&1931.030274	1.547882	0.45612	0.213448388	
IGHG2	&1897.548911	&1898.317697	1.537572	0.28638	0.21497957	
AGR2	&792.606973	&793.373189	1.532432	999	0.215747812	
WFDC8	&1414.877904	&1415.624182	1.492556	0.35747	0.221820305	
CYB561	&1914.479545	&1915.217349	1.475608	0.32908	0.224462958	
LIPA	&2212.871781	&2213.592039	1.440516	0.56711	0.230055859	
CTSO	&1609.167995	&1609.862502	1.389014	0.21524	0.238571682	
DDAH1	&1301.486424	&1302.178768	1.384688	0.28702	0.239304222	
SEMA3C	&591.469554	&592.160749	1.38239	0.25912	0.239694463	
F11R	&1623.087589	&1623.768344	1.36151	7.53055	0.243275957	
PRKAR2A	&2023.015184	&2023.689323	1.348278	0.38438	0.245579385	
GLA	&2065.770018	&2066.414433	1.28883	0.38841	0.256263679	
CPO	&2176.415496	&2177.050915	1.270838	0.46848	0.259609531	
SERPINB5	&1776.609986	&1777.239789	1.259606	0.31837	0.261725683	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
ACE2	&4525.205882	&4525.817038	1.222312	1.30143	0.268907398	
CAP1	&2295.250133	&2295.859735	1.219204	0.39744	0.269516924	
DPP4	&3557.634057	&3558.243593	1.219072	0.30138	0.269542849	
GLO1	&898.299485	&898.901174	1.203378	0.32041	0.272647569	
RAB27B	&999.756901	&1000.312788	1.111774	7.21658	0.291696645	
LCN1	&1024.506004	&1025.025407	1.038806	0.5175	0.308099327	
VTN	&2593.326705	&2593.821682	0.989954	0.55471	0.319753618	
APOE	&1813.381162	&1813.875723	0.989122	0.40646	0.31995706	
ACR	&2431.656732	&2432.119735	0.926006	0.52774	0.335902919	
SOD1	&861.65567	&862.116708	0.922076	0.50744	0.336930472	
SEMG2	&3578.612786	&3579.047973	0.870374	0.66608	0.35085179	
LGALS3	&1334.372921	&1334.779599	0.813356	0.3661	0.367129905	
DNASE2	&1920.706606	&1921.099662	0.786112	0.56595	0.375278367	
GM2A	&1026.973383	&1027.3652	0.783634	0.49837	0.376032033	
DBI	&658.137807	&658.523999	0.772384	0.4666	0.379480552	
QPCT	&1826.243978	&1826.624337	0.760718	0.56432	0.38310392	
LAMP2	&1922.566409	&1922.937914	0.74301	0.21219	0.388698371	
MMP7	&1413.354446	&1413.714599	0.720306	0.53725	0.396043554	
PSMB4	&1248.500356	&1248.850182	0.699652	0.42637	0.402900652	
PGK1	&1900.761858	&1901.097463	0.67121	0.25819	0.412630064	
PRDX4	&1291.588639	&1291.920881	0.664484	999	0.414981372	
pla2g2A	&857.439165	&857.757624	0.636918	0.46535	0.424829042	
B4GALT4	&1758.233365	&1758.542358	0.617986	2.22183	0.431796687	
WFDC2	&657.568146	&657.871193	0.606094	0.48879	0.43626229	
GP2	&2925.311815	&2925.610927	0.598224	0.5971	0.439256454	
TEX101	&1483.896499	&1484.192812	0.592626	1.79667	0.441405454	
GSTZ1	&1095.802117	&1096.097477	0.59072	999	0.442140834	
SERPINA3	&2836.550863	&2836.82738	0.553034	0.72113	0.457080647	
SERPINA4	&2416.161419	&2416.430794	0.53875	0.61762	0.462951229	
FAM12B	&709.046591	&709.314116	0.53505	999	0.464491438	
CD38	&1612.221255	&1612.485322	0.528134	0.56764	0.467392423	
PLA2G7	&2164.334787	&2164.572275	0.474976	0.52047	0.490706839	
SPINK2	&513.291606	&513.514193	0.445174	0.38089	0.5046357	
PFN2	&782.061769	&782.273253	0.422968	5.10459	0.515459773	
LIPI	&2583.161127	&2583.368489	0.414724	0.7376	0.519581476	
LYZ	&799.957372	&800.159426	0.404108	0.39924	0.524975304	
RAB27A	&1047.317886	&1047.508806	0.38184	0.39916	0.536620141	
CRYZ	&1749.356575	&1749.526347	0.339544	0.64684	0.560092552	
CAMP	&1003.295435	&1003.456229	0.321588	1.54065	0.570654874	
PRDX5	&1042.831233	&1042.983631	0.304796	0.45299	0.580891265	
ANXA7	&2297.977482	&2298.129214	0.303464	0.59594	0.581718909	
CRISP3	&1300.765345	&1300.897525	0.26436	0.4671	0.607140475	
SDC1	&1665.094346	&1665.22362	0.258548	1.48939	0.611119458	
BASP1	&921.642657	&921.767043	0.248772	0.62567	0.61794108	
IGKC	&593.483564	&593.606504	0.24588	1.46845	0.619991154	
CA4	&1908.232189	&1908.350857	0.237336	0.75325	0.626136852	
SEPP1	&1952.751096	&1952.863472	0.224752	0.73865	0.635442745	
DNAJB9	&1082.159841	&1082.271052	0.222422	0.55071	0.63720064	
CYB5R2	&1467.492249	&1467.589896	0.195294	0.6726	0.658546513	
EGF	&6295.239814	&6295.332597	0.185566	0.80586	0.666632908	
ACRBP	&3029.213762	&3029.304827	0.18213	0.80488	0.669549106	
CST1	&1078.495127	&1078.582332	0.17441	0.79513	0.676221876	
KRT9	&3257.667605	&3257.736863	0.138516	0.89086	0.709760789	
HDHD2	&1220.637011	&1220.701134	0.128246	0.71679	0.720257623	
GGH	&1666.793171	&1666.850623	0.114904	0.64919	0.73462862	
SPACA3	&1235.390796	&1235.432911	0.08423	1.25893	0.771644837	
TFPI2	&1255.849387	&1255.890553	0.082332	0.75671	0.774161683	
HPX	&2735.924532	&2735.9564	0.063736	0.80107	0.800685607	
AGA	&1770.601645	&1770.632653	0.062016	1.2186	0.803337484	
SEMG1	&3120.931282	&3120.96111	0.059656	1.08331	0.807040475	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CA2	&1300.268631	&1300.298284	0.059306	0.80607	0.807596217	
IGJ	&899.442229	&899.468464	0.05247	0.81672	0.81881971	
PGCP	&2253.874825	&2253.900944	0.052238	0.86236	0.819213763	
NPC2	&714.422904	&714.44739	0.048972	1.2896	0.824861823	
RNASE1	&845.610814	&845.634287	0.046946	0.76853	0.828465329	
MDH1	&1611.964903	&1611.986607	0.043408	0.77061	0.834958921	
DEFB129	&916.520442	&916.538518	0.036152	1.24204	0.849201939	
TTR	&787.044075	&787.054302	0.020454	1.18653	0.886276375	
EDIL3	&2208.955877	&2208.965965	0.020176	0	0.887046636	
CLN5	&2182.194037	&2182.201562	0.01505	0.90131	0.902361736	
fam3B	&1384.005927	&1384.011539	0.011224	0.92825	0.915627275	
Park7	&838.32672	&838.33177	0.0101	0.88303	0.91994837	
TIMP1	&1322.319919	&1322.321755	0.003672	0.95953	0.951680139	
IGFBP2	&1365.928316	&1365.929887	0.003142	0.66976	0.955299151	
DCD	&649.01765	&649.018912	0.002524	0.93883	0.959931593	
WFDC9	&484.052685	&484.053659	0.001948	1.03808	0.964795875	
PSMB8	&1421.251817	&1421.252732	0.00183	0.96064	0.965878103	
CD59	&865.551874	&865.552455	0.001162	0.97557	0.972806881	
B2M	&642.20546	&642.205647	0.000374	1.03004	0.984570609	
ANG	&874.55919	&874.559345	0.00031	1.01606	0.985952518	
RAB14	&906.933411	&906.933453	8.4E&05	0	0.99268737	
TPT1	&767.034396	&767.034436	8E&05	0	0.992863599	
UBE2N	&635.71498	&635.715012	6.4E&05	0	0.993616992	
PAICS	&2099.556662	&2099.556687	5E&05	1.00837	0.994358151	
GNG12	&817.92306	&817.923074	2.8E&05	0	0.995778011	
RPLP0	&1380.982917	&1380.98293	2.6E&05	0	0.995931589	
VAMP2	&492.558883	&492.558889	1.2E&05	0	0.997236052	
PSMA4	&1162.065779	&1162.065784	1E&05	0	0.997476872	
ARF6	&713.214285	&713.214289	8E&06	0	0.997743245	
RALA	&1071.3447	&1071.344703	6E&06	0	0.998045592	
CKB	&1620.280949	&1611.09262	&18.376658	0	#NUM!	
PURA	&1247.663255	&1247.663254	&2E&06	0	#NUM!	
RAD23B	&1935.866095	&1923.167924	&25.396342	67.15385	#NUM!	
SCGB2A1	&677.676614	&559.946453	&235.460322	0.09542	#NUM!	
VCL	&5505.570282	&5096.145309	&818.849946	0	#NUM!	

Gibbon

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPG2	&31790.3307	&32121.29001	661.918626	0.79408	5.7158E&146	
MYH9	&8819.308536	&8898.67884	158.740608	0.00699	2.13215E&36	
FCGBP	&26824.67463	&26886.40909	123.468922	0.1791	1.10097E&28	
LAMA5	&19256.01836	&19315.69607	119.355406	0.16042	8.75501E&28	
PTPRS	&9624.989046	&9670.769073	91.560054	0.16509	1.08256E&21	
COL6A2	&6142.845553	&6187.643427	89.595748	0.45262	2.92151E&21	
PLXNB2	&9374.669945	&9411.641902	73.943914	0.13047	8.03684E&18	
PYGB	&4712.003815	&4745.397426	66.787222	0.23593	3.02452E&16	
FBLN2	&5915.60157	&5947.483657	63.764174	0.07872	1.40241E&15	
PFKP	&4114.272541	&4142.94168	57.338278	0.1794	3.66944E&14	
AHCY	&2324.858354	&2351.849172	53.981636	0.86124	2.02372E&13	
CRTAC1	&3031.055659	&3057.395497	52.679676	0.03324	3.92633E&13	
LAP3	&3038.713757	&3064.745408	52.063302	0.84915	5.37399E&13	
MUC6	&13541.05756	&13566.21808	50.321038	0.29465	1.30543E&12	
COL6A1	&5742.020055	&5766.331741	48.623372	0.30651	3.10151E&12	
CPAMD8	&10033.0526	&10057.15247	48.19974	0.19892	3.84939E&12	
EEF2	&4121.869718	&4145.416612	47.093788	0	6.76698E&12	
ANXA11	&4305.224103	&4325.331413	40.21462	0.89127	2.27539E&10	
ODZ2	&12811.35188	&12830.43929	38.174824	0.02937	6.46816E&10	
COMP	&3817.401532	&3836.324603	37.846142	0.07886	7.65496E&10	
FLNB	&12657.6898	&12676.25355	37.127502	0.0271	1.10652E&09	
MMP2	&3185.585052	&3204.131556	37.093008	0.19728	1.12627E&09	
CACNA2D1	&4976.084081	&4994.240161	36.31216	0.26028	1.68112E&09	
RELN	&16739.09994	&16756.19117	34.182466	0.05768	5.0179E&09	
RRBP1	&4909.49491	&4925.422839	31.855858	0.3302	1.66048E&08	
FASN	&13845.0358	&13860.75766	31.443724	0.10024	2.05305E&08	
col12A1	&14640.91712	&14656.39764	30.961042	0.23754	2.6326E&08	
CANT1	&2219.131245	&2234.474069	30.685648	0.24402	3.03401E&08	
CAPN1	&3438.021032	&3452.691745	29.341426	0.02789	6.06844E&08	
DDB1	&5175.527067	&5190.107502	29.16087	0.01784	6.6611E&08	
AGRN	&10948.89633	&10963.35145	28.910242	0.16815	7.5811E&08	
ATRN	&7591.531005	&7605.910956	28.759902	0.23049	8.19299E&08	
PTPRF	&9059.946408	&9074.065034	28.237252	0.04415	1.07319E&07	
TMEM8	&4066.591575	&4080.677161	28.171172	0.16166	1.11046E&07	
RUVBL2	&2136.595682	&2150.410249	27.629134	0.0484	1.46949E&07	
THBS1	&5464.527302	&5478.094967	27.13533	0.03604	1.89699E&07	
SORL1	&10869.63703	&10883.09327	26.91248	0.14085	2.1288E&07	
FN1	&12062.94309	&12076.36159	26.837014	0.11279	2.21357E&07	
THBS2	&5835.564225	&5848.764703	26.400956	0.1367	2.77403E&07	
CLSTN1	&4929.81861	&4942.813013	25.988806	0.02718	3.43403E&07	
HSPA5	&2981.106734	&2994.092816	25.972164	0.18586	3.46376E&07	
ACE	&6846.842699	&6859.777378	25.869358	0.20576	3.65323E&07	
SERPINB6	&2140.458715	&2153.372528	25.827626	0.08014	3.73307E&07	
CPD	&6384.139771	&6396.013468	23.747394	0.20868	1.09844E&06	
IGFBP2	&1365.929919	&1377.464704	23.06957	0	1.56244E&06	
CTSD	&2194.599536	&2205.874172	22.549272	0.05441	2.04822E&06	
UGCGL1	&7216.104736	&7227.186267	22.163062	0.11239	2.50446E&06	
PSME4	&8501.637064	&8512.649463	22.024798	0.04644	2.6915E&06	
CNDP2	&2405.049077	&2416.010895	21.923636	0.05405	2.83718E&06	
P4HB	&2491.767035	&2502.688373	21.842676	0.16902	2.95944E&06	
NEO1	&6916.78813	&6927.511793	21.447326	0.15093	3.63683E&06	
IDH1	&2141.455062	&2152.067349	21.224574	0.71513	4.08493E&06	
HSPA8	&3010.867894	&3021.392673	21.049558	0	4.47556E&06	
MME	&3523.458718	&3533.973729	21.030022	0.16879	4.52143E&06	
OS9	&3132.109878	&3142.56476	20.909764	0.10303	4.81434E&06	
KPNB1	&3990.918646	&4001.199523	20.561754	0	5.77382E&06	
SMS	&1886.056541	&1895.932871	19.75266	0.62297	8.81389E&06	
RAB1A	&879.223046	&888.981319	19.516546	0.20416	9.97321E&06	
PACSIN2	&2686.910598	&2696.587594	19.353992	0	1.08592E&05	
MGAM	&9726.971119	&9736.585775	19.229312	0.11873	1.1592E&05	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
ADAMTS1	&4874.973416	&4884.505067	19.063302	0.09118	1.26453E&05	
SPON2	&1579.385496	&1588.608956	18.44692	0.06264	1.74703E&05	
PGK1	&1891.550562	&1900.769027	18.43693	0.85606	1.75621E&05	
PRSS22	&1602.486653	&1611.667392	18.361478	0.19353	1.82715E&05	
ADAMTSL1	&8529.891384	&8538.921119	18.05947	0.17261	2.14111E&05	
GAS6	&8528.782733	&8537.583925	17.602384	0.24389	2.72247E&05	
SMOC2	&2171.498071	&2180.26502	17.533898	0	2.82231E&05	
XPNPEP1	&2971.073826	&2979.72791	17.308168	0	3.17818E&05	
RTN4RL1	&2265.866585	&2274.518043	17.302916	0.05418	3.18697E&05	
C3	&8543.195584	&8551.791349	17.19153	0.31881	3.3794E&05	
ACO1	&4245.80374	&4254.35991	17.11234	0.50494	3.52326E&05	
PSMA1	&1246.004041	&1254.456988	16.905894	0.32801	3.92794E&05	
sez6L2	&4432.61155	&4441.016801	16.810502	0.05389	4.13041E&05	
CYB561	&1906.189951	&1914.481342	16.582782	0.63706	4.65719E&05	
BPNT1	&1435.867019	&1444.153431	16.572824	0.86215	4.68171E&05	
PFAS	&6777.268828	&6785.45656	16.375464	0.43629	5.19534E&05	
TIMP3	&899.044111	&907.080395	16.072568	8.36484	6.09607E&05	
CFL1	&744.019856	&752.025456	16.0112	0	6.29689E&05	
CCT8	&2457.309482	&2465.284269	15.949574	0.09575	6.50524E&05	
PLOD3	&3727.215202	&3735.188797	15.94719	0.28151	6.51344E&05	
LEFTY2	&2008.400529	&2016.349163	15.897268	0.04603	6.68752E&05	
ALDOA	&2009.99901	&2017.892698	15.787376	0.02331	7.08738E&05	
RAB11B	&959.630271	&967.43856	15.616578	0	7.75715E&05	
TPP2	&6056.610667	&6064.399851	15.578368	0.184	7.9155E&05	
FUT3	&2253.048606	&2260.741522	15.385832	0.22958	8.7643E&05	
CDH1	&4611.635535	&4619.219157	15.167244	0.11629	9.83956E&05	
ENO1	&2053.757369	&2061.338961	15.163184	0.02939	9.86074E&05	
TFRC	&4085.307706	&4092.855029	15.094646	0.30015	0.000102253	
GPC1	&2722.604543	&2730.148059	15.087032	0.07972	0.000102666	
CNTN3	&5074.29461	&5081.792561	14.995902	0.20736	0.000107745	
EFHD2	&1219.422128	&1226.832154	14.820052	0.0626	0.000118271	
KRT8	&2758.632205	&2766.035247	14.806084	0.38557	0.00011915	
KRT10	&3013.825558	&3021.151188	14.65126	0.09384	0.000129348	
PSMA6	&1108.124475	&1115.367713	14.486476	0.54431	0.000141169	
GAA	&4986.300687	&4993.477987	14.3546	0.13472	0.000151409	
SYT7	&2155.070962	&2162.118026	14.094128	0.07062	0.000173886	
GPI	&2903.640645	&2910.649517	14.017744	0.01868	0.000181094	
ST14	&4409.76704	&4416.730038	13.925996	0.12842	0.00019015	
CA6	&1744.078457	&1750.955032	13.75315	0.07253	0.000208471	
EDIL3	&2208.899743	&2215.730747	13.662008	0.12564	0.000218837	
CCT5	&2475.93317	&2482.6485	13.43066	0	0.000247545	
ANXA6	&3525.582542	&3532.264551	13.364018	0.0423	0.000256498	
VCP	&3667.871826	&3674.519485	13.295318	0.10774	0.00026607	
SORT1	&3974.084011	&3980.620756	13.07349	0.17221	0.000299505	
GOT1	&2037.935419	&2044.395946	12.921054	0	0.000324907	
PLOD2	&3514.830426	&3521.286822	12.912792	0.11112	0.000326344	
PPP5C	&2319.540733	&2325.990636	12.899806	0.11993	0.000328616	
CTSB	&1793.474668	&1799.842762	12.736188	0.17213	0.000358648	
HSPA1L	&3827.723577	&3833.921868	12.396582	0.03543	0.00043012	
SPOCK3	&2096.615398	&2102.578577	11.926358	0.10966	0.000553453	
UBE2L3	&714.46638	&720.389071	11.845382	0.46648	0.000578045	
MFAP4	&1277.774613	&1283.661365	11.773504	0	0.000600798	
IL6ST	&4250.054861	&4255.90738	11.705038	0.17986	0.000623311	
OLFM1	&2197.544163	&2203.38073	11.673134	0.06342	0.000634091	
GPD1L	&1727.985487	&1733.806135	11.641296	0.12337	0.000645036	
HSPA4	&3746.386169	&3752.160578	11.548818	0.11898	0.000677923	
RAC1	&943.742847	&949.48256	11.479426	0.67042	0.000703709	
GGH	&1661.040214	&1666.758471	11.436514	3.88631	0.000720148	
MYO1C	&5453.548103	&5459.230959	11.365712	0.03767	0.000748124	
C9	&3132.153896	&3137.797026	11.28626	0.17755	0.000780828	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
FMOD	&1738.204273	&1743.830972	11.253398	0.05667	0.000794774	
MMP14	&2637.68855	&2643.262344	11.147588	0	0.00084141	
QSCN6	&3085.718687	&3091.269541	11.101708	0.20808	0.000862482	
NRP1	&4386.01644	&4391.544622	11.056364	0.12917	0.000883833	
PSAP	&2459.839554	&2465.351169	11.02323	0.27724	0.000899772	
GNB2	&1550.855134	&1556.331886	10.953504	0	0.000934268	
KIF5B	&4445.344017	&4450.792889	10.897744	0	0.000962815	
CCT7	&2534.567327	&2539.99707	10.859486	0.03527	0.00098291	
ANXA2	&1663.246531	&1668.64382	10.794578	0	0.001017978	
PPP2R4	&2041.608113	&2046.972536	10.728846	0.63342	0.001054782	
LAMB2	&9314.872682	&9320.036276	10.327188	0.28369	0.001310848	
APEH	&360.20704	&365.328694	10.243308	0.02693	0.001371814	
DAG1	&4329.276071	&4334.359576	10.16701	0.11816	0.00142976	
BAIAP2	&2717.149921	&2722.186735	10.073628	0.02025	0.001504066	
IQGAP1	&7510.321768	&7515.347011	10.050486	0.03533	0.001523078	
LNPEP	&4993.377872	&4998.379324	10.002904	0.59999	0.001562936	
MMP7	&1410.231303	&1415.184372	9.906138	2.30251	0.001647284	
LPL	&2389.280559	&2394.22645	9.891782	0.10104	0.001660185	
CST1	&1077.804724	&1082.705868	9.802288	0.20756	0.001742949	
PSMA4	&1158.487889	&1163.373561	9.771344	0.22177	0.001772528	
ALDH7A1	&2686.886258	&2691.736886	9.701256	0.22553	0.001841421	
KRT1	&3124.429857	&3129.273944	9.688174	0.08802	0.001854577	
KAL1	&3348.625219	&3353.423384	9.59633	0.64201	0.001949667	
LMAN2	&1581.150105	&1585.843262	9.386314	0.06983	0.002186113	
COLEC12	&3646.128928	&3650.791843	9.32583	0.02823	0.00225946	
BPIL1	&2383.684752	&2388.276513	9.183522	0.24894	0.002442037	
CCT2	&2332.258329	&2336.848335	9.180012	0.06579	0.002446724	
PRDX2	&976.821841	&981.377656	9.11163	0.2892	0.002539894	
KRT5	&2977.796333	&2982.349364	9.106062	0.07994	0.002547638	
B4GALT1	&2162.810308	&2167.330958	9.0413	0.35424	0.002639479	
PTGDS	&982.839694	&987.353151	9.026914	0.09036	0.002660332	
PGCP	&2253.911009	&2258.414803	9.007588	0.17888	0.00268861	
IL1RL1	&3843.616087	&3848.060324	8.888474	0.77757	0.002869765	
GMPPA	&2234.793542	&2239.230443	8.873802	0.2573	0.00289292	
YWHAQ	&1122.917499	&1127.344469	8.85394	1.04541	0.002924569	
VCL	&5089.78474	&5094.174765	8.78005	0.09465	0.003045429	
PROM2	&4692.57993	&4696.967966	8.776072	0.36988	0.003052077	
TGFB3	&1781.772272	&1786.119914	8.695284	0	0.003190344	
Hyou1	&4705.466031	&4709.81159	8.691118	0.04558	0.003197644	
GLG1	&5645.708634	&5650.016437	8.615606	0.02813	0.003332949	
GAPDH	&1562.515613	&1566.801118	8.57101	0.02174	0.003415576	
NPEPPS	&4004.662243	&4008.901019	8.477552	0.21215	0.003595556	
LTF	&4528.383295	&4532.616231	8.465872	0.26024	0.003618717	
TAGLN2	&902.967147	&907.149042	8.36379	0.26161	0.003827714	
TCP1	&2481.479087	&2485.651992	8.34581	0.06301	0.003865778	
NCSTN	&3553.098711	&3557.253454	8.309486	0.37214	0.003943855	
ZPBP	&1823.897917	&1828.050955	8.306076	0.3751	0.003951267	
FH	&2428.172843	&2432.313419	8.281152	0.1965	0.004005871	
RAB27A	&1045.994344	&1050.125963	8.263238	0	0.004045591	
EEF1G	&2358.750202	&2362.860612	8.22082	0.22702	0.004141248	
CD81	&1098.325156	&1102.432992	8.215672	0	0.004153013	
NRCAM	&6122.275164	&6126.36332	8.176312	0.10495	0.004244096	
SERPINB5	&1776.346217	&1780.427555	8.162676	0.34632	0.004276123	
SMPD1	&3205.719399	&3209.794841	8.150884	0.38444	0.004304018	
GALC	&3334.014234	&3338.082601	8.136734	0.25527	0.004337734	
PIGR	&4428.34778	&4432.408835	8.12211	0.30833	0.004372863	
PTPRJ	&7429.438105	&7433.488209	8.100208	0.37796	0.004426018	
GALNS	&2944.125444	&2948.149661	8.048434	0.16843	0.004554301	
CLTC	&7272.366088	&7276.345818	7.95946	0.08021	0.004783668	
ARF1	&802.333419	&806.310983	7.955128	0	0.004795132	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PPT1	&1498.55342	&1502.452275	7.79771	0.20274	0.005231249	
GPRC5C	&2503.102016	&2506.988942	7.773852	0.11106	0.005300789	
PDCD6IP	&3898.681872	&3902.54372	7.723696	0	0.005450071	
DNASE1	&1529.490634	&1533.33952	7.697772	0.108	0.005528903	
MATN2	&4673.665347	&4677.44788	7.565066	0.20803	0.005951048	
MPST	&1729.025836	&1732.796429	7.541186	0.1375	0.006030434	
ANXA4	&1494.796905	&1498.535405	7.477	0.33734	0.006249211	
GNAI3	&1543.818883	&1547.557124	7.476482	0	0.006251009	
CTBS	&1984.77749	&1988.512289	7.469598	0.05361	0.006274956	
IL1RAP	&3278.438686	&3282.169006	7.46064	0.03648	0.006306258	
SMPDL3B	&2535.659145	&2539.382958	7.447626	0.20808	0.006352017	
SDCBP2	&1529.033399	&1532.752426	7.438054	0.12	0.00638589	
TMC5	&5449.876049	&5453.523087	7.294076	0.66344	0.006918234	
LTA4H	&2793.228728	&2796.812558	7.16766	0.35625	0.007422954	
SLC44A4	&577.1096	&580.682361	7.145522	0.13987	0.00751514	
PSMB5	&1223.035493	&1226.605145	7.139304	0.08173	0.007541242	
KRT9	&3258.683379	&3262.249363	7.131968	0.10736	0.007572157	
TIMP2	&997.06466	&1000.595488	7.061656	0.0472	0.007875117	
ACTN1	&4234.238719	&4237.764247	7.051056	0.01264	0.007921854	
PGC	&1949.530065	&1953.045768	7.031406	0.25136	0.008009245	
GNPTG	&1707.978285	&1711.48837	7.02017	0.08694	0.008059658	
IGFBP5	&1175.612387	&1179.0736	6.922426	0.0616	0.008512142	
PGAM2	&1125.258989	&1128.716857	6.915736	0	0.008544047	
CAPNS1	&1633.6713	&1637.103808	6.865016	0.03173	0.008789946	
PRCP	&2720.35227	&2723.769593	6.834646	0.62088	0.008940641	
MPI	&1969.041247	&1972.45226	6.822026	0	0.009004037	
CA4	&1905.238148	&1908.631885	6.787474	0.21058	0.009179971	
LGALS3BP	&3226.972907	&3230.359549	6.773284	0.18225	0.009253241	
SDC1	&1666.727999	&1670.078641	6.701284	0.45484	0.009634351	
SOD3	&1097.487719	&1100.776054	6.57667	0.02304	0.010332401	
YWHAG	&1078.462822	&1081.744555	6.563466	0	0.010409343	
NAGA	&2039.231095	&2042.487416	6.512642	0.11012	0.010711025	
NEU1	&2052.330359	&2055.584312	6.507906	0.26388	0.01073959	
ACR	&2431.699616	&2434.921041	6.44285	0.45225	0.011139978	
LAMP1	&2235.651978	&2238.819952	6.335948	0.27726	0.011831486	
DCXR	&1305.353718	&1308.501456	6.295476	0.10233	0.012104651	
CD109	&7432.4694	&7435.606832	6.274864	0.30823	0.012246252	
ARF6	&713.214313	&716.33875	6.248874	0	0.012427228	
GRN	&3083.954704	&3087.069771	6.230134	0.67058	0.012559423	
MANBA	&4390.462146	&4393.573179	6.222066	0.29852	0.01261678	
PPP2CA	&1404.4078	&1407.488276	6.160952	0	0.01306009	
SYT1	&1899.250711	&1902.318087	6.134752	0	0.013255014	
NUCB2	&2064.043816	&2067.090679	6.093726	0.09328	0.01356627	
NELL1	&4124.526906	&4127.571425	6.089038	0.0873	0.013602313	
PKM2	&2962.942516	&2965.930381	5.97573	0.23147	0.014504076	
MAN2A1	&5436.753324	&5439.733897	5.961146	0.26539	0.014624532	
RAB14	&906.933496	&909.899003	5.931014	0	0.014876679	
GDI2	&2124.663933	&2127.607317	5.886768	0	0.015255073	
NBL1	&996.240383	&999.181059	5.881352	0.07746	0.015302067	
ACLY	&5462.574243	&5465.493144	5.837802	0	0.015685409	
ARSA	&2673.349293	&2676.260887	5.823188	0.19068	0.015816253	
PPIB	&976.801969	&979.709319	5.8147	0.0855	0.015892764	
PPAP2A	&1294.796003	&1297.70015	5.808294	0	0.015950761	
CKB	&1604.395747	&1607.291839	5.792184	0.0663	0.016097578	
LRG1	&1929.134388	&1932.015981	5.763186	0.12723	0.016365371	
CD151	&1220.248825	&1223.120019	5.742388	0.45655	0.016560263	
GNS	&2820.000267	&2822.87032	5.740106	0.11459	0.016581792	
RNASE4	&747.110492	&749.968283	5.715582	1.63274	0.016814989	
GSS	&2204.188378	&2207.019166	5.661576	0.09071	0.017340535	
ABP1	&4017.935685	&4020.755218	5.639066	0.17649	0.017564562	0.019512195

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PTN	&768.432831	&771.244296	5.62293	0.18224	0.017726989	0.019593496
F11R	&1623.295634	&1626.096545	5.601822	0.10795	0.017941809	0.019674797
MDH2	&1637.61574	&1640.394185	5.55689	0	0.018408088	0.019756098
ASAH1	&2199.196814	&2201.970276	5.546924	0.07485	0.018513194	0.019837398
ALCAM	&2705.13093	&2707.894882	5.527904	0.12397	0.018715512	0.019918699
RAB13	&919.801983	&922.530601	5.457236	0	0.019487449	0.02
GALNT7	&2932.487362	&2935.209582	5.44444	0.467	0.019630707	0.020081301
TUBB1	&2181.894144	&2184.607109	5.42593	0.13211	0.019839866	0.020162602
ASRGL1	&1617.838515	&1620.541056	5.405082	0.32231	0.020078205	0.020243902
RAB3B	&1024.134133	&1026.813703	5.35914	0	0.020613937	0.020325203
OLFM4	&2762.152998	&2764.832412	5.358828	0.60722	0.020617625	
GSR	&2856.746379	&2859.417541	5.342324	0.31104	0.020813707	
SCPEP1	&2264.309216	&2266.968268	5.318104	0.08469	0.021104963	
CD47	&1466.203754	&1468.853595	5.299682	0	0.021329318	
HEXA	&2618.763295	&2621.407696	5.288802	0.35718	0.02146298	
PSMB1	&1155.315322	&1157.956207	5.28177	0.10507	0.02154983	
NUCB1	&2216.172618	&2218.791018	5.2368	0.1023	0.022113914	
PSAT1	&1798.413999	&1801.03227	5.236542	0.04939	0.022117194	
A1BG	&2640.390239	&2643.004033	5.227588	0.48268	0.022231341	
LDHB	&1500.35107	&1502.956547	5.210954	0	0.022445016	0.021138211
ANXA3	&1635.00934	&1637.614485	5.21029	0.22483	0.022453589	
MAMDC2	&3253.894432	&3256.483175	5.177486	0.11372	0.022881408	
LSAMP	&1596.576888	&1599.165264	5.176752	0	0.022891076	
FBP1	&1664.44722	&1667.032877	5.171314	0.15145	0.02296284	
PDGFA	&1304.344354	&1306.905971	5.123234	0.23386	0.023607581	
ACTR1A	&1747.712288	&1750.270859	5.117142	0	0.023690603	
PLA2G7	&2163.048728	&2165.59472	5.091984	0.06024	0.024036678	
GNMT	&1451.388475	&1453.898804	5.020658	0.09683	0.025046649	
HEBP2	&1011.745733	&1014.230012	4.968558	0.21896	0.025812159	
RAP1B	&777.570235	&780.050684	4.960898	0	0.02592674	0.02195122
TGFBR3	&4154.307625	&4156.777814	4.940378	0.17228	0.026236298	
ACE2	&4533.137273	&4535.605687	4.936828	0.36379	0.026290241	
PSMB6	&1148.242238	&1150.705419	4.926362	0	0.026449945	
GPR115	&4130.01309	&4132.473012	4.919844	0.5365	0.026549914	
EEF1A1	&2041.953382	&2044.403076	4.899388	0	0.026866215	
IDI1	&1549.114118	&1551.56153	4.894824	1.7092	0.026937319	
PPP1CC	&1397.753986	&1400.199715	4.891458	0	0.026989884	
SEMA3F	&869.788483	&872.232136	4.887306	0.08033	0.027054871	
VAMP8	&450.203331	&452.642837	4.879012	0	0.027185176	
PPP1R7	&1599.734201	&1602.166781	4.86516	0.07785	0.027404257	0.022764228
IQGAP2	&7135.160916	&7137.592162	4.862492	0.15675	0.027446665	
MAN2B2	&5888.576314	&5891.003294	4.85396	0.31904	0.027582738	
RUVBL1	&2020.851407	&2023.271064	4.839314	0	0.027817959	
CAPZA2	&1219.684291	&1222.102109	4.835636	0	0.027877356	
ALDH1A1	&397.582009	&399.983267	4.802516	0.1046	0.028418207	
GPC4	&540.135788	&542.521026	4.770476	0.57818	0.02895182	
DNAJC3	&291.109268	&293.461716	4.704896	0.04398	0.030076822	
tmpRSS2	&228.354718	&230.681882	4.654328	0.43949	0.030975355	
FUCA2	&250.417508	&252.739285	4.643554	0.73603	0.031170387	
STEAP2	&249.042943	&251.35636	4.626834	0.22721	0.031475594	
LAMC1	&7895.200301	&7897.509919	4.619236	0.0687	0.031615317	
CAPG	&1646.906874	&1649.214232	4.614716	0.04718	0.031698744	
TP53I3	&1651.4381	&1653.744579	4.612958	0.07468	0.031731254	
CD59	&865.888284	&868.166036	4.555504	6.14994	0.032813105	
ACP5	&1619.371874	&1621.642995	4.542242	0.03195	0.033068254	
IL1R1	&2818.149153	&2820.406583	4.51486	0.35792	0.033601636	
PDCD6	&1147.017683	&1149.251548	4.46773	0.23277	0.034540852	
TF	&4067.665209	&4069.895014	4.45961	0.84424	0.03470542	
SDCBP	&1416.911746	&1419.136962	4.450432	0.10416	0.034892419	
SORD	&1998.289842	&2000.504689	4.429694	0.14339	0.035318839	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SERPING1	&2615.330779	&2617.543818	4.426078	0.30078	0.035393749	
CAB39L	&1526.277277	&1528.489256	4.423958	0	0.035437744	
SERPINC1	&2499.997964	&2502.204292	4.412656	0.1671	0.035673258	
CRISP1	&1446.789241	&1448.937321	4.29616	0.13234	0.03819853	
LCN1	&1024.861198	&1027.007652	4.292908	0.32921	0.038271653	
CRISP3	&1299.610183	&1301.749587	4.278808	999	0.038590402	
EFEMP1	&2220.395031	&2222.523946	4.25783	0.237	0.039069799	
RNASET2	&1451.69341	&1453.822167	4.257514	0.38552	0.039077068	
SFN	&1070.800803	&1072.888879	4.176152	0	0.040996683	
LCP1	&2872.413242	&2874.498666	4.170848	0	0.041125211	
ANXA5	&1411.906186	&1413.991151	4.16993	0.26489	0.0411475	
SERPINA4	&2415.563759	&2417.646708	4.165898	0.50649	0.041245543	
HIST2H2BE	&531.300085	&533.369079	4.137988	0	0.04193098	
PRKCSH	&2724.271406	&2726.335322	4.127832	0.15029	0.04218336	
ORM2	&1234.37109	&1236.416038	4.089896	0.0799	0.043140297	
SIL1	&2461.699686	&2463.74278	4.086188	0.32717	0.043235048	
CAB39	&1447.2991	&1449.330424	4.062648	0	0.043841699	
HPRT1	&1068.632804	&1070.639297	4.012986	0.82402	0.045151119	
APCS	&1271.400486	&1273.406799	4.012626	3.47478	0.04516076	
TPT1	&765.039898	&767.034436	3.989076	2.23581	0.045796172	
CPE	&2253.254945	&2255.244976	3.980062	0.28348	0.046041868	
PRDX6	&1048.736047	&1050.720657	3.96922	0.07575	0.046339233	
YWHAE	&1079.0251	&1081.003998	3.957796	0.10216	0.046654751	
TXN	&467.073659	&469.042748	3.938178	0	0.047201875	
PSMA7	&1180.179054	&1182.13659	3.915072	0.14095	0.047854965	
CAPZB	&2005.03651	&2006.992484	3.911948	0.2868	0.047943994	
MDH1	&613.225275	&615.149083	3.847616	0.09443	0.049816752	0.026585366
apoa1BP	&1424.212139	&1426.125945	3.827612	0.04845	0.050414712	
CAMP	&1001.546695	&1003.440493	3.787596	999	0.051633757	
GPX3	&102.600282	&104.481101	3.761638	0.21731	0.052441182	
B4GALT4	&1759.805935	&1761.681509	3.751148	0.13576	0.052771256	
CD38	&1610.668887	&1612.534655	3.731536	3.86121	0.053394272	
CNP	&1955.055175	&1956.918818	3.727286	0	0.053530306	
UGDH	&2199.851605	&2201.709707	3.716204	0	0.053886748	
APLP2	&675.674869	&677.529199	3.70866	0.1414	0.054130832	
BCAN	&4543.769573	&4545.601492	3.663838	0.23131	0.055605404	
FSTL1	&1389.665911	&1391.470685	3.609548	0	0.057448732	
DDR1	&4202.897994	&4204.66156	3.527132	0.04415	0.060372133	
HDHD2	&1219.051406	&1220.726616	3.35042	0	0.067187869	
SERPINA3	&2835.687872	&2837.354577	3.33341	1.01828	0.067885991	
GC	&486.144675	&487.799668	3.309986	0.17358	0.068860079	
GNB2L1	&1451.515393	&1453.161136	3.291486	0	0.069639969	
RAB27B	&1001.943458	&1003.568855	3.250794	0.25817	0.071388868	
CLU	&586.46583	&588.074611	3.217562	0.17564	0.07285206	
CAP1	&2295.063153	&2296.668442	3.210578	0.10489	0.073163633	
CPVL	&2494.670886	&2496.256051	3.17033	0.31545	0.074987294	
PSMB4	&1249.406261	&1250.990368	3.168214	0	0.075084512	
SLC35F2	&1868.037978	&1869.620459	3.164962	0.2087	0.075234187	
CP	&5166.046812	&5167.610228	3.126832	0.09612	0.077013263	
RAD23B	&1918.079369	&1919.641366	3.123994	0.34529	0.077147476	
Rab18	&1027.34863	&1028.908465	3.11967	0	0.077352447	
MAN2B1	&5063.236209	&5064.780229	3.08804	0.1238	0.078869756	
VAT1	&1980.712694	&1982.252009	3.07863	0.0916	0.07932732	
FDPS	&2086.8037	&2088.319574	3.031748	0.23036	0.081650009	
KLK3	&1482.174776	&1483.685741	3.02193	0.36798	0.082145652	
AKR7A2	&2000.039652	&2001.544427	3.00955	0.23362	0.082775268	
GM2A	&1025.733868	&1027.215952	2.964168	0.1004	0.08512824	
CTSZ	&1651.537242	&1653.013235	2.951986	0.1956	0.085772094	
LYZ	&798.623019	&800.089086	2.932134	0.21267	0.086832646	
UBE2N	&635.714983	&637.134733	2.8395	0	0.091972829	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SERPINA6	&2120.160082	&2121.574224	2.828284	0.41284	0.092617274	
RNASE1	&844.741009	&846.15246	2.822902	0.08725	0.092928252	
PRDX1	&896.587643	&897.99813	2.820974	999	0.09303993	
GSTP1	&1060.656713	&1062.063597	2.813768	0.29898	0.093458625	
CST6	&707.798979	&709.180773	2.763588	0.08328	0.096431741	
VAMP2	&492.558883	&493.939866	2.761966	0	0.096529545	
AGT	&2692.800943	&2694.181466	2.761046	0.14233	0.096585068	
PFN1	&646.901616	&648.28184	2.760448	999	0.096621176	
TWSG1	&990.310533	&991.675208	2.72935	0	0.098519374	
IDS	&2682.719241	&2684.079348	2.720214	0.34861	0.09908473	
PRKAR2A	&2022.862525	&2024.218256	2.711462	0.15466	0.099629646	
YWHAB	&1085.130045	&1086.479082	2.698074	0	0.10046955	
GP2	&2925.464693	&2926.813645	2.697904	0.40595	0.100480265	
LIFR	&5259.461917	&5260.808079	2.692324	0.17245	0.100832651	
PGD	&2494.459123	&2495.799995	2.681744	0.19285	0.10150451	
AKR1A1	&1502.637273	&1503.976226	2.677906	0	0.101749442	
GNB1	&1523.458979	&1524.794	2.670042	0	0.102253325	
PURA	&1246.333542	&1247.663255	2.659426	0.3227	0.102937876	
VPS28	&1274.511028	&1275.840684	2.659312	0.07217	0.102945254	
THBS4	&4698.819642	&4700.13509	2.630896	0.09064	0.104802556	
ALB	&3215.117925	&3216.4215	2.60715	0.2557	0.106382795	
CAPZA1	&1243.632727	&1244.934194	2.602934	0.19021	0.106666082	
PGLS	&1263.31579	&1264.599688	2.567796	0.04526	0.109059583	
APP	&3790.908997	&3792.162935	2.507876	0.0925	0.113278516	
ESD	&1288.468457	&1289.711426	2.485938	0	0.114867848	
PITPNA	&1222.510945	&1223.74628	2.47067	0.22746	0.115988473	
QPCT	&1827.295938	&1828.528655	2.465434	0.25778	0.116375554	
TSNAX	&1310.383889	&1311.577422	2.387066	0.13895	0.122343054	
TSN	&997.593312	&998.78391	2.381196	0	0.122803497	
CLIC1	&1148.117408	&1149.305999	2.377182	999	0.123119462	
PIP	&979.357249	&980.536762	2.359026	1.33026	0.124559938	
EXTL2	&1508.965025	&1510.13815	2.34625	0.11785	0.125584788	
ANXA1	&1595.040134	&1596.21223	2.344192	0	0.125750749	
CTSF	&2580.318175	&2581.487238	2.338126	0.53859	0.126241342	
DNASE2	&1921.021923	&1922.177519	2.311192	0.2571	0.128445516	
CPO	&2176.342273	&2177.496224	2.307902	0.30389	0.12871768	
CAT	&2660.666814	&2661.808515	2.283402	0.3019	0.130764763	
KLK11	&1493.314553	&1494.449962	2.270818	0.15436	0.131830304	
GDF15	&1711.222644	&1712.353997	2.262706	0.8448	0.132522318	
PRSS8	&1907.010168	&1908.13158	2.242824	0.19999	0.134235624	
FAM3C	&978.923862	&980.026592	2.20546	0.12004	0.137522866	
SPACA3	&1235.761752	&1236.857595	2.191686	0.53781	0.138757356	
GRHPR	&1677.588076	&1678.670805	2.165458	0.30407	0.141142565	
TMEFF2	&1662.498225	&1663.580821	2.165192	0.14313	0.14116699	
MINPP1	&2559.32144	&2560.400286	2.157692	0.28195	0.141857626	
GLO1	&898.644608	&899.711571	2.133926	0.10595	0.144071336	
BGN	&1722.241361	&1723.305475	2.128228	0.04132	0.144607843	
TALDO1	&1588.888016	&1589.943168	2.110304	0.14533	0.14631025	
INHBB	&1721.092529	&1722.133701	2.082344	0	0.149011199	
LDHA	&1655.522466	&1656.544652	2.044372	0.08235	0.152770016	
LZTFL1	&1303.326245	&1304.34509	2.03769	10.03568	0.153442509	
MARCKS	&1422.438434	&1423.437556	1.998244	0.41513	0.157481559	
SERPINA5	&2277.068615	&2278.048046	1.958862	0.12356	0.161635078	
CST3	&696.933448	&697.899753	1.93261	0.21552	0.16447318	
PLA1A	&2498.998733	&2499.954817	1.912168	0.39149	0.166722632	
SEPP1	&1952.445776	&1953.364727	1.837902	0.51079	0.175197045	
LGALS3	&1334.104263	&1335.022028	1.83553	1.03571	0.175475763	
PRDX5	&1042.189581	&1043.103083	1.827004	0.108	0.176481828	
FTH1	&831.776731	&832.688279	1.823096	0.19605	0.176945193	
SERPINF1	&2281.642342	&2282.547018	1.809352	0.11781	0.178585983	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SLC1A1	&2563.54173	&2564.430462	1.777464	0.04601	0.182461041	
ECM1	&2916.460238	&2917.34016	1.759844	0.40673	0.184643975	
ORM1	&1198.219526	&1199.085918	1.732784	0.26541	0.188055745	
SPINK2	&512.833953	&513.689214	1.710522	0.38027	0.190917658	
C1RL	&2663.641536	&2664.485029	1.686986	0.40567	0.193998758	
ENPP3	&4424.131662	&4424.962379	1.661434	0.32196	0.197409819	
CA2	&1300.879285	&1301.697248	1.635926	0.15225	0.200885355	
SEMA3C	&3591.545925	&3592.357437	1.623024	0.07328	0.202670649	
GNG12	&817.113883	&817.923074	1.618382	0.2255	0.203317542	
TGM4	&3677.975731	&3678.783615	1.615768	0.35309	0.203682891	
CRYZ	&1747.651356	&1748.45809	1.613468	1.10273	0.204004993	
VTN	&2593.38194	&2594.178239	1.592598	0.47097	0.206955344	
PCMT1	&1289.005936	&1289.798049	1.584226	0	0.208153021	
APOH	&1788.267691	&1789.049607	1.563832	0.16446	0.211105023	
PSMB2	&1082.04345	&1082.807058	1.527216	0	0.216530755	
HEXB	&2927.712014	&2928.452513	1.480998	0.42367	0.223618441	
FKBP4	&2243.748281	&2244.47652	1.456478	0.12127	0.22749134	
SEMA7A	&3323.062704	&3323.788999	1.45259	0.13231	0.228112819	
PFN2	&782.14411	&782.864791	1.441362	2.18313	0.229919066	
MLPH	&3875.977039	&3876.6777	1.401322	0.64036	0.23650235	
NP	&1452.459777	&1453.156188	1.392822	0.36006	0.237929109	
GLB1L	&3239.143074	&3239.837754	1.38936	2.32298	0.23851321	
TEX101	&1484.314573	&1485.002487	1.375828	0.48565	0.240813071	
IGKC	&593.576828	&594.262765	1.371874	999	0.241490165	
RAB5C	&1147.374247	&1148.052424	1.356354	0.07029	0.244170366	
NIF3L1	&1932.743175	&1933.411166	1.335982	0.53174	0.247743795	
WFDC8	&1414.489325	&1415.155443	1.332236	0.33157	0.24840782	
AZGP1	&1710.801784	&1711.449743	1.295918	0.73347	0.254960196	
CD44	&3893.376904	&3894.015149	1.27649	0.43485	0.258552682	
RAB5B	&1050.210283	&1050.846234	1.271902	0	0.259410169	
GLB1	&3849.044163	&3849.673126	1.257926	0.38743	0.262044036	
IDE	&4641.039475	&4641.66182	1.24469	0.04139	0.264569087	
GANAB	&4579.226744	&4579.847709	1.24193	0.10542	0.26509942	
PSMB7	&1343.214358	&1343.832889	1.237062	0.444	0.26603803	
ACYP1	&476.973678	&477.581387	1.215418	0	0.270261749	
LCN2	&1102.405085	&1103.011378	1.212586	0.30007	0.270820575	
MSMB	&700.74661	&701.344079	1.194938	0.52619	0.274335761	
TSG101	&1726.358954	&1726.947091	1.176274	0	0.278115843	
ADAM7	&4045.78776	&4046.362525	1.14953	1.01228	0.283647559	
FUCA1	&2440.811094	&2441.362744	1.1033	0.28394	0.293543031	
PGK2	&1982.959453	&1983.502771	1.086636	0.42425	0.297217766	
PTPRD	&9071.447696	&9071.968598	1.041804	0.12117	0.30740228	
C19orf10	&834.36158	&834.879013	1.034866	0.2249	0.309018518	
AKR1B1	&1486.299079	&1486.811156	1.024154	0.04784	0.311535691	
CD9	&1041.73294	&1042.243341	1.020802	0	0.312328848	
CD14	&1922.736957	&1923.245317	1.01672	0.65242	0.3132983	
ACAT2	&2217.016931	&2217.517405	1.000948	0.97641	0.317081228	
APOA2	&562.12144	&562.618031	0.993182	0.88292	0.318965908	
tor1B	&1561.586921	&1562.057244	0.940646	0.14833	0.332111762	
pla2g2A	&857.395127	&857.856449	0.922644	0.55984	0.336781701	
TNFSF10	&1406.70091	&1407.153056	0.904292	0.71673	0.341633469	
SOD1	&861.691912	&862.134958	0.886092	0.59187	0.346538541	
HRSP12	&647.201655	&647.632215	0.86112	0	0.353425457	
EGF	&6295.310298	&6295.739455	0.858314	0.71687	0.354210937	
GAPDHS	&2136.472734	&2136.875323	0.805178	0.32581	0.369549728	
IDUA	&3708.410113	&3708.810188	0.80015	0.1501	0.371048526	
DNAJB9	&1082.064677	&1082.458393	0.787432	0.3196	0.374877764	
NAGLU	&3595.850756	&3596.238701	0.77589	0.03287	0.378401079	
ACRBP	&3030.102403	&3030.473306	0.741806	0.47942	0.389082965	
APOD	&1109.031132	&1109.379146	0.696028	1.4186	0.404121571	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TFPI2	&1255.767383	&1256.107082	0.679398	0.36516	0.409794098	
GSTO1	&1164.079787	&1164.396593	0.633612	0.31684	0.426033496	
PSMB8	&1421.747869	&1422.047765	0.599792	0.57431	0.438657399	
APOE	&1813.54518	&1813.815922	0.541484	0.26562	0.461818359	
ACPP	&2126.025972	&2126.296456	0.540968	0.6942	0.462031833	
HINT1	&579.755893	&580.023511	0.535236	0.15148	0.464413816	
SLIT2	&7464.441143	&7464.697512	0.512738	0.22739	0.473955993	
AGA	&1771.497138	&1771.75049	0.506704	0.42134	0.476569161	
IGJ	&899.234616	&899.485266	0.5013	2.08911	0.47892947	
GSN	&3874.797066	&3875.046889	0.499646	0.11221	0.479655708	
DEFB129	&916.302065	&916.543734	0.483338	1.25874	0.486914218	
IGLV1&40	&697.327968	&697.546128	0.43632	1.65491	0.508904004	
COPB2	&4073.710222	&4073.913652	0.40686	0.05547	0.523567563	
s100A11	&496.920386	&497.122251	0.40373	0	0.525169189	
PRDX4	&1292.396361	&1292.597492	0.402262	0.34852	0.525923372	
GCHFR	&890.168157	&890.366008	0.395702	0.10247	0.529317313	
DDT	&576.569605	&576.76471	0.39021	999	0.532189038	
PAM	&4585.476236	&4585.669944	0.387416	0.40137	0.533660799	
LIPI	&2583.189501	&2583.360445	0.341888	0.64849	0.558741455	
GSTZ1	&1095.753673	&1095.923769	0.340192	0.13638	0.559718417	
NPC2	&720.532273	&720.695902	0.327258	0	0.567278155	
B2M	&642.186104	&642.341012	0.309816	0.30596	0.577793117	
FAM12A	&792.283275	&792.433151	0.299752	0.70386	0.584037936	
fam3B	&1384.05975	&1384.208302	0.297104	0.91393	0.585703675	
RAB3D	&1031.546499	&1031.691781	0.290564	0	0.589859332	
SEMG2	&579.128029	&579.255709	0.25536	0.89342	0.61332597	
GSTM3	&1077.304013	&1077.425595	0.243164	0.15374	0.621930189	
ALDH9A1	&2588.965149	&2589.079202	0.228106	0.19704	0.632931771	
WFDC2	&658.122981	&658.224899	0.203836	0.12026	0.651642192	
ACRV1	&1556.828537	&1556.913972	0.17087	0.73696	0.679339766	
TTR	&787.106962	&787.187499	0.161074	1.07661	0.68816963	
PAEP	&996.743435	&996.821345	0.15582	0.71057	0.693034469	
SEMG1	&121.123052	&121.197857	0.14961	0.9869	0.698908335	
CD63	&1057.640413	&1057.698331	0.115836	0.1242	0.733595316	
BASP1	&922.687144	&922.703716	0.033144	0.19995	0.855539613	
RALB	&1037.120299	&1037.124445	0.008292	0	0.927444583	
FAM12B	&709.381619	&709.384541	0.005844	0.91369	0.939064227	
DCD	&649.028505	&649.029896	0.002782	0.82257	0.957935349	
PSMD14	&1271.536848	&1271.537069	0.000442	0	0.983226673	
NUTF2	&661.358714	&661.358909	0.00039	0	0.984244067	
YWHAZ	&991.250665	&991.25081	0.00029	0	0.986413172	
PSMA5	&1038.294519	&1038.294553	6.8E&05	0	0.99342055	
WFDC9	&484.05381	&484.05384	6E&05	0	0.993819675	
RAB2A	&862.788137	&862.788165	5.6E&05	0	0.994029234	
RAB10	&817.552669	&817.552679	2E&05	0	0.996431764	
Park7	&840.628468	&840.628473	1E&05	0	0.997476872	
ACTN4	&4223.495936	&4170.305285	&106.381302	12.48345	#NUM!	
ADAM10	&3310.191164	&3309.548402	&1.285524	0	#NUM!	
AGR2	&794.71242	&794.347793	&0.729254	0	#NUM!	
ALAD	&1834.872155	&1834.335082	&1.074146	0.26409	#NUM!	
AMBP	&1761.529266	&1760.376689	&2.305154	0.1166	#NUM!	
ANPEP	&5014.000858	&5012.769153	&2.46341	0.43911	#NUM!	
ANTXR2	&2363.262564	&2358.531467	&9.462194	0.1181	#NUM!	
ANXA7	&2298.683052	&2297.99059	&1.384924	0.23294	#NUM!	
APOB	&23798.48311	&23798.28396	&0.398304	0.47267	#NUM!	
BTD	&2766.958224	&2765.874771	&2.166906	0.44314	#NUM!	
CACYBP	&1005.793265	&1001.550618	&8.485294	0.13247	#NUM!	
CALR	&1871.955399	&1870.63431	&2.642178	0.04036	#NUM!	
CCT3	&2975.94264	&2969.441039	&13.003202	0.20867	#NUM!	
CCT4	&2398.00113	&2397.737151	&0.527958	0	#NUM!	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CFB	&3283.411522	&3282.829768	&1.163508	0.19969	#NUM!	
CLN5	&2182.448386	&2181.998822	&0.899128	0.61487	#NUM!	
CNTNAP2	&7123.40189	&7115.132941	&16.537898	0.09267	#NUM!	
COL9A1	&4610.231317	&4606.166876	&8.128882	0.27814	#NUM!	
CPM	&2181.497171	&2177.556546	&7.88125	278.93361	#NUM!	
CREG1	&1115.66634	&1115.04758	&1.23752	0.0696	#NUM!	
Crisp2	&1479.65791	&1477.592076	&4.131668	0.22373	#NUM!	
CTSH	&1641.267516	&1640.965993	&0.603046	0.10951	#NUM!	
CTSO	&1609.319176	&1608.523114	&1.592124	0.456	#NUM!	
CUL3	&3336.212394	&3335.239294	&1.9462	0.03396	#NUM!	
CYB5R2	&1467.665914	&1466.567088	&2.197652	0.16015	#NUM!	
DDAH1	&1302.338567	&1300.960033	&2.757068	0.04857	#NUM!	
DPEP3	&2750.365346	&2750.192041	&0.34661	0.685	#NUM!	
DPP4	&3557.627888	&3555.613212	&4.029352	0.25314	#NUM!	
DPP7	&2587.783361	&2586.132839	&3.301044	0.09614	#NUM!	
DSC2	&4651.759344	&4623.309845	&56.898998	14.74033	#NUM!	
EPHA5	&4895.272234	&4885.957635	&18.629198	0.13725	#NUM!	
FOLH1	&3750.536491	&3744.890589	&11.291804	0.22315	#NUM!	
GALNT6	&2897.689432	&2887.514893	&20.349078	21.07208	#NUM!	
GBA	&3370.482245	&3364.013917	&12.936656	0.04842	#NUM!	
GGT1	&3050.207783	&3046.054746	&8.306074	0.16587	#NUM!	
GLA	&2065.559138	&2065.369172	&0.379932	0.21252	#NUM!	
GNPDA1	&1287.860273	&1287.156324	&1.407898	0.04034	#NUM!	
GPR64	&4793.717269	&4793.304764	&0.82501	0.45293	#NUM!	
GSTT1	&1142.791594	&1142.289941	&1.003306	0.16919	#NUM!	
GUSB	&3811.636433	&3810.751807	&1.769252	0.377	#NUM!	
HPX	&2733.777409	&2733.483752	&0.587314	0.2606	#NUM!	
IMPA1	&1618.528583	&1609.219509	&18.618148	0.48849	#NUM!	
ITIH5	&5267.275727	&5263.377523	&7.796408	0.23808	#NUM!	
LAMP2	&1922.618218	&1922.574982	&0.086472	0.55366	#NUM!	
LDHC	&1561.422732	&1560.712587	&1.42029	0.13507	#NUM!	
LGMN	&2360.218296	&2347.787166	&24.86226	0.15282	#NUM!	
LIPA	&2212.82632	&2212.725293	&0.202054	0.43768	#NUM!	
LIPG	&2621.646146	&2618.636401	&6.01949	0.31564	#NUM!	
MSLN	&3967.846354	&3967.687188	&0.318332	0.3491	#NUM!	
NME3	&751.632493	&750.740322	&1.784342	0	#NUM!	
PAICS	&2100.303864	&2099.456493	&1.694742	0.24685	#NUM!	
PDIA3	&2418.576848	&2406.94703	&23.259636	0.14697	#NUM!	
PEBP4	&1277.514497	&1277.467989	&0.093016	0.49954	#NUM!	
PGM1	&2775.792833	&2774.79882	&1.988026	0.08878	#NUM!	
PGM2	&3783.176772	&3759.985968	&46.381608	0.14414	#NUM!	
PHGDH	&2552.807913	&2551.461869	&2.692088	0.08882	#NUM!	
PI15	&1214.786653	&1214.685603	&0.2021	0.12676	#NUM!	
PODXL2	&2867.962693	&2867.618687	&0.688012	0.22761	#NUM!	
PPIA	&756.898294	&752.994604	&7.80738	0	#NUM!	
PPIC	&1091.49007	&1090.727937	&1.524266	0.2344	#NUM!	
PRKAR1A	&1752.632816	&1749.8799	&5.505832	0	#NUM!	
PROS1	&3326.273918	&3325.441354	&1.665128	0.33052	#NUM!	
PSCA	&648.865194	&648.001909	&1.72657	0.16529	#NUM!	
PSMA2	&1086.859645	&1077.218695	&19.2819	0	#NUM!	
PSMA3	&1294.640693	&1282.694898	&23.89159	0	#NUM!	
PSMD2	&4158.003401	&4153.976108	&8.054586	0.0844	#NUM!	
RAB1B	&983.374228	&972.299495	&22.149466	0	#NUM!	
RALA	&1069.365987	&1061.662033	&15.407908	0	#NUM!	
RBP4	&891.90676	&888.996049	&5.821422	17.15225	#NUM!	
RDX	&2858.418707	&2840.784203	&35.269008	0.02781	#NUM!	
RHOA	&812.291506	&812.291489	&3.4E&05	0	#NUM!	
RPLP0	&1380.6089	&1378.571181	&4.075438	0	#NUM!	
SCGB2A1	&560.014319	&559.89134	&0.245958	0.48544	#NUM!	
SELENBP1	&2613.818703	&2612.93395	&1.769506	0.12503	#NUM!	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SERPINA1	&2322.066413	&2321.504092	&1.124642	0.57109	#NUM!	
SERPINI1	&1936.676723	&1936.203198	&0.94705	0.19677	#NUM!	
SH3BGRL2	&468.874796	&467.661613	&2.426366	0	#NUM!	
SLC15A2	&3496.536405	&3495.726186	&1.620438	0.43593	#NUM!	
SLPI	&797.372796	&797.220178	&0.305236	0.79014	#NUM!	
smpdl3A	&2309.634252	&2309.172107	&0.92429	0.37166	#NUM!	
SPINT1	&2729.125603	&2727.518518	&3.21417	0.6354	#NUM!	
SPINT3	&506.469633	&506.311902	&0.315462	0.42257	#NUM!	
STXBP2	&3028.914686	&3028.359004	&1.111364	0.05772	#NUM!	
TGFB1	&1757.508279	&1743.376214	&28.26413	16.18257	#NUM!	
TKT	&3006.216857	&3004.208171	&4.017372	0.02026	#NUM!	
TOLLIP	&1330.379152	&1322.151512	&16.45528	0	#NUM!	
TPI1	&1184.841297	&1184.094718	&1.493158	0	#NUM!	
TSTA3	&1604.246022	&1604.08178	&0.328484	0.02719	#NUM!	
USP14	&2151.688316	&2149.294333	&4.787966	0	#NUM!	

Macaque

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PTPRS	%9629.927823	%9807.067451	354.279256	0.00369	4.95778E%79	
LAMA5	%19255.67827	%19424.33842	337.320298	0.1179	2.44607E%75	
FASN	%13845.70872	%13989.66077	287.904102	0.12244	1.42311E%64	
SDK2	%10118.72493	%10260.92754	284.405216	0.03626	8.23473E%64	
HSPG2	%32082.54306	%32206.34461	247.603114	0.04892	8.64953E%56	
MYH9	%8819.02845	%8938.760487	239.464074	0.00671	5.14709E%54	
ODZ2	%12811.04162	%12927.89578	233.708318	0.01361	9.26078E%53	
PLXNB2	%9381.131633	%9493.033579	223.803892	0.04373	1.33872E%50	
FLNB	%12658.69976	%12765.2184	213.037292	0.05128	2.98701E%48	
RELN	%16739.42386	%16841.80675	204.76578	0.07593	1.90499E%46	
MUC5B	%33206.98623	%33308.82329	203.67412	0.31912	3.2968E%46	
PTPRF	%9059.770763	%9157.616639	195.691752	0.05304	1.81986E%44	
VWF	%13693.71209	%13785.45195	183.479716	0.15468	8.42745E%42	
AGRN	%10948.77368	%11040.38128	183.215198	0.11602	9.626E%42	
MYO1C	%5446.603823	%5532.4676	171.727554	0.01126	3.10358E%39	
COL6A1	%5750.234662	%5834.675303	168.881282	0.04305	1.2987E%38	
ACTN4	%4155.284931	%4239.157457	167.745052	0	2.29979E%38	
ACE	%6845.706945	%6926.098777	160.783664	0.05995	7.62833E%37	
EEF2	%4122.230877	%4199.702821	154.943888	0.00216	1.44031E%35	
PYGB	%4716.273717	%4787.956786	143.366138	0.02214	4.88852E%33	
THBS2	%5838.532722	%5908.153998	139.242552	0.0488	3.8981E%32	
LAMC1	%7893.033184	%7956.372922	126.679476	0.05196	2.18336E%29	
THBS1	%5463.985192	%5524.43455	120.898716	0.03079	4.02148E%28	
SORL1	%10869.72919	%10928.98227	118.506152	0.08286	1.34337E%27	
col12A1	%14645.80904	%14700.62533	109.632572	0.12393	1.17946E%25	
CLSTN1	%4930.384759	%4984.820367	108.871216	0.0492	1.7318E%25	
COL6A2	%6172.266808	%6225.996542	107.459468	0.13449	3.53052E%25	
C3	%8538.083685	%8590.682244	105.197118	0.12385	1.10571E%24	
CNTNAP2	%7119.909315	%7172.165688	104.512746	0.06305	1.56185E%24	
SLIT2	%7467.373039	%7518.659634	102.57319	0.06483	4.15721E%24	
PTPRD	%9070.833489	%9121.383968	101.100958	0.04707	8.74126E%24	
CAPN1	%3437.852173	%3487.639743	99.57514	0.03526	1.8886E%23	
MMP2	%3190.217857	%3239.76497	99.094226	0.00742	2.40769E%23	
GLG1	%5642.58047	%5690.295883	95.430826	0	1.5315E%22	
ACTN1	%4234.822777	%4281.478491	93.311428	0.03257	4.46805E%22	
RUVBL2	%2137.246489	%2183.635848	92.778718	0	5.84806E%22	
FN1	%12062.54571	%12108.89891	92.7064	0.13526	6.06571E%22	
DDB1	%5172.885422	%5218.736758	91.702672	0	1.00729E%21	
GAS6	%3531.550489	%3576.272985	89.444992	0.06753	3.15284E%21	
PFKP	%4125.565264	%4170.145224	89.15992	0.02633	3.64152E%21	
IGF2R	%12687.87549	%12731.68473	87.61848	0.27453	7.93795E%21	
CPAMD8	%10033.02348	%10076.5833	87.119642	0.16954	1.02151E%20	
COL18A1	%9613.151128	%9656.458795	86.615334	0.22946	1.31821E%20	
ADAMTSL1	%8529.01596	%8571.95088	85.86984	0.1153	1.92178E%20	
ANPEP	%5009.525901	%5051.411755	83.771708	0.10364	5.55339E%20	
ADAMTS1	%4873.298463	%4914.683525	82.770124	0.0476	9.21726E%20	
UGCGL1	%7216.104533	%7257.311419	82.413772	0.12912	1.10382E%19	
TKT	%3006.127447	%3047.325999	82.397104	0.02246	1.11317E%19	
BGN	%1720.422604	%1761.153034	81.46086	0.00701	1.78767E%19	
GSN	%3871.466193	%3911.657411	80.382436	0.03888	3.08525E%19	
COMP	%3817.623219	%3857.694513	80.142588	0.10498	3.48343E%19	
ST14	%4409.943577	%4449.920448	79.953742	0.07585	3.83279E%19	
PLOD3	%3732.145034	%3771.914207	79.538346	0.06613	4.72956E%19	
CLTC	%7273.995814	%7313.038125	78.084622	0.02059	9.87195E%19	
HSPA8	%3010.867894	%3049.862011	77.988234	0	1.03656E%18	
BAIAP2	%2716.522279	%2755.36513	77.685702	0.05614	1.20813E%18	
GPC1	%2722.809882	%2760.650922	75.68208	0.05928	3.33218E%18	
PFAS	%6777.075897	%6813.903233	73.654672	0.13473	9.30513E%18	
TFRC	%4084.239564	%4120.885892	73.292656	0.169	1.11783E%17	
RRBP1	%4915.158047	%4951.571304	72.826514	0.07048	1.41562E%17	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
GAA	%4986.232473	%5021.970965	71.476984	0.13461	2.80511E%17	
CCT5	%2474.76841	%2509.982277	70.427734	0	4.7744E%17	
KRT5	%2976.676083	%3011.869473	70.38678	0.02792	4.87455E%17	
TMEM8	%4067.158628	%4102.184278	70.0513	0.12461	5.7782E%17	
MAN2B1	%5063.018437	%5097.962064	69.887254	0.12283	6.27929E%17	
KPNB1	%3989.326638	%4024.207984	69.762692	0	6.68861E%17	
IQGAP1	%7510.495528	%7545.154477	69.317898	0.04836	8.38056E%17	
DDR1	%4202.475825	%4236.81122	68.67079	0.04565	1.16352E%16	
ATRN	%7584.395072	%7618.558462	68.32678	0.099	1.38527E%16	
GGT1	%3049.911916	%3083.707542	67.591252	0.09109	2.01158E%16	
PSMD2	%4157.323335	%4190.767063	66.887456	0.02507	2.87458E%16	
ACLY	%5465.893973	%5498.978224	66.168502	0.05591	4.13975E%16	
SEMA3F	%3868.760262	%3901.436855	65.353186	0.05977	6.26086E%16	
CCT7	%2530.495395	%2562.86474	64.73869	0	8.55191E%16	
ACO1	%4246.515534	%4278.735975	64.440882	0.06983	9.94726E%16	
PSME4	%8502.614321	%8534.320196	63.41175	0.09077	1.67715E%15	
sez6L2	%4430.704242	%4462.197495	62.986506	0.0445	2.08128E%15	
GALNS	%2942.870185	%2973.471982	61.203594	0.07191	5.14675E%15	
TOLLIP	%1329.630177	%1359.877641	60.494928	0.00834	7.37683E%15	
LAMB2	%9314.070774	%9343.706016	59.270484	0.23574	1.37422E%14	
LDLR	%4411.387916	%4440.439715	58.103598	0.17839	2.48671E%14	
GPRC5C	%2502.639955	%2531.69144	58.10297	0.072	2.4875E%14	
APOB	%23796.82278	%23825.16701	56.688454	0.42855	5.10625E%14	
COLEC12	%3646.640974	%3674.748098	56.214248	0.06438	6.49889E%14	
PGD	%2489.118756	%2516.941061	55.64461	0.01488	8.68307E%14	
VPS28	%1273.569765	%1301.391009	55.642488	0.02498	8.69245E%14	
INHBB	%1717.785321	%1745.541441	55.51224	0.00941	9.28789E%14	
RTN4RL1	%2265.337138	%2293.047186	55.420096	0.09156	9.73362E%14	
ITIH5	%5266.17023	%5293.757787	55.175114	0.14885	1.10256E%13	
COPB2	%4069.83217	%4097.069536	54.474732	0.01544	1.57459E%13	
STXBP2	%3028.622084	%3055.729479	54.21479	0.04609	1.79729E%13	
CNTN3	%5074.509018	%5101.571734	54.125432	0.11036	1.88091E%13	
GFRA2	%2076.327442	%2103.003694	53.352504	0.02086	2.78756E%13	
OLFM1	%2197.81427	%2224.263784	52.899028	0.02792	3.51143E%13	
PRKCSH	%2724.359173	%2750.570583	52.42282	0.09782	4.47494E%13	
MGAM	%9728.292021	%9754.499765	52.415488	0.25189	4.49168E%13	
Hyou1	%4706.740815	%4732.621423	51.761216	0.11037	6.26778E%13	
FBP1	%1664.762749	%1690.494484	51.46347	0.06345	7.29418E%13	
HSPA4	%3745.958532	%3771.677239	51.437414	0.03915	7.39163E%13	
SFN	%1070.945582	%1096.602445	51.313726	0.00963	7.87233E%13	
NRP1	%4385.535278	%4411.067209	51.063862	0.088	8.94093E%13	
TUBB1	%2181.49665	%2206.913046	50.832792	0.03643	1.00579E%12	
CALR	%1871.499414	%1896.874449	50.75007	0.01467	1.04909E%12	
BCAN	%4543.767629	%4568.909529	50.2838	0.18243	1.33043E%12	
VCL	%5089.86528	%5114.478518	49.226476	0.06557	2.28052E%12	
GPR56	%3511.418522	%3535.743652	48.65026	0.13724	3.05928E%12	
APLP2	%3675.551538	%3699.685931	48.268786	0.11447	3.71621E%12	
SERPINF1	%2281.528036	%2305.300359	47.544646	0.11933	5.37654E%12	
VCP	%3670.833831	%3694.507086	47.34651	0.01726	5.94839E%12	
ACTR1A	%1747.712288	%1771.347716	47.270856	0	6.18246E%12	
TGFB1	%1739.201787	%1762.698568	46.993562	0	7.12203E%12	
VAT1	%1978.941316	%2002.219229	46.555826	0.09841	8.90451E%12	
EFHD2	%1215.15498	%1238.334593	46.359226	0	9.84429E%12	
IDE	%4641.323765	%4664.24626	45.84499	0.07883	1.2799E%11	
ALDOA	%2009.97274	%2032.775724	45.605968	0.02943	1.446E%11	
RDX	%2852.934108	%2875.715854	45.563492	0	1.4777E%11	
CANT1	%2223.036038	%2245.80898	45.545884	0.09476	1.49105E%11	
KRT8	%2755.963802	%2778.636318	45.345032	0	1.65207E%11	
ENO1	%2054.113923	%2076.638135	45.048424	0.0168	1.92222E%11	
CKB	%1605.156089	%1627.649727	44.987276	0.01911	1.98319E%11	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPB1	%959.51003	%981.978603	44.937146	0	2.03461E%11	
TPP2	%6049.339788	%6071.722131	44.764686	0.22752	2.22194E%11	
CCT2	%2333.600358	%2355.676627	44.152538	0	3.03758E%11	
PHGDH	%2552.774481	%2574.77025	43.991538	0.07793	3.29799E%11	
HSPA5	%2987.73188	%3009.586854	43.709948	0	3.80831E%11	
EPHA5	%4892.023051	%4913.736827	43.427552	0.04866	4.3995E%11	
GPI	%2905.712216	%2927.338359	43.252286	0.08313	4.81175E%11	
PPP5C	%2320.823334	%2342.249141	42.851614	0.01466	5.90533E%11	
PGM2	%3776.725602	%3798.102788	42.754372	0.10334	6.2063E%11	
LPL	%2386.871682	%2408.234646	42.725928	0.0185	6.29721E%11	
ANXA2	%1662.824205	%1684.178564	42.708718	0	6.35285E%11	
PROM2	%4694.064204	%4715.37669	42.624972	0.22428	6.63074E%11	
MME	%3524.649867	%3545.902269	42.504804	0.07906	7.05088E%11	
A4GALT	%1746.19358	%1767.429467	42.471774	0.09438	7.17096E%11	
LEFTY2	%2008.135498	%2029.312522	42.354048	0.08864	7.61585E%11	
SEMA7A	%3322.620811	%3343.77088	42.300138	0.08317	7.8287E%11	
DPP7	%2587.92436	%2608.919966	41.991212	0.11646	9.16845E%11	
PACSIN2	%2686.202344	%2707.144337	41.883986	0.22083	9.68526E%11	
NEO1	%6916.779062	%6937.619864	41.681604	0.14315	1.07415E%10	
CYB561	%1906.211655	%1927.006498	41.589686	0.08578	1.12586E%10	
PGM1	%2775.125238	%2795.667537	41.084598	0.06229	1.45781E%10	
UGDH	%2200.006696	%2220.274937	40.536482	0.03485	1.92979E%10	
RAB11B	%959.630271	%979.880882	40.501222	0	1.96493E%10	
ANXA11	%4311.475192	%4331.558843	40.167302	0.13487	2.33118E%10	
NAGLU	%3596.687267	%3616.701546	40.028558	0.11597	2.50277E%10	
NCSTN	%3551.545997	%3571.396226	39.700458	0.06493	2.96056E%10	
SLC44A4	%3576.790868	%3596.515846	39.449956	0.13224	3.36575E%10	
ABP1	%4017.617441	%4037.300766	39.36665	0.201	3.51245E%10	
IDUA	%3708.676045	%3728.279297	39.206504	0.20039	3.81268E%10	
APOE	%1810.427621	%1829.973191	39.09114	0.10485	4.04475E%10	
CUL3	%3336.205054	%3355.691005	38.971902	0.03543	4.29949E%10	
GSTP1	%1055.879003	%1075.285826	38.813646	0	4.66257E%10	
SERPINB6	%2139.822075	%2159.157564	38.670978	0.09051	5.01612E%10	
MAN2B2	%5888.901175	%5908.135572	38.468794	0.20626	5.56362E%10	
DNAJC3	%2290.814808	%2309.941381	38.253146	0.03602	6.21368E%10	
PSMA4	%1160.129998	%1179.246709	38.233422	0	6.27681E%10	
SORT1	%3973.58341	%3992.650098	38.133376	0.09994	6.60703E%10	
CD151	%1221.053605	%1240.111695	38.11618	0.05393	6.66551E%10	
NAPA	%1260.183872	%1279.08181	37.795876	0	7.85476E%10	
LGMN	%2355.935684	%2374.725601	37.579834	0.03423	8.7747E%10	
PDCD6IP	%3898.175897	%3916.809956	37.268118	0	1.02954E%09	
THBS4	%4698.981955	%4717.606217	37.248524	0.15732	1.03994E%09	
CACNA2D1	%4980.663535	%4999.212137	37.097204	0.08558	1.12385E%09	
FMOD	%1737.730155	%1756.115048	36.769786	0.02122	1.32935E%09	
PGK1	%1892.174332	%1910.301526	36.254388	0	1.7317E%09	
KIF5B	%4443.867053	%4461.879914	36.025722	0.18965	1.9473E%09	
RAB1B	%980.631084	%998.5372	35.812232	0	2.17279E%09	
SEMA3C	%3591.680246	%3609.376062	35.391632	0.08978	2.69643E%09	
EEF1A1	%2041.953382	%2059.598121	35.289478	0	2.84163E%09	
SELENBP1	%2613.782509	%2631.371607	35.178196	0.12913	3.00873E%09	
CNDP2	%2405.514825	%2423.015292	35.000934	0.10524	3.29547E%09	
CCT3	%2972.164201	%2989.612763	34.897124	0.0773	3.47594E%09	
DSC3	%4388.896616	%4406.320967	34.848702	0.20894	3.56347E%09	
SPINT1	%2726.73057	%2744.140098	34.819056	0.15034	3.61815E%09	
GALNT6	%2889.599902	%2906.964035	34.728266	0.13145	3.79087E%09	
GNB1	%1522.933884	%1540.287602	34.707436	0	3.83165E%09	
RAB3D	%1029.741685	%1047.060517	34.637664	0	3.97147E%09	
CTSD	%2193.009514	%2210.324055	34.629082	0.11959	3.98902E%09	
IL1RAP	%3278.612152	%3295.87715	34.529996	0.0722	4.19733E%09	
KRT10	%3012.68969	%3029.949322	34.519264	0.0995	4.22054E%09	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PGC	%1949.413881	%1966.583471	34.33918	0.11116	4.62967E%09	
LGALS3BP	%3226.862968	%3244.00029	34.274644	0.15595	4.78577E%09	
KAL1	%3350.408648	%3367.450998	34.0847	0.1588	5.27645E%09	
CTSF	%2578.527723	%2595.549001	34.042556	0.1263	5.39198E%09	
NRCAM	%6121.663951	%6138.619062	33.910222	0.15212	5.77147E%09	
ARSA	%2672.247872	%2689.173561	33.851378	0.14624	5.94869E%09	
CD81	%1095.760722	%1112.617513	33.713582	0.04367	6.38533E%09	
DAG1	%4328.504077	%4345.333638	33.659122	0.1094	6.56662E%09	
CPE	%2252.881513	%2269.541835	33.320644	0.02443	7.81486E%09	
MMP14	%2639.388377	%2655.971615	33.166476	0.05449	8.45965E%09	
TCP1	%2481.645649	%2498.12111	32.950922	0.02227	9.45149E%09	
COL9A1	%4607.753075	%4624.040567	32.574984	0.17156	1.14681E%08	
RUVBL1	%2020.851407	%2037.112287	32.52176	0	1.17865E%08	
PDIA3	%2416.882148	%2433.007383	32.25047	0.06947	1.35524E%08	
GNPTG	%1708.304164	%1724.389279	32.17023	0.12625	1.41238E%08	
GMPPA	%2233.907094	%2249.933713	32.053238	0.02551	1.50005E%08	
LCP1	%2872.470951	%2888.460005	31.978108	0.04395	1.5592E%08	
SYT7	%2154.76132	%2170.703743	31.884846	0.03848	1.63588E%08	
IL6ST	%4249.875539	%4265.769967	31.788856	0.17195	1.71876E%08	
MAMDC2	%3253.861069	%3269.666173	31.610208	0.10283	1.88436E%08	
XPNPEP1	%2971.591477	%2987.243659	31.304364	0.04698	2.20583E%08	
QSCN6	%3083.877309	%3099.456619	31.15862	0.16305	2.37781E%08	
CAP1	%2291.264839	%2306.7979	31.066122	0.02549	2.49386E%08	
C19orf10	%835.203051	%850.532652	30.659202	0.02212	3.07564E%08	
YWHAG	%1078.462822	%1093.72499	30.524336	0	3.29705E%08	
KRT1	%3124.458702	%3139.625962	30.33452	0.10389	3.63597E%08	
ADAM10	%3311.810011	%3326.892867	30.165712	0.08383	3.96661E%08	
GPD1L	%1727.244358	%1742.278125	30.067534	0.0456	4.17259E%08	
LIPG	%2620.227983	%2635.062404	29.668842	0.11252	5.1252E%08	
AHCY	%2343.734923	%2358.381835	29.293824	0.11989	6.21936E%08	
P4HB	%2492.567493	%2507.19604	29.257094	0.10628	6.33837E%08	
ALDH1A1	%2397.53832	%2412.094857	29.113074	0.08145	6.82747E%08	
MATN2	%4673.635301	%4687.984979	28.699356	0.17516	8.45318E%08	
MPST	%1728.855266	%1743.188704	28.666876	0.15759	8.59616E%08	
PSMA1	%1250.939568	%1265.235646	28.592156	0	8.93434E%08	
GAPDH	%1562.778995	%1577.05277	28.54755	0.04148	9.14254E%08	
PSAP	%2462.039101	%2476.187863	28.297524	0.10005	1.04029E%07	
DDAH1	%1299.676282	%1313.814917	28.27727	0	1.05123E%07	
PRKAR1A	%1752.782341	%1766.826241	28.0878	0.02737	1.15934E%07	
IQGAP2	%7135.035794	%7149.05543	28.039272	0.2225	1.18878E%07	
PRKACA	%1825.926877	%1839.791573	27.729392	0.13804	1.39527E%07	
SDCBP2	%1528.36665	%1542.166968	27.600636	0.11253	1.4913E%07	
NELL1	%4124.750734	%4138.483616	27.465764	0.12465	1.599E%07	
GNB2	%1550.920319	%1564.599192	27.357746	0.02035	1.69086E%07	
NUCB1	%2215.898666	%2229.551568	27.305804	0.1503	1.73689E%07	
PSMB4	%1248.797097	%1262.435163	27.276132	0.02925	1.76375E%07	
GUSB	%3812.177975	%3825.777008	27.198066	0.24562	1.83642E%07	
FUT3	%2254.09782	%2267.65307	27.1105	0.15111	1.92151E%07	
GNB2L1	%1451.515393	%1464.99952	26.968254	0	2.06825E%07	
MFAP4	%1277.635856	%1291.118474	26.965236	0.0556	2.07148E%07	
FH	%2428.426109	%2441.893158	26.934098	0.10938	2.10512E%07	
SERPINA4	%2414.512858	%2427.959566	26.893416	0.17253	2.1499E%07	
OS9	%3132.172688	%3145.58566	26.825944	0.12527	2.22628E%07	
LIFR	%5259.571222	%5272.901073	26.659702	0.2167	2.42629E%07	
PLOD2	%3514.778659	%3528.045823	26.534328	0.10445	2.58896E%07	
APEH	%3360.88534	%3374.081022	26.391364	0.12511	2.78784E%07	
AGT	%2693.164183	%2706.248759	26.169152	0.2641	3.12779E%07	
GSR	%2856.555006	%2869.559717	26.009422	0.16829	3.39755E%07	
SLC35F2	%1867.497619	%1880.334751	25.674264	0.13214	4.04181E%07	
PSMA7	%1179.052835	%1191.748636	25.391602	0	4.67951E%07	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PSMB7	%1343.179754	%1355.74037	25.121232	0.03143	5.38368E%07	
GNS	%2820.029299	%2832.553643	25.048688	0.12824	5.59008E%07	
LMAN2	%1581.140705	%1593.635835	24.99026	0.02339	5.76207E%07	
PPP2CA	%1403.551641	%1416.033504	24.963726	0	5.84191E%07	
MARCKS	%1422.975918	%1435.39819	24.844544	0.03018	6.21447E%07	
GDI2	%2124.784878	%2137.19742	24.825084	0.10648	6.27752E%07	
LAP3	%3056.717201	%3069.081295	24.728188	0.11265	6.60116E%07	
SOD3	%1098.558789	%1110.860987	24.604396	0.08937	7.0391E%07	
TAGLN2	%905.470794	%917.748286	24.554984	0	7.22193E%07	
SYT1	%1898.958512	%1911.231662	24.5463	0	7.25455E%07	
LAMP1	%2236.179428	%2248.334261	24.309666	0.14863	8.20264E%07	
IGFBP2	%1366.026989	%1378.175042	24.296106	0.05332	8.26059E%07	
ANXA6	%3520.379547	%3532.513441	24.267788	0.32465	8.38293E%07	
TGFBR3	%4154.183733	%4166.301808	24.23615	0.216	8.52177E%07	
LNPEP	%4993.028108	%5004.95856	23.860904	0.22575	1.03554E%06	
SI	%9012.818092	%9024.734265	23.832346	0.39729	1.05101E%06	
RAB3B	%1023.531487	%1035.346861	23.630748	0	1.16708E%06	
CFL1	%743.382566	%755.197474	23.629816	0.02402	1.16764E%06	
IL1RL1	%3842.945735	%3854.719032	23.546594	0.23902	1.21925E%06	
PGAM2	%1125.013958	%1136.780607	23.533298	0.05463	1.22771E%06	
NAGA	%2039.314531	%2051.078774	23.528486	0.12843	1.23078E%06	
PRDX2	%978.016319	%989.683891	23.335144	0	1.36091E%06	
ALCAM	%2705.087729	%2716.720735	23.266012	0.10941	1.41071E%06	
RAD23B	%1918.027592	%1929.514344	22.973504	0.0333	1.6425E%06	
GANAB	%4579.779408	%4591.258247	22.957678	0.2138	1.65607E%06	
MANBA	%4390.406108	%4401.869643	22.92707	0.24293	1.68265E%06	
ALDOC	%1676.155466	%1687.557951	22.80497	0.05926	1.79301E%06	
APP	%3782.538756	%3793.913529	22.749546	0.30359	1.84548E%06	
PKM2	%2962.763543	%2974.127446	22.727806	0.08926	1.86647E%06	
MDH2	%1639.553	%1650.896854	22.687708	0.11866	1.90583E%06	
ACP5	%1620.437691	%1631.603656	22.33193	0.0905	2.29361E%06	
NPEPPS	%4004.589138	%4015.704305	22.230334	0.03496	2.41823E%06	
PPIB	%976.198544	%987.202938	22.008788	0	2.71405E%06	
ANXA7	%2296.705549	%2307.701234	21.99137	0.08281	2.73879E%06	
NPC2	%718.615367	%729.592922	21.95511	0	2.79103E%06	
LDHB	%1500.35107	%1511.317454	21.932768	0	2.82371E%06	
CAPG	%1646.629171	%1657.479501	21.70066	0.0347	3.18682E%06	
PSMB6	%1148.156719	%1158.979316	21.645194	0.03685	3.28031E%06	
TALDO1	%1587.970622	%1598.747813	21.554382	0.05615	3.43936E%06	
PPP1R7	%1599.65869	%1610.387426	21.457472	0.03172	3.61764E%06	
TIMP3	%904.544163	%915.222943	21.35756	0	3.81115E%06	
SPON2	%1579.861834	%1590.454802	21.185936	0.11394	4.16812E%06	
FOLH1	%3749.694302	%3760.202638	21.016672	0.20942	4.55304E%06	
ALDH7A1	%2686.455726	%2696.939136	20.96682	0.09157	4.67307E%06	
CD63	%1055.468679	%1065.92473	20.912102	0	4.80847E%06	
CNP	%1957.401729	%1967.808446	20.813434	0.13461	5.06266E%06	
SMPD1	%3206.440497	%3216.847047	20.8131	0.1829	5.06354E%06	
CLU	%2586.533015	%2596.937309	20.808588	0.21698	5.07549E%06	
ALDH9A1	%2588.878508	%2599.248768	20.74052	0.16232	5.25913E%06	
TIMP2	%996.127074	%1006.492017	20.729886	0	5.28841E%06	
PSMA2	%1085.541183	%1095.881453	20.68054	0	5.42647E%06	
CAPNS1	%1633.109788	%1643.366205	20.512834	0.00392	5.92328E%06	
BPNT1	%1441.158658	%1451.337298	20.35728	0.0592	6.42482E%06	
TSG101	%1726.151997	%1736.329287	20.35458	0	6.43389E%06	
DNASE1	%1529.385406	%1539.53715	20.303488	0.12221	6.608E%06	
GNMT	%1451.539297	%1461.625479	20.172364	0.05563	7.0768E%06	
EEF1G	%2358.501341	%2368.586862	20.171042	0.11794	7.08169E%06	
TSTA3	%1605.471968	%1615.379442	19.814948	0.07166	8.53129E%06	
CDH1	%4609.654495	%4619.514164	19.719338	0.31605	8.96892E%06	
GNPDA1	%1287.817868	%1297.6294	19.623064	0.03217	9.43237E%06	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
B4GALT4	%1757.618204	%1767.343501	19.450594	0.12787	1.03236E%05	
ARF1	%802.333419	%812.025321	19.383804	0	1.0691E%05	
CD109	%7431.614641	%7441.289849	19.350416	0.43434	1.08796E%05	
SIL1	%2461.600903	%2471.274839	19.347872	0.14933	1.08941E%05	
AKR7A2	%2000.202176	%2009.829963	19.255574	0.17922	1.14336E%05	
ELSPBP1	%1097.581578	%1107.198451	19.233746	0.10116	1.15651E%05	
BPIL1	%2383.467276	%2393.042406	19.15026	0.197	1.20821E%05	
PITPNA	%1222.716624	%1232.289067	19.144886	0.06811	1.21162E%05	
SMOC2	%2172.866179	%2182.369948	19.007538	0.12118	1.30203E%05	
GSTM3	%1077.121953	%1086.62205	19.000194	0.07464	1.30705E%05	
GAPDHS	%2136.815543	%2146.309576	18.988066	0.21978	1.31539E%05	
HEXA	%2619.46247	%2628.950932	18.976924	0.16289	1.32309E%05	
CST3	%697.372535	%706.842589	18.940108	0.0504	1.34887E%05	
GPC4	%2542.011141	%2551.422986	18.82369	0.12509	1.43375E%05	
AKR1B1	%1486.728794	%1495.998672	18.539756	0.09917	1.66397E%05	
ANXA1	%1595.336655	%1604.42173	18.17015	0.07158	2.02021E%05	
RPLP0	%1379.977973	%1389.034159	18.112372	0	2.08244E%05	
FSTL1	%1389.546971	%1398.59747	18.100998	0	2.09492E%05	
MDH1	%1612.676216	%1621.711169	18.069906	0.06843	2.12941E%05	
PRKAR2A	%2022.866892	%2031.819193	17.904602	0.22935	2.32259E%05	
RAB13	%919.801983	%928.747792	17.891618	0	2.33849E%05	
B4GALT1	%2163.198834	%2172.122885	17.848102	0.21843	2.39258E%05	
CTSB	%1794.355334	%1803.253129	17.79559	0.11056	2.45953E%05	
SPOCK3	%2096.179568	%2105.068442	17.777748	0.0617	2.4827E%05	
IGHG4	%1803.638318	%1812.493003	17.70937	0.22309	2.57356E%05	
MSLN	%8968.0331	%8976.84521	17.62422	0.38037	2.69139E%05	
MAN2A1	%5436.72246	%5445.519248	17.593576	0.2592	2.73511E%05	
CAB39L	%1524.798907	%1533.570639	17.543464	0.07546	2.80814E%05	
CFB	%3283.765383	%3292.505837	17.480908	0.3023	2.90207E%05	
DDT	%575.760655	%584.493995	17.46668	0.04137	2.92388E%05	
SLC1A1	%2564.687529	%2573.412169	17.44928	0.14431	2.95076E%05	
CCT8	%2457.295536	%2466.015185	17.439298	0.09034	2.9663E%05	
PSMB5	%1223.047397	%1231.711574	17.328354	0.0715	3.1446E%05	
AMBP	%1761.752201	%1770.411614	17.318826	0.17218	3.1604E%05	
SMS	%1888.459634	%1897.046136	17.173004	0.06816	3.41252E%05	
SERPINA5	%2277.775186	%2286.327876	17.10538	0.23411	3.5362E%05	
SORD	%1998.558319	%2007.106218	17.095798	0.19596	3.55409E%05	
tor1B	%1562.032808	%1570.445784	16.825952	0.09291	4.09692E%05	
IGFBP5	%1175.1352	%1183.509922	16.749444	0.03036	4.26548E%05	
RNASET2	%1452.211554	%1460.583793	16.744478	0.14218	4.27665E%05	
CP	%5168.51522	%5176.841196	16.651952	0.32447	4.49041E%05	
PPT1	%1498.734132	%1507.056789	16.645314	0.10384	4.50615E%05	
PPP2R4	%2044.03973	%2052.282276	16.485092	0.1316	4.90341E%05	
IDI1	%1550.394808	%1558.636633	16.48365	0.1512	4.90714E%05	
CCT4	%2397.191119	%2405.417681	16.453124	0.0971	4.98679E%05	
NEU1	%2052.087431	%2060.285292	16.395722	0.19997	5.14011E%05	
CAT	%2660.744629	%2668.927004	16.36475	0.23664	5.22479E%05	
AKR1A1	%1503.620612	%1511.732026	16.222828	0.04505	5.63115E%05	
TWSG1	%989.791124	%997.878433	16.174618	0	5.77629E%05	
DPP4	%3557.142187	%3565.161291	16.038208	0.20285	6.2077E%05	
PCMT1	%1289.712691	%1297.650089	15.874796	0.08076	6.7674E%05	
CYB5R2	%1466.702971	%1474.633046	15.86015	0.14735	6.81998E%05	
TPI1	%1185.166461	%1193.000146	15.66737	0.13745	7.55158E%05	
FKBP4	%2243.816446	%2251.607585	15.582278	0.17237	7.89915E%05	
FTH1	%831.943656	%839.707741	15.52817	0.0427	8.12849E%05	
EDIL3	%2207.963603	%2215.710255	15.493304	0.15864	8.2798E%05	
STEAP2	%2249.202826	%2256.907638	15.409624	0.07912	8.65464E%05	
HSPA1L	%3828.456676	%3836.14496	15.376568	0.03418	8.80737E%05	
USP14	%2151.404363	%2159.066268	15.32381	0	9.05678E%05	
PI15	%1214.215995	%1221.790394	15.148798	0.04694	9.93615E%05	

Gene	lnL&free	lnL&ixed	2ΔlnL	branch_w	P&value	k
RAB27B	%998.703725	%1006.231459	15.055468	0	0.000104397	
QPCT	%1826.761508	%1834.263998	15.00498	0.1681	0.000107228	
HPRT1	%1067.02643	%1074.504727	14.956594	0	0.000110013	
EFEMP1	%2220.17728	%2227.611879	14.869198	0.04752	0.000115229	
PSMD14	%1271.537111	%1278.964603	14.854984	0	0.000116101	
CA2	%1299.56752	%1306.976361	14.817682	0.12642	0.00011842	
KRT9	%3260.263373	%3267.657525	14.788304	0.22554	0.000120279	
FUCA1	%2440.828859	%2448.182479	14.70724	0.2502	0.000125563	
PSMB2	%1082.781502	%1090.09322	14.623436	0.14844	0.000131272	
PTPRJ	%7428.641639	%7435.939004	14.59473	0.52234	0.000133287	
NME3	%751.595476	%758.834559	14.478166	0.03197	0.000141794	
TSNAX	%1310.491102	%1317.725914	14.469624	0.10217	0.000142438	
TMC5	%5451.492959	%5458.681752	14.377586	0.40722	0.000149572	
Park7	%838.999984	%846.125814	14.25166	0	0.00015992	
PAM	%4585.694746	%4592.744232	14.098972	0.25088	0.000173439	
PRDX1	%896.797172	%903.811605	14.028866	0	0.000180026	
PSCA	%648.787629	%655.716574	13.85789	0.10017	0.000197167	
CTSH	%1641.361794	%1648.26877	13.813952	0.16349	0.000201832	
GALNT7	%2933.766057	%2940.573026	13.613938	0.12161	0.000224512	
IGHG2	%1897.359315	%1904.101373	13.484116	0.31946	0.000240591	
LDHC	%1561.49501	%1568.211932	13.433844	0.18294	0.000247125	
APOA2	%556.953228	%563.612165	13.317874	0	0.000262888	
PSMB1	%1155.260658	%1161.898078	13.27484	0.14304	0.000268992	
PGK2	%1983.400753	%1989.949522	13.097538	0.19735	0.000295684	
PROS1	%3326.245686	%3332.72811	12.964848	0.34295	0.000317394	
DSC2	%4623.245188	%4629.644937	12.799498	0.36577	0.000346712	
CAB39	%1446.943435	%1453.333519	12.780168	0	0.000350313	
PSMA5	%1038.294519	%1044.674358	12.759678	0	0.000354172	
PFN1	%644.294054	%650.669843	12.751578	0	0.000355709	
NBL1	%995.980842	%1002.348075	12.734466	0.1172	0.000358978	
FDPS	%2086.397419	%2092.751669	12.7085	0.1595	0.000363997	
PAICS	%2099.378405	%2105.731435	12.70606	0.13626	0.000364473	
CACYBP	%1004.427365	%1010.746448	12.638166	0.04474	0.000377951	
PSAT1	%1798.98734	%1805.263696	12.552712	0.18357	0.000395632	
MMP7	%1413.073254	%1419.289391	12.432274	0.18248	0.000421978	
LDHA	%1655.368819	%1661.581082	12.424526	0.12266	0.000423732	
GNAI3	%1543.818883	%1550.030294	12.422822	0	0.000424119	
SERPING1	%2615.274365	%2621.459772	12.370814	0.38102	0.000436097	
MPI	%1971.242983	%1977.427316	12.368666	0.22742	0.000436599	
GGH	%1665.530482	%1671.694706	12.328448	0.21706	0.000446107	
GRHPR	%1677.354279	%1683.494115	12.279672	0.27872	0.000457919	
GPR115	%4130.619211	%4136.736206	12.23399	0.38336	0.000469267	
PPP1CC	%1397.753986	%1403.813127	12.118282	0	0.000499299	
YWHAB	%1085.130045	%1091.102099	11.944108	0	0.000548205	
CA6	%1744.749442	%1750.694216	11.889548	0.27803	0.000564498	
smpdl3A	%2309.421175	%2315.24294	11.64353	0.29106	0.000644262	
DPEP3	%2751.278686	%2757.07742	11.597468	0.3796	0.000660417	
ENPP3	%4423.989232	%4429.730095	11.481726	0.34416	0.000702838	
PDCD6	%1147.320129	%1153.059457	11.478656	0.13975	0.000704	
IDS	%2682.745938	%2688.465114	11.438352	0.2961	0.000719436	
SCGB2A1	%556.003185	%561.658884	11.311398	0.19113	0.000770328	
ACRV1	%1556.441662	%1562.057652	11.23198	0.29928	0.000803998	
MINPP1	%2559.317543	%2564.908927	11.182768	0.28469	0.000825605	
CTSZ	%1651.583768	%1657.165562	11.163588	0.22371	0.000834184	
GLO1	%898.418594	%903.98566	11.134132	0.08943	0.000847536	
CD9	%1044.970543	%1050.51831	11.095534	0.09862	0.000865359	
PDGFA	%1304.3759	%1309.897516	11.043232	0.26428	0.000890115	
GOT1	%2037.274633	%2042.753629	10.957992	0.22481	0.000932008	
RAB27A	%1047.254805	%1052.668924	10.828238	0.08918	0.000999637	
FAM3C	%977.768391	%983.091845	10.646908	0	0.001102551	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
FUCA2	%2251.604021	%2256.898404	10.588766	0.267	0.001137769	
PSMA6	%1112.46948	%1117.745183	10.551406	0	0.001160997	
AGR2	%793.354349	%798.603088	10.497478	0.06536	0.001195376	
IDH1	%2147.950536	%2153.191842	10.482612	0.11716	0.001205033	
ALAD	%1834.873909	%1840.078418	10.409018	0.25412	0.001254014	
PPIA	%756.438467	%761.640746	10.404558	0	0.001257046	
PRDX6	%1048.614615	%1053.661386	10.093542	0.11026	0.001487898	
SCPEP1	%2265.051046	%2270.040481	9.97887	0.31568	0.001583468	
PSMA3	%1294.642982	%1299.615329	9.944694	0	0.001613137	
ACR	%2431.652662	%2436.624484	9.943644	0.35518	0.001614057	
ANTXR2	%2363.383468	%2368.352708	9.93848	0.15083	0.001618591	
ESD	%1288.63705	%1293.585293	9.896486	0.16053	0.001655947	
GRN	%3084.354831	%3089.290775	9.871888	0.41368	0.001678232	
SERPINA6	%2120.180139	%2125.051009	9.74174	0.33061	0.001801303	
GLA	%2065.580194	%2070.410667	9.660946	0.12349	0.001882267	
CD14	%1922.493946	%1927.1167	9.245508	0.32675	0.002360738	
HIST2H2BE	%531.300085	%535.902083	9.203996	0	0.002414874	
LSAMP	%1596.895091	%1601.496018	9.201854	0.07208	0.002417701	
PPIC	%1091.391102	%1095.922221	9.062238	0.1758	0.002609424	
GALC	%3332.63959	%3337.145448	9.011716	0.36173	0.002682544	
tmpRSS2	%3228.40526	%3232.895902	8.981284	0.48963	0.002727589	
LRG1	%1929.993283	%1934.470401	8.954236	0.36971	0.002768269	
C1RL	%2663.492731	%2667.968033	8.950604	0.36432	0.002773779	
WFDC2	%658.216619	%662.676509	8.91978	0.19491	0.002820985	
TF	%4068.519467	%4072.978659	8.918384	0.47381	0.002823142	
GSTT1	%142.684524	%147.128981	8.888914	0.19095	0.002869073	
RAB14	%906.933411	%911.375028	8.883234	0	0.002878013	
IMPA1	%1611.090384	%1615.525079	8.86939	0.22028	0.00289992	
GPR64	%4793.743391	%4798.088851	8.69092	0.39847	0.003197992	
RHOA	%812.291507	%816.628632	8.67425	0	0.003227376	
RAB5C	%147.382578	%151.718661	8.672166	0.12146	0.003231069	
s100A11	%495.921887	%500.254138	8.664502	0.14791	0.003244687	
PLA2G7	%2164.329451	%2168.524509	8.390116	0.39457	0.003772668	
PTN	%768.970012	%773.145903	8.351782	0.07086	0.003853093	
TPT1	%764.561777	%768.707768	8.291982	0	0.00398205	
SDCBP	%1416.740288	%1420.850832	8.221088	0.1989	0.004140637	
CD47	%1467.752938	%1471.840572	8.175268	0.15387	0.004246539	
TGFB3	%1780.558376	%1784.590616	8.06448	0.06481	0.004514143	
LIPA	%2211.861194	%2215.89192	8.061452	0.32812	0.004521693	
ACAT2	%2217.305337	%2221.307403	8.004132	0.3668	0.004667073	
GPX3	%1101.762683	%1105.757078	7.98879	0.26517	0.004706786	
SH3BGRL2	%468.250258	%472.239894	7.979272	0	0.004731597	
RAP1B	%777.425012	%781.404519	7.959014	0	0.004784847	
PODXL2	%2868.05013	%2872.014502	7.928744	0.28441	0.004865556	
HDHD2	%1220.987648	%1224.937892	7.900488	0.13288	0.004942146	
ACE2	%4532.548945	%4536.48196	7.86603	0.40473	0.005037212	
KLK2	%1340.486922	%1344.41699	7.860136	0.28497	0.005053659	
ANXA4	%1495.327168	%1499.253151	7.851966	0.16919	0.005076547	
SERPINB5	%1776.881423	%1780.805351	7.847856	0.15774	0.005088101	
RALB	%1037.307329	%1041.199315	7.783972	0.11155	0.005271178	
PIP	%979.495991	%983.335561	7.67914	3.07433	0.005586278	
PGLS	%1263.024114	%1266.854411	7.660594	0.17833	0.005643992	
RALA	%1069.367648	%1073.1845	7.633704	0	0.005728753	
CAPZA1	%1243.16633	%1246.978517	7.624374	0	0.005758465	
SLC15A2	%3496.612677	%3500.419511	7.613668	0.35951	0.005792753	
PRSS8	%1907.32211	%1911.119785	7.59535	0.34331	0.005851903	
Rab18	%1027.342461	%1031.135478	7.586034	0	0.005882221	
ANXA3	%1634.997248	%1638.77202	7.549544	0.23268	0.006002526	
GSS	%2203.725757	%2207.445176	7.438838	0.34029	0.006383109	
ASRGL1	%1617.861892	%1621.559004	7.394224	0.26496	0.006543365	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
DNASE2	%1921.00529	%1924.691172	7.371764	0.38237	0.006625591	
EGF	%6295.309388	%6298.970354	7.321932	0.5505	0.006811815	
VAMP8	%450.203331	%453.858751	7.31084	0	0.006853988	
BASP1	%922.538745	%926.173923	7.270356	0.13284	0.007010191	
CPM	%2171.532818	%2175.116478	7.16732	0.33715	0.007424361	
TSN	%997.593312	%1001.13474	7.082856	0	0.007782487	
ACRBP	%3030.164014	%3033.681147	7.034266	0.34083	0.007996464	
RAC1	%946.828479	%950.340428	7.023898	0	0.008042895	
DCXR	%1306.054571	%1309.467763	6.826384	0.30455	0.008982093	
TNFSF10	%1406.87773	%1410.260214	6.764968	0.28794	0.009296459	
GSTO1	%1164.003832	%1167.385198	6.762732	0.23307	0.009308115	
AZGP1	%1711.806359	%1715.084183	6.555648	0.38054	0.010455176	
PRCP	%2722.396111	%2725.629954	6.467686	0.31612	0.010985348	
BTD	%2766.99864	%2770.226156	6.455032	0.37849	0.011063855	
GLB1L	%3242.096363	%3245.23551	6.278294	0.36555	0.012222571	
GP2	%2925.185421	%2928.286886	6.20293	0.49476	0.012753901	
TMEFF2	%1662.598774	%1665.689224	6.1809	0.09563	0.012913658	
PGCP	%2254.699969	%2257.786355	6.172772	0.26297	0.012973118	
NIF3L1	%1932.957319	%1936.037007	6.159376	0.33603	0.013071731	
LCN1	%1024.776552	%1027.653021	5.752938	0.27201	0.016461104	
UBE2N	%635.714986	%638.53007	5.630168	0	0.017653939	
EXTL2	%1509.119152	%1511.92698	5.615656	0.1895	0.017800717	
GBA	%3379.390001	%3382.197449	5.614896	0.49723	0.017808438	
CPO	%2175.332219	%2178.105603	5.546768	0.548	0.018514844	
VTN	%2593.360815	%2596.132098	5.542566	0.4858	0.01855935	
CST6	%707.610909	%710.344284	5.46675	0.20996	0.019381635	
GNG12	%317.113938	%319.806639	5.385402	0	0.020305909	
SDC1	%1666.731529	%1669.366534	5.27001	0.42291	0.021695888	
SEMG2	%3576.294414	%3578.917989	5.24715	1.97947	0.021982748	
HEBP2	%1011.269253	%1013.830399	5.122292	0.27221	0.023620399	0.040412044
ZPBP	%1823.904243	%1826.404627	5.000768	0.32756	0.025336074	
RNASE4	%749.460522	%751.959274	4.997504	0.14883	0.0253839	
UBE2L3	%717.983819	%720.465286	4.962934	0	0.025896233	
KLK11	%1493.647061	%1496.125181	4.95624	0.313	0.025996675	
CLN5	%2182.563621	%2185.026659	4.926076	0.46147	0.026454323	
RAB2A	%862.788139	%865.240008	4.903738	0	0.026798627	
CRYZ	%1749.678917	%1752.11118	4.864526	0.23976	0.027414328	
LZTFL1	%1304.169995	%1306.551556	4.763122	0.22911	0.029075763	
CTBS	%1987.203943	%1989.541288	4.67469	0.43011	0.030610227	
ADAM7	%4046.704822	%4049.031809	4.653974	0.56659	0.030981743	0.041204437
IGKC	%593.130178	%595.456881	4.653406	5.16933	0.030991995	0.041283677
PSMB8	%1421.589968	%1423.894416	4.608896	0.24991	0.031806504	0.041362916
LTF	%4531.239478	%4533.490946	4.502936	0.65582	0.033836709	0.041442155
PURA	%1247.653373	%1249.853665	4.400584	0.07947	0.035926626	0.041521395
NUTF2	%658.165389	%660.295596	4.260414	0.36541	0.039010413	0.041600634
CD44	%3893.17709	%3895.290112	4.226044	0.5363	0.039808122	0.041679873
PLA1A	%2497.889692	%2499.990494	4.201604	0.5462	0.040385762	0.041759113
TP53I3	%1650.621522	%1652.700096	4.157148	0.40653	0.041459157	0.041838352
GDF15	%1711.834224	%1713.904619	4.14079	0.47085	0.041861629	0.041917591
MLPH	%3876.702314	%3878.720321	4.036014	0.52956	0.044538902	0.04199683
AGA	%1771.442999	%1773.389283	3.892568	0.41355	0.048500211	0.04207607
SERPINA1	%2322.104793	%2324.017137	3.824688	0.50661	0.05050275	
LAMP2	%1922.457045	%1924.36828	3.82247	0.35938	0.050569639	
ASAH1	%2202.595392	%2204.483194	3.775604	0.506	0.052005122	
F11R	%1624.946177	%1626.821702	3.75105	0.3784	0.05277435	
apoa1BP	%1426.146723	%1427.952475	3.611504	0.32216	0.057381204	
SPINT3	%504.098723	%505.897104	3.596762	5.0677	0.057892227	
CREG1	%1114.003438	%1115.800558	3.59424	0.35116	0.057980134	
LGALS3	%1333.99253	%1335.772287	3.559514	0.42517	0.059205071	
DBI	%658.285339	%660.054878	3.539078	0.31735	0.059938771	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HEXB	%2927.650565	%2929.402269	3.503408	0.51347	0.06124268	
ALB	%3213.507293	%3215.243628	3.47267	0.58335	0.062390529	
RAB5B	%1045.734838	%1047.451784	3.433892	0.4411	0.063871414	
PRDX5	%1042.731864	%1044.322528	3.181328	0.39028	0.074484171	
HRSP12	%646.563301	%648.14235	3.158098	0.36106	0.075551159	
ARF6	%713.214315	%714.777207	3.125784	0	0.077062795	
ARHGDIA	%1706.544018	%1708.106052	3.124068	0.45896	0.077143973	
GSTZ1	%1096.515779	%1098.046488	3.061418	0.34996	0.080171677	
CDC42	%983.067696	%984.598286	3.06118	0.15807	0.08018342	
HINT1	%579.714406	%581.231322	3.033832	0	0.081545217	
YWHAQ	%1126.481026	%1127.997158	3.032264	0.20047	0.081624049	
MSMB	%700.234654	%701.718891	2.968474	2.58022	0.084901908	
pla2g2A	%857.447927	%858.906308	2.916762	0.41789	0.087663615	
SOD1	%861.182566	%862.62588	2.886628	0.36832	0.089317686	
PFN2	%781.998427	%783.414083	2.831312	0	0.09244281	
CRISP1	%1437.267103	%1438.673189	2.812172	1.93204	0.093551636	
CPVL	%2495.219974	%2496.618343	2.796738	0.52157	0.094456299	
SERPINI1	%1935.664219	%1937.056419	2.7844	0.43286	0.095186337	
ENPP5	%2240.889671	%2242.261791	2.74424	0.52647	0.097605475	
VAMP2	%492.558883	%493.916502	2.715238	0	0.099394145	
YWHAZ	%991.250673	%992.595586	2.689826	0	0.100990842	
RAB10	%817.552669	%818.897365	2.689392	0	0.101018353	
APCS	%1273.023591	%1274.290524	2.533866	0.4902	0.111426914	
SERPINC1	%2493.569718	%2494.79647	2.453504	0.65959	0.117262842	
ECM1	%2916.621542	%2917.840387	2.43769	0.58786	0.118450543	
GCHFR	%390.359187	%391.537974	2.357574	0.16007	0.124675944	
C9	%3134.700332	%3135.873275	2.345886	0.61075	0.125614124	
PEBP4	%1277.337036	%1278.491862	2.309652	0.5045	0.128572832	
SMPDL3B	%2534.346615	%2535.490609	2.287988	0.66334	0.130378838	
CLIC1	%1147.396568	%1148.532134	2.271132	0.4423	0.131803599	
LTA4H	%2792.12327	%2793.255307	2.264074	0.42071	0.132405333	
OLFM4	%2760.203118	%2761.292779	2.179322	0.62659	0.13987607	
IL1R1	%2815.680885	%2816.726564	2.091358	0.60983	0.148134341	
KLK3	%1481.389771	%1482.424486	2.06943	0.58029	0.150277677	
CST1	%1079.124854	%1080.1142	1.978692	0.53511	0.15952827	
PIGR	%4426.212662	%4427.166718	1.908112	0.7221	0.167173132	
IGLV1%40	%698.712916	%699.660238	1.894644	0.48821	0.168679053	
ORM1	%1197.546372	%1198.484462	1.87618	0.52797	0.170768952	
CTSO	%1609.12673	%1610.042992	1.832524	0.52719	0.175829714	
TGM4	%3675.908439	%3676.802583	1.788288	0.6528	0.181134892	
CRISP3	%1299.925669	%1300.803511	1.755684	0.59727	0.185163767	
PRDX4	%1292.364233	%1293.214299	1.700132	0.38597	0.192270715	
fam3B	%1383.779324	%1384.618531	1.678414	0.53972	0.195135328	
DNAJB9	%1082.174119	%1083.008371	1.668504	0.36999	0.196459031	
LYZ	%797.2946	%798.085704	1.582208	2.13918	0.208442935	
B2M	%642.338172	%643.045781	1.415218	0.50004	0.234192103	
APOH	%1787.278052	%1787.981395	1.406686	0.55922	0.235607316	
TEX101	%1482.534511	%1483.196818	1.324614	1.81301	0.249765658	
SERPINA3	%2836.551271	%2837.168413	1.234284	0.71202	0.266575517	
SPINK2	%513.294197	%513.872503	1.156612	1.70043	0.282169292	
APOD	%1108.904424	%1109.403677	0.998506	1.53417	0.317672282	
SLPI	%797.48011	%797.952716	0.945212	0.55478	0.330941043	
WFDC8	%1415.042432	%1415.511849	0.938834	0.70363	0.332577888	
TIMP1	%1321.085672	%1321.518411	0.865478	1.73279	0.352210239	
GC	%2480.711152	%2481.090304	0.758304	0.75953	0.383859803	
ORM2	%1234.614093	%1234.991903	0.75562	0.6312	0.384702718	
DEFB129	%916.641152	%917.003345	0.724386	0.62726	0.394708979	
NP	%1451.343941	%1451.678617	0.669352	0.65805	0.413277621	
GM2A	%1025.946176	%1026.267792	0.643232	0.6928	0.422542861	
HPX	%2735.908793	%2736.211291	0.604996	0.73841	0.43667815	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
TFPI2	%1255.76238	%1256.063751	0.602742	0.68295	0.437533737	
PTGDS	%978.678386	%978.979534	0.602296	0.5762	0.437703337	
RNASE1	%844.941881	%845.216207	0.548652	0.66153	0.45886901	
LCN2	%1101.003892	%1101.26984	0.531896	0.71649	0.465810831	
SEMG1	%3121.040345	%3121.298722	0.516754	0.82026	0.472229627	
TXN	%464.78076	%465.035155	0.50879	2.13104	0.475663125	
RAB1A	%880.63943	%880.865942	0.453024	0	0.500902392	
FAM12B	%709.486322	%709.702907	0.43317	0.60835	0.510437563	
ANG	%874.590141	%874.780666	0.38105	1.25866	0.537041829	
YWHAE	%1078.339263	%1078.522748	0.36697	0.41464	0.544660528	
PAEP	%996.435726	%996.58901	0.306568	0.77927	0.579793873	
LIPI	%2582.378684	%2582.51458	0.271792	0.85699	0.602132209	
CD59	%865.46164	%865.588799	0.254318	1.3053	0.614050919	
TTR	%787.175461	%787.298398	0.245874	0.72154	0.619995423	
NUCB2	%2055.504991	%2055.585436	0.16089	1.16885	0.688338434	
SPACA3	%1235.568726	%1235.639238	0.141024	0.84027	0.707265133	
FAM12A	%792.085951	%792.152244	0.132586	1.21273	0.71576571	
CAMP	%1003.370838	%1003.436161	0.130646	1.185	0.717763182	
Crisp2	%1476.54311	%1476.607619	0.129018	0.82451	0.719452391	
WFDC9	%483.944056	%483.995926	0.10374	0.81393	0.747386828	
SEPP1	%1952.563577	%1952.613215	0.099276	0.87357	0.752700198	
CAPZB	%2003.309868	%2003.346658	0.07358	1.13846	0.786193886	
ACPP	%2125.016828	%2125.03883	0.044004	1.08378	0.833846171	
CA4	%1906.521626	%1906.540537	0.037822	1.07604	0.845801001	
DCD	%648.975572	%648.987053	0.022962	0.9104	0.879555932	
ACYP1	%473.811858	%473.823333	0.02295	0.90464	0.879587168	
IGJ	%899.493864	%899.501269	0.01481	1.08753	0.903139509	
CD38	%1612.214876	%1612.220481	0.01121	1.05262	0.915679715	
PPAP2A	%1293.66516	%1293.665906	0.001492	1.03373	0.969188241	
CAPZA2	%1226.420687	%1224.291327	%4.25872	0	#NUM!	
GLB1	%3896.641906	%3850.385012	%92.513788	0.69241	#NUM!	

Human-Chimp Ancestor

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
LAMA5	%19256.17848	%19292.63439	72.911824	0.10469	1.35574E%17	
VWF	%13693.88988	%13711.42154	35.06333	0.15761	3.19155E%09	
GAS6	%3529.164634	%3544.031039	29.73281	0	4.95884E%08	
MUC5B	%33208.51091	%33222.91366	28.805496	0.45922	8.00237E%08	
TMEM8	%4067.123307	%4081.344078	28.441542	0.09848	9.65707E%08	
CPAMD8	%10032.87251	%10044.44604	23.147066	0.13651	1.50072E%06	
IGFBP2	%1366.09521	%1377.027599	21.864778	0	2.92555E%06	
PTPRF	%9058.851942	%9068.560918	19.417952	0	1.05015E%05	
FASN	%13845.64132	%13855.15603	19.029438	0.10308	1.28717E%05	
CACNA2D1	%4979.534557	%4988.990477	18.91184	0	1.369E%05	
UGCGL1	%7215.932274	%7225.2085	18.552452	0.08978	1.65292E%05	
PTPRS	%9651.819275	%9660.777409	17.916268	0	2.30839E%05	
VPS28	%1273.4649	%1281.66187	16.39394	0	5.14495E%05	
FN1	%12061.255	%12069.35077	16.191558	0	5.72487E%05	
RELN	%16739.81486	%16747.50601	15.382312	0.04457	8.78064E%05	
IQGAP1	%7509.739585	%7517.253441	15.027712	0	0.000105944	
MYH9	%8819.319895	%8826.068337	13.496884	0	0.00023896	
ODZ2	%12811.43248	%12818.06794	13.270922	0.04562	0.000269555	
COLEC12	%3645.775504	%3652.233152	12.915296	0	0.000325908	
CAPN1	%3437.487601	%3443.923562	12.871922	0	0.000333549	
RALA	%1067.909669	%1074.297858	12.776378	0	0.000351024	
STXBP2	%3027.990838	%3034.118944	12.256212	0	0.000463712	
AHCY	%2342.474062	%2348.495995	12.043866	0	0.000519631	
HSPG2	%32097.46817	%32103.47768	12.019032	0.06378	0.0005266	
LGALS3BP	%3224.333221	%3230.311621	11.9568	0	0.000544483	
MARCKS	%1424.42689	%1430.220319	11.586858	0.05623	0.000664195	
ACE2	%4530.105536	%4535.859135	11.507198	0.11386	0.000693272	
CLSTN1	%4929.803195	%4935.116822	10.627254	0	0.001114331	
OS9	%3131.879792	%3137.168099	10.576614	0.05902	0.001145272	
PTPRJ	%7427.596482	%7432.830364	10.467764	0.10621	0.001214757	
PLXNB2	%9382.816778	%9388.027939	10.422322	0.09853	0.001245013	
TPP2	%6055.714794	%6060.843984	10.25838	0	0.001360651	
COL6A1	%5764.612268	%5769.734364	10.244192	0	0.001371156	
AGRN	%10949.16136	%10954.22064	10.118562	0.07366	0.001467835	
MYO1C	%5453.614797	%5458.608445	9.987296	0	0.001576239	
TKT	%3006.162211	%3011.13953	9.954638	0.05555	0.001604447	
CNDP2	%2404.390353	%2409.302568	9.82443	0	0.001722091	
RAD23B	%1918.469802	%1923.370346	9.801088	0	0.001744087	
MME	%3523.852642	%3528.703532	9.70178	0	0.001840896	
IGF2R	%12689.88722	%12694.70717	9.639898	0.13611	0.001903958	
PDCD6IP	%3899.292949	%3904.055611	9.525324	0	0.002026558	
MAMDC2	%3252.960252	%3257.645249	9.369994	0	0.002205662	
HSPA5	%2990.375428	%2994.923596	9.096336	0	0.002561221	
PIGR	%4426.853373	%4431.357389	9.008032	0.10113	0.002687957	
IGHG2	%1896.46334	%1900.888137	8.849594	0.10739	0.002931541	
PDCD6	%1147.138211	%1151.551923	8.827424	0.09284	0.00296737	
GUSB	%3811.686282	%3816.085688	8.798812	0.12994	0.003014268	
LAMB2	%9312.952016	%9317.262381	8.62073	0	0.003323586	
C19orf10	%834.950992	%839.246952	8.59192	0	0.003376578	
GNMT	%1450.922295	%1455.217898	8.591206	0	0.003377902	0.003930818
RDX	%2859.704453	%2863.964994	8.521082	0	0.003510557	0.004009434
MPST	%1727.529681	%1731.78192	8.504478	0	0.003542735	0.00408805
IGHG4	%1801.245247	%1805.449927	8.40936	0	0.00373294	0.004166667
SYT7	%2154.3358	%2158.434979	8.198358	0	0.004192832	0.004245283
APP	%3790.04228	%3794.081342	8.078124	0	0.00448028	0.004323899
RNASET2	%1451.403608	%1455.434795	8.062374	0	0.004519393	0.004402516
SELENBP1	%2612.92413	%2616.923353	7.998446	0	0.004681751	0.004481132
COMP	%3817.620237	%3821.603025	7.965576	0.0403	0.004767532	0.004559748
MMP14	%2639.09061	%2643.023612	7.866004	0	0.005037285	0.004638365
SPON2	%1579.824359	%1583.748794	7.84887	0.08878	0.005085248	0.004716981

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
SMS	%1888.861282	%1892.718797	7.71503	0	0.005476295	
SERPING1	%2614.905821	%2618.66354	7.515438	0.20787	0.006117241	
GALC	%3333.966307	%3337.67488	7.417146	0.1942	0.006460521	
IGFBP5	%1174.942619	%1178.629129	7.37302	0	0.006620965	
SEMA3F	%3869.837714	%3873.48692	7.298412	0.07086	0.006901558	
CLTC	%7273.879192	%7277.512657	7.26693	0	0.007023575	
Park7	%839.930038	%843.475198	7.09032	0	0.007750141	
IL1R1	%2816.277683	%2819.702281	6.849196	0	0.008868117	
CTSZ	%1650.256939	%1653.534993	6.556108	0	0.010452473	
PSMA3	%1295.372046	%1298.53235	6.320608	0	0.01193427	0.005503145
RTN4RL1	%2264.951454	%2268.103926	6.304944	0	0.012040172	
IGLV1%40	%696.446117	%699.575871	6.259508	0	0.01235285	
PFKP	%4127.072102	%4130.167393	6.190582	0	0.012843194	
A1BG	%2640.727365	%2643.821332	6.187934	0.09199	0.012862426	
CLN5	%2181.090912	%2184.132648	6.083472	0.08857	0.013645233	
ANXA6	%3525.929542	%3528.947993	6.036902	0	0.014009848	
CANT1	%2222.274864	%2225.279581	6.009434	0	0.014229591	
NAGLU	%3597.275018	%3600.263944	5.977852	0.09797	0.014486635	
LIFR	%5259.167251	%5262.118153	5.901804	0.08192	0.015125385	
NAGA	%2038.542296	%2041.4354	5.786208	0	0.016152394	
CRISP1	%1446.424316	%1449.312652	5.776672	0	0.016240263	
CRISP3	%1299.228031	%1302.011382	5.566702	0	0.018305207	
APLP2	%3675.659784	%3678.442848	5.566128	0.10057	0.018311209	
TF	%4066.706652	%4069.482128	5.550952	0	0.018470638	
IL1RAP	%3278.299717	%3280.974411	5.349388	0	0.020729546	
COL6A2	%6173.311453	%6175.96225	5.301594	0.06602	0.021305918	
FOLH1	%3749.428439	%3752.079194	5.30151	0	0.021306946	
ACLY	%5465.605232	%5468.254739	5.299014	0	0.0213375	
SDK2	%10118.59675	%10121.24506	5.296632	0	0.0213667	
MUC6	%13541.46339	%13544.08158	5.236388	0.33711	0.022119152	
CNTNAP2	%7123.412581	%7126.020917	5.216672	0	0.022371325	
ARHGDIA	%1706.802795	%1709.380058	5.154526	0	0.023185863	
NPEPPS	%4005.586877	%4008.163854	5.153954	0	0.023193502	
IDI1	%1550.608367	%1553.152647	5.08856	0	0.024084182	
ITIH5	%5266.277262	%5268.813971	5.073418	0	0.024295433	
PLOD2	%3514.224213	%3516.760805	5.073184	0	0.024298712	
SPOCK3	%2096.600337	%2099.106399	5.012124	0.09279	0.025170407	
LRG1	%1929.50343	%1932.000016	4.993172	0	0.02544752	
Hyou1	%4706.330928	%4708.817013	4.97217	0	0.025758311	
PHGDH	%2552.399162	%2554.864025	4.929726	0	0.026398503	
MATN2	%4672.857677	%4675.304336	4.893318	0	0.026960824	
PSMB4	%1249.601254	%1252.029368	4.856228	0	0.027546498	
LAMC1	%7895.480621	%7897.904225	4.847208	0.10071	0.02769092	
ASRGL1	%1617.79512	%1620.179243	4.768246	0.21942	0.028989346	
BGN	%1722.22351	%1724.605557	4.764094	0.05468	0.02905935	
VCL	%5089.578741	%5091.915359	4.673236	0	0.03063615	
PRDX5	%1041.741478	%1044.065603	4.64825	0	0.031085223	
CCT3	%2974.937272	%2977.250395	4.626246	0	0.031486384	
GAPDHS	%2135.932468	%2138.238826	4.612716	0	0.031735732	
PSMD2	%4158.01821	%4160.308396	4.580372	0	0.032340193	
TIMP1	%1320.279734	%1322.535379	4.51129	0.17417	0.033671836	
LPL	%2388.894196	%2391.130407	4.472422	0	0.034446131	
KRT8	%2764.659294	%2766.891104	4.46362	0	0.034624047	
FLNB	%12658.57803	%12660.80602	4.45599	0	0.034779051	
GDI2	%2125.17648	%2127.401543	4.450126	0	0.034898672	
PDIA3	%2417.876392	%2419.982632	4.21248	0	0.040127629	
ACTN4	%4157.530048	%4159.60506	4.150024	0	0.041633934	
IL6ST	%4250.071862	%4252.116709	4.089694	0.21824	0.043145453	
ACRV1	%1555.995481	%1558.010271	4.02958	0	0.04470907	
ADAMTS1	%4874.945131	%4876.934039	3.977816	0.11858	0.046103304	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
ALDH9A1	%2588.398715	%2590.370731	3.944032	0	0.047037909	
tmpRSS2	%3227.818217	%3229.780552	3.92467	0.23061	0.047582528	
CST6	%707.821493	%709.775838	3.90869	0.0873	0.048037028	0.009669811
IDE	%4641.35838	%4643.215276	3.713792	0.09855	0.05396466	
LAMP2	%1921.485432	%1923.340816	3.710768	0	0.05406251	
CPD	%6384.521913	%6386.36602	3.688214	0.3989	0.054798264	
FCGBP	%26832.87002	%26834.69049	3.640948	0.12618	0.056374826	
col12A1	%14645.49955	%14647.31011	3.62112	0.24608	0.057050454	
PSMA4	%1161.93353	%1163.732018	3.596976	0	0.057884775	
SEMG1	%3119.424292	%3121.210909	3.573234	0	0.058717852	
SORL1	%10869.68836	%10871.45406	3.531396	0	0.060217068	
BCAN	%4543.78791	%4545.549821	3.523822	0.13629	0.060492798	
NPC2	%720.36199	%722.116198	3.508416	0	0.061057806	
PACSIN2	%2693.862203	%2695.603262	3.482118	0	0.062035293	
ACE	%6850.210931	%6851.94675	3.471638	0.12588	0.062429462	
SLC44A4	%3576.595682	%3578.329801	3.468238	0	0.062557914	
NEO1	%6916.295875	%6918.018463	3.445176	0	0.063436665	
KAL1	%3350.267245	%3351.954896	3.375302	0	0.06618045	
ACYP1	%476.59874	%478.263023	3.328566	0	0.068086213	
SEMA7A	%3323.085916	%3324.724278	3.276724	0.13791	0.070269061	
WFDC2	%657.611632	%659.220523	3.217782	0	0.072842268	
QPCT	%1826.88769	%1828.48055	3.18572	0	0.074284265	
AKR7A2	%1999.650223	%2001.188893	3.07734	0	0.07939027	
SLIT2	%7468.426051	%7469.957555	3.063008	0	0.080093273	
KIF5B	%4448.476614	%4449.976394	2.99956	0.12672	0.083287133	
GGT1	%3049.625657	%3051.107944	2.964574	0	0.085106872	
PGLS	%1263.301212	%1264.777951	2.953478	0	0.085692955	
TGFB1	%1740.414593	%1741.883033	2.93688	0	0.086577816	
UBE2N	%635.71498	%637.134912	2.839864	0	0.091951996	
GSTM3	%1077.116212	%1078.529478	2.826532	0	0.092718382	
PRCP	%2721.790022	%2723.197078	2.814112	0	0.093438591	
MMP2	%3195.022142	%3196.426069	2.807854	0	0.093803782	
AKR1B1	%1486.495971	%1487.882241	2.77254	0	0.095893886	
BASP1	%922.204072	%923.586001	2.763858	0	0.096415471	
GSR	%2856.982718	%2858.357791	2.750146	0.25026	0.097245548	
ST14	%4410.300792	%4411.672975	2.744366	0.10257	0.097597781	
CTSH	%1640.949573	%1642.316295	2.733444	0	0.098267171	
GSTT1	%1142.310169	%1143.676439	2.73254	0	0.0983228	
ARSA	%2672.865474	%2674.223563	2.716178	0	0.099335614	
NUTF2	%660.814897	%662.171583	2.713372	0	0.099510447	
CTSF	%2577.666955	%2579.023437	2.712964	999	0.099535897	
TSNAX	%1310.240245	%1311.584239	2.687988	0	0.10110741	
SERPINC1	%2500.34045	%2501.679883	2.678866	0	0.101688117	
AZGP1	%1711.075834	%1712.411972	2.672276	0	0.102109905	
CST1	%1079.245796	%1080.580698	2.669804	0.43618	0.102268617	
LDLR	%4412.512411	%4413.842479	2.660136	0.02641	0.102891937	
PSAT1	%1798.829149	%1800.156045	2.653792	0	0.103303208	
TPI1	%1185.621564	%1186.93906	2.634992	0	0.104532588	
RALB	%1037.152768	%1038.46822	2.630904	0	0.104802028	
GLG1	%5645.371184	%5646.685648	2.628928	0.15445	0.104932539	
PAICS	%2099.761346	%2101.073464	2.624236	0	0.105243151	
PGK1	%1900.315887	%1901.62598	2.620186	0	0.105512072	
CALR	%1871.922313	%1873.227096	2.609566	0	0.106220829	
CD63	%1057.485993	%1058.781258	2.59053	0	0.107504357	
ACTR1A	%1747.712288	%1748.998953	2.57333	0	0.108678741	
RPLP0	%1380.870132	%1382.15231	2.564356	0	0.109297058	
PLOD3	%3733.269698	%3734.549263	2.55913	0	0.109658915	
LAMP1	%2236.192159	%2237.471149	2.55798	0.1323	0.109738719	
CD38	%1611.193737	%1612.472364	2.557254	0	0.109789133	
ESD	%1288.464477	%1289.738427	2.5479	0	0.110440962	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
ANXA3	%1634.561652	%1635.835236	2.547168	0	0.110492151	
THBS4	%4698.893331	%4700.162459	2.538256	0	0.11111746	
LCN2	%1102.104648	%1103.36634	2.523384	0.14859	0.112169641	
CRYZ	%1749.600388	%1750.86184	2.522904	0.15344	0.112203782	
CAT	%2660.256507	%2661.516887	2.52076	0	0.112356422	
RAB27B	%1001.532046	%1002.787343	2.510594	0	0.1130833	
EDIL3	%2208.73594	%2209.990356	2.508832	0	0.113209811	
GPRC5C	%2503.105879	%2504.359081	2.506404	0.13165	0.113384395	
EPHA5	%4894.925306	%4896.178316	2.50602	0	0.113412034	
PRDX4	%1291.776493	%1293.026777	2.500568	0	0.113805246	
RAB3B	%1024.293615	%1025.53977	2.49231	0	0.114403699	
CTSO	%1608.575057	%1609.817791	2.485468	0	0.114902165	
FAM12B	%708.757465	%709.995931	2.476932	0.15139	0.115527408	
LYZ	%798.978568	%800.214238	2.47134	0	0.115939045	
OLFM4	%2762.146482	%2763.381515	2.470066	0	0.116033052	
GC	%2486.539387	%2487.772993	2.467212	0	0.116243952	
TCP1	%2481.624845	%2482.855968	2.462246	0	0.116611932	
RAB2A	%862.788137	%864.011743	2.447212	0	0.117733815	
ELSPBP1	%1097.67184	%1098.895127	2.446574	0	0.117781687	
NCSTN	%3555.132505	%3556.35341	2.44181	0	0.118139837	
NUCB1	%2215.713437	%2216.932445	2.438016	0	0.118425926	
CAP1	%2295.292557	%2296.507342	2.42957	0	0.119065555	
PGD	%2494.848751	%2496.060905	2.424308	0.08016	0.119465987	
SERPINB5	%1776.547565	%1777.752012	2.408894	0	0.120647578	
IDUA	%3709.44406	%3710.644514	2.400908	0	0.121264846	
EFEMP1	%2220.51491	%2221.712698	2.395576	0	0.121678925	
MGAM	%9728.76529	%9729.961645	2.39271	0.13846	0.121902143	
VCP	%3670.858446	%3672.048871	2.38085	0	0.122830697	
FH	%2428.204158	%2429.387643	2.36697	0	0.123927381	
ANPEP	%5015.219147	%5016.392552	2.34681	0	0.125539671	
MAN2B1	%5063.306975	%5064.471965	2.32998	0.15189	0.126903508	
SERPINI1	%1936.279904	%1937.437313	2.314818	0	0.128146299	
SLC15A2	%3496.355791	%3497.512796	2.31401	0	0.128212908	
B4GALT4	%1759.995773	%1761.152079	2.312612	0	0.128328245	
PGM2	%3783.1652	%3784.306744	2.283088	0	0.130791233	
MMP7	%1413.308283	%1414.446955	2.277344	0	0.131276515	
CDH1	%4611.883592	%4612.991561	2.215938	0	0.13659202	
GSN	%3874.793906	%3875.893381	2.19895	0.14478	0.138104781	
PGK2	%1983.397672	%1984.49625	2.197156	0.16909	0.138265628	
XPNPEP1	%2971.843495	%2972.926107	2.165224	0	0.141164051	
C3	%8542.539718	%8543.619902	2.160368	0.49289	0.141610772	
PODXL2	%2867.637937	%2868.697841	2.119808	0	0.145404771	
CFB	%3283.42557	%3284.480446	2.109752	0	0.146363036	
CAB39	%1447.371362	%1448.423887	2.10505	0	0.146813544	
GOT1	%2039.284891	%2040.317758	2.065734	0	0.150642382	
LZTFL1	%1303.887679	%1304.910457	2.045556	0	0.152651204	
CAB39L	%1526.411324	%1527.433062	2.043476	0	0.152859997	
SMOC2	%2173.077797	%2174.08254	2.009486	0	0.156318271	
PLA1A	%2496.836955	%2497.829786	1.985662	999	0.158795195	
LNPEP	%4994.37335	%4995.343144	1.939588	0.29216	0.163713275	
KRT5	%2977.786034	%2978.747847	1.923626	0	0.165457483	
PSMB2	%1082.796046	%1083.727957	1.863822	0.19815	0.172184334	
OLFM1	%2197.743797	%2198.675659	1.863724	0	0.172195612	
ACR	%2431.200569	%2432.123266	1.845394	0	0.174320051	
LIPI	%2582.76353	%2583.676329	1.825598	0.30627	0.176648374	
EEF2	%4122.236937	%4123.143302	1.81273	0	0.178181087	
ALDOA	%2009.92435	%2010.823621	1.798542	0	0.17988886	
CNTN3	%5074.713772	%5075.591938	1.756332	0.19719	0.185082688	
GPI	%2905.490184	%2906.36819	1.756012	0	0.185122722	
GLB1L	%3242.378839	%3243.241854	1.72603	0.39126	0.188918698	

Gene	lnL	lnL	2ΔlnL	branch_w	PQvalue	k
NRCAM	%6122.164495	%6123.017157	1.705324	0.20437	0.191593183	
IGKC	%593.324843	%594.13482	1.619954	999	0.203098202	
SMPDL3B	%2535.378719	%2536.187574	1.61771	999	0.203411391	
ADAM7	%4046.559201	%4047.3639	1.609398	0.21878	0.204576445	
PTPRD	%9072.19296	%9072.990174	1.594428	0.20569	0.206694635	
ENPP3	%4424.179619	%4424.972222	1.585206	0.2833	0.208012402	
PRKCSH	%2724.258118	%2725.045973	1.57571	0	0.209379717	
NELL1	%4125.825805	%4126.596536	1.541462	0	0.214400321	
PITPNA	%1218.717442	%1219.47675	1.518616	999	0.217829054	
GPR64	%4792.170206	%4792.92712	1.513828	999	0.218555895	
SCGB2A1	%558.685091	%559.429216	1.48825	999	0.222488181	
CA4	%1907.18753	%1907.918109	1.461158	999	0.226745961	
FUCA2	%2251.5669	%2252.284463	1.435126	0	0.230929691	
PFAS	%6779.459865	%6780.171022	1.422314	0.22795	0.233022905	
GAPDH	%1562.680765	%1563.389082	1.416634	0	0.233958226	
FBLN2	%5916.646339	%5917.333575	1.374472	0.26562	0.241045016	
PRDX2	%981.041287	%981.72229	1.362006	0	0.243190127	
ALDH7A1	%2684.568883	%2685.217291	1.296816	999	0.254795638	
KRT9	%3261.943573	%3262.580324	1.273502	0.3908	0.259110734	
SERPINA4	%2416.613893	%2417.245609	1.263432	0	0.261002458	
COL18A1	%9613.797347	%9614.422421	1.250148	0	0.263524212	
THBS2	%5839.411372	%5840.0343	1.245856	0.15723	0.264345437	
KRT10	%3012.10215	%3012.724823	1.245346	999	0.264443231	
ENPP5	%2241.09733	%2241.718433	1.242206	999	0.265046327	
ACRBP	%3029.077023	%3029.684719	1.215392	999	0.270266873	
GP2	%2924.262574	%2924.855279	1.18541	56.24386	0.276257373	
TGM4	%3677.98079	%3678.570314	1.179048	0.31577	0.277549889	
GCHFR	%387.896641	%388.457092	1.120902	999	0.289724313	
ORM1	%1196.94662	%1197.485366	1.077492	999	0.299259291	
VTN	%2592.376593	%2592.901057	1.048928	999	0.305754107	
GPR56	%3512.55374	%3513.046743	0.986006	0.17136	0.320720506	
MAN2A1	%5435.474974	%5435.956537	0.963126	999	0.326400539	
ANXA11	%4324.365858	%4324.846607	0.961498	0.28007	0.326809746	
LIPA	%2212.100068	%2212.57858	0.957024	999	0.32793782	
CA6	%1744.777837	%1745.251299	0.946924	0.34953	0.330503504	
QSCN6	%3085.729787	%3086.197023	0.934472	0.46604	0.333703568	
pla2g2A	%856.507006	%856.961881	0.90975	999	0.34018076	
PIP	%979.689926	%980.13287	0.885888	999	0.346594059	
FAM12A	%791.898595	%792.338426	0.879662	999	0.348294272	
MAN2B2	%5888.151313	%5888.589663	0.8767	999	0.349107119	
SERPINA1	%2322.147057	%2322.577506	0.860898	0.37918	0.353487515	
GLB1	%3849.07793	%3849.498168	0.840476	0.39171	0.35926067	
TMC5	%5451.439916	%5451.858072	0.836312	0.25914	0.360453675	
RAB3D	%1031.428502	%1031.845793	0.834582	0.24662	0.360950933	
DNASE1	%1529.837432	%1530.254673	0.834482	0.20654	0.360979706	
PYGB	%4728.15381	%4728.563266	0.818912	0	0.365498464	
SPINT1	%2728.829852	%2729.23476	0.809816	999	0.368174656	
C9	%3134.536571	%3134.934583	0.796024	999	0.372284793	
NP	%1452.456959	%1452.847501	0.781084	0.40354	0.376809819	
HDHD2	%1220.371109	%1220.759465	0.776712	999	0.378148617	
PSMB6	%1146.836587	%1147.206774	0.740374	999	0.389541099	
CPVL	%2494.59596	%2494.964994	0.738068	999	0.39028047	
CCT7	%2532.343094	%2532.700599	0.71501	447.3655	0.397785614	
LTA4H	%2792.385186	%2792.734546	0.69872	999	0.403214127	
CD59	%866.31271	%866.661197	0.696974	160.38533	0.403802346	
LGMN	%2360.014474	%2360.360298	0.691648	0	0.4056044	
PRSS8	%1907.473619	%1907.817966	0.688694	0.2816	0.406608955	
DSC3	%4388.360518	%4388.703183	0.68533	266.84737	0.407757378	
APCS	%1272.944708	%1273.277889	0.666362	999	0.414322862	
MANBA	%4389.587117	%4389.919816	0.665398	999	0.41466069	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
APEH	%3359.667328	%3359.993799	0.652942	999	0.419062798	
GBA	%3379.470906	%3379.79305	0.644288	0.29097	0.422162302	
DSC2	%4622.533379	%4622.854993	0.643228	999	0.422544303	
PAM	%4584.948636	%4585.269277	0.641282	999	0.423246947	
SLPI	%796.958689	%797.278678	0.639978	999	0.423718764	
CD109	%7431.891638	%7432.210899	0.638522	999	0.42424651	
ECM1	%2916.140407	%2916.458898	0.636982	999	0.424805776	
ATRN	%7591.408792	%7591.718313	0.619042	0	0.431403508	
HEXA	%2618.656636	%2618.964586	0.6159	999	0.432574965	
MLPH	%3876.644172	%3876.950615	0.612886	0.31947	0.433703245	
C1RL	%2663.957866	%2664.264307	0.612882	0.29956	0.433704745	
IL1RL1	%3848.051053	%3848.354705	0.607304	0.31704	0.435804711	
GSTZ1	%1095.787645	%1096.089841	0.604392	999	0.436907169	
INHBB	%1720.262388	%1720.564043	0.60331	0.33489	0.437317891	
LDHC	%1560.414706	%1560.716332	0.603252	999	0.437339924	
AGA	%1770.967353	%1771.264131	0.593556	999	0.441047321	
P4HB	%2492.300597	%2492.593917	0.58664	0.31836	0.443721359	
IMPA1	%1611.69328	%1611.976767	0.566974	0.32652	0.45146388	
CAMP	%1003.125283	%1003.405851	0.561136	102.14965	0.453802893	
PKM2	%2962.549287	%2962.827896	0.557218	999	0.455383329	
CAPG	%1645.337841	%1645.615118	0.554554	999	0.456462879	
HPX	%2735.561159	%2735.837436	0.552554	999	0.457276005	
SDCBP	%1416.692685	%1416.962776	0.540182	0	0.46235731	
CPO	%2175.893828	%2176.158655	0.529654	49.79925	0.466752361	
HSPA1L	%3827.489501	%3827.747452	0.515902	0.33897	0.472595027	
GAA	%4985.206957	%4985.445796	0.477678	93.92694	0.489475974	
RNASE1	%845.280079	%845.516691	0.473224	999	0.491507705	
ASAH1	%2202.922587	%2203.159157	0.47314	0.36513	0.491546157	
THBS1	%5463.67023	%5463.903047	0.465634	0.34486	0.49500262	
GSTP1	%1060.661199	%1060.891665	0.460932	999	0.497188724	
SI	%9016.447845	%9016.672809	0.449928	999	0.502369148	
SERPINA5	%2277.04277	%2277.264663	0.443786	999	0.505300752	
CAPZA1	%1243.269489	%1243.491199	0.44342	0.38032	0.505476369	
PSCA	%647.769896	%647.988802	0.437812	999	0.508180405	
ABP1	%4017.059036	%4017.277511	0.43695	60.08438	0.508598246	
SERPINA3	%2836.26575	%2836.482422	0.433344	999	0.510352644	
SIL1	%2462.173677	%2462.386769	0.426184	0.35716	0.513867367	
A4GALT	%1745.775972	%1745.98893	0.425916	0.33962	0.51399974	
PGC	%1949.132672	%1949.345247	0.42515	999	0.514378417	
SMPD1	%3206.696835	%3206.905646	0.417622	0.38015	0.518126011	
SEMA3C	%3591.320561	%3591.523283	0.405444	0.39148	0.524291056	
ALDH1A1	%2397.104265	%2397.306329	0.404128	0.39785	0.524965049	
smpdl3A	%2309.135537	%2309.337523	0.403972	999	0.525045047	
LMAN2	%1579.270323	%1579.471598	0.40255	999	0.525775261	
CP	%5168.584731	%5168.784919	0.400376	0.45566	0.526895139	
PROS1	%3326.091314	%3326.286991	0.391354	0	0.531588539	
CA2	%1301.174783	%1301.366215	0.382864	0.40896	0.536074444	
AMBP	%1760.925118	%1761.113711	0.377186	999	0.539113102	
ALCAM	%2704.692536	%2704.87479	0.364508	0.40211	0.546013205	
IDS	%2682.717966	%2682.899443	0.362954	0.4184	0.546870219	
PAEP	%996.504663	%996.683989	0.358652	999	0.549255835	
LCN1	%1024.690328	%1024.861486	0.342316	0	0.558495424	
PGCP	%2255.016723	%2255.187678	0.34191	0.43143	0.558728803	
TFPI2	%1255.75874	%1255.916446	0.315412	999	0.574377999	
ALAD	%1834.79394	%1834.949982	0.312084	0.44091	0.576404166	
MINPP1	%2559.303456	%2559.449171	0.29143	0.4494	0.589305607	
RAP1B	%777.425012	%777.570218	0.290412	0	0.589956632	
ACAT2	%2218.005094	%2218.136666	0.263144	0.62976	0.607968366	
KLK3	%1481.862749	%1481.993323	0.261148	999	0.609332558	
PPIC	%1091.346977	%1091.474512	0.25507	0.47533	0.613527544	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
TFRC	%4084.995548	%4085.113705	0.236314	0.63032	0.626881106	
IQGAP2	%7135.084129	%7135.200681	0.233104	0.48608	0.62923175	
ALB	%3215.528098	%3215.639869	0.223542	0.51578	0.636354244	
SCPEP1	%2264.734038	%2264.845662	0.223248	999	0.636576172	
SEPP1	%1952.749745	%1952.848872	0.198254	0.65939	0.656133873	
DAG1	%4330.358608	%4330.457306	0.197396	0	0.656830981	
PRSS22	%1602.919319	%1603.017621	0.196604	999	0.657476077	
SDCBP2	%1528.713795	%1528.799808	0.172026	0.56487	0.678317479	
SOD3	%1098.067853	%1098.148685	0.161664	999	0.687629111	
MSLN	%3967.359483	%3967.439092	0.159218	1.69196	0.689877508	
RRBP1	%4917.494466	%4917.558546	0.12816	0.48105	0.720347494	
CPZ	%2996.715406	%2996.772051	0.11329	999	0.736429163	
CTSB	%1794.322156	%1794.37839	0.112468	0	0.73735166	
KLK2	%1340.72218	%1340.772358	0.100356	0.7796	0.751402838	
ORM2	%1235.103354	%1235.147629	0.08855	999	0.766028687	
LTF	%4531.839651	%4531.883721	0.08814	0.80017	0.766555213	
PDGFA	%1304.206728	%1304.250436	0.087416	0.65386	0.767488244	
SORD	%1998.854795	%1998.894093	0.078596	0.69069	0.779209161	
apoa1BP	%1425.848814	%1425.877662	0.057696	0.73232	0.810175278	
EGF	%6295.420664	%6295.441522	0.041716	0.77317	0.838162086	
GRN	%3084.144342	%3084.161979	0.035274	0.81968	0.851022666	
BPIL1	%2383.221897	%2383.238085	0.032376	0.78334	0.857204916	
ADAMTSL1	%8528.143628	%8528.159175	0.031094	1.25981	0.860030839	
PROM2	%4693.669948	%4693.684882	0.029868	0.81092	0.862790079	
BTD	%2766.995321	%2767.006368	0.022094	8.63107	0.881837309	
LIPG	%2620.796882	%2620.803914	0.014064	1.17771	0.905598812	
DPEP3	%2750.773207	%2750.778992	0.01157	1.13299	0.914341607	
PSMB1	%1153.727936	%1153.73027	0.004668	0.91746	0.945528704	
PSME4	%8502.627973	%8502.62918	0.002414	0	0.960813724	
ANXA7	%2298.693432	%2298.694569	0.002274	0	0.961966112	
PRKACA	%1827.255881	%1827.256983	0.002204	0	0.962555645	
GNB2	%1551.137894	%1551.138818	0.001848	0	0.965710804	
CTSD	%2194.772475	%2194.773354	0.001758	0	0.966555688	
ANXA1	%1595.336485	%1595.337348	0.001726	0	0.966861295	
FUT3	%2254.144903	%2254.145729	0.001652	0	0.967579066	
Crisp2	%1477.306745	%1477.307481	0.001472	0	0.969395349	
PPAP2A	%1295.91088	%1295.911606	0.001452	0	0.969603871	
PSAP	%2462.100575	%2462.101259	0.001368	0	0.970495783	
PSMA5	%1038.294519	%1038.295195	0.001352	0	0.970668751	
SYT1	%1899.670326	%1899.670971	0.00129	0	0.971348883	
ACO1	%4249.264113	%4249.264731	0.001236	0	0.971954716	
TALDO1	%1588.910208	%1588.910824	0.001232	0	0.972000115	
FBP1	%1664.970149	%1664.970756	0.001214	0	0.972205329	
TOLLIP	%1331.187369	%1331.187895	0.001052	0	0.97412551	
LEFTY2	%2008.760859	%2008.761367	0.001016	0	0.974571931	
CCT5	%2476.099957	%2476.100464	0.001014	0	0.974596963	
SORT1	%3974.158216	%3974.158716	0.001	0	0.974772879	
PURA	%1247.663078	%1247.663578	0.001	0	0.974772879	
KLK11	%1493.698427	%1493.6989	0.000946	0	0.975463243	
HEXB	%2927.742158	%2927.742629	0.000942	0	0.975515156	
TEX101	%1484.678719	%1484.679157	0.000876	0	0.976388221	
DCXR	%1306.331847	%1306.332284	0.000874	0	0.976415183	
RAB5B	%1050.845993	%1050.846392	0.000798	0	0.977463641	
STEAP2	%2249.393267	%2249.393657	0.00078	0	0.977719193	
CCT4	%2398.591777	%2398.592153	0.000752	0	0.978122658	
DDB1	%5175.568482	%5175.568823	0.000682	0	0.979165509	
APOB	%23797.97222	%23797.97255	0.00065	0.98356	0.979660059	
GGH	%1666.89622	%1666.896524	0.000608	0	0.98032803	
ANXA2	%1663.301326	%1663.301627	0.000602	0	0.980425317	
HSPA4	%3746.765222	%3746.765518	0.000592	0	0.980588546	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
TMEFF2	%1662.603594	%1662.603872	0.000556	0	0.981187903	
GRHPR	%1677.652413	%1677.65266	0.000494	0	0.982267589	
ACP5	%1620.544594	%1620.54483	0.000472	0	0.982666874	
APOH	%1788.805521	%1788.805745	0.000448	0	0.983113228	
SDC1	%1666.731274	%1666.731495	0.000442	0	0.983226673	
CAPNS1	%1634.045253	%1634.045466	0.000426	0	0.983533017	
SEMG2	%3579.305348	%3579.305551	0.000406	0	0.983924159	
DNASE2	%1921.150806	%1921.151009	0.000406	0	0.983924159	
PTGDS	%982.883005	%982.883204	0.000398	0	0.984083309	
SPACA3	%1235.813698	%1235.813896	0.000396	0	0.984123346	
GPC4	%2542.324079	%2542.324262	0.000366	0	0.984736501	
LGALS3	%1334.476183	%1334.476363	0.00036	0	0.984862113	
RAB11B	%959.630271	%959.63043	0.000318	0	0.985772434	
SLC35F2	%1868.049695	%1868.049852	0.000314	0	0.985862189	
EEF1G	%2358.943814	%2358.943967	0.000306	0	0.986043432	
PPP5C	%2321.511129	%2321.511272	0.000286	0	0.986507191	
DDR1	%4202.525528	%4202.525669	0.000282	0	0.98660187	
PPP2R4	%2046.304743	%2046.304868	0.00025	0	0.987384863	
CD81	%1099.112028	%1099.112149	0.000242	0	0.98758833	
GNAI3	%1543.818883	%1543.818994	0.000222	0	0.988112228	
GALNS	%2944.562112	%2944.562222	0.00022	0	0.988165893	
CRTAC1	%3032.641823	%3032.641928	0.00021	0	0.988437959	
GNPTG	%1708.304177	%1708.304275	0.000196	0	0.988829981	
ADAM10	%3311.838502	%3311.838599	0.000194	0	0.988887113	
TUBB1	%2182.509646	%2182.509742	0.000192	0	0.988944541	
FDPS	%2086.537526	%2086.537619	0.000186	0.96792	0.989118643	
PSMB7	%1343.912063	%1343.912154	0.000182	0	0.989236275	
CKB	%1605.378926	%1605.379016	0.00018	0	0.989295576	
APOE	%1813.688209	%1813.688298	0.000178	0	0.989355208	
DEFB129	%916.675777	%916.675866	0.000178	0	0.989355208	
NRP1	%4386.025457	%4386.025542	0.00017	0	0.989597153	
HSPA8	%3010.867894	%3010.867979	0.00017	0	0.989597153	
CCT8	%2457.392438	%2457.392522	0.000168	0	0.989658524	
GPR115	%4130.653071	%4130.653155	0.000168	0	0.989658524	
CD44	%3893.388996	%3893.389078	0.000164	0	0.989782371	
NUCB2	%2066.585857	%2066.585938	0.000162	0	0.989844862	
GLA	%2065.8065	%2065.806581	0.000162	0	0.989844862	
TIMP2	%997.28575	%997.28583	0.00016	0	0.989907739	
CCT2	%2334.160568	%2334.160642	0.000148	0	0.990293555	
PLA2G7	%2164.415514	%2164.415585	0.000142	0	0.990492333	
ZPBP	%1823.908333	%1823.908404	0.000142	0	0.990492333	
CFL1	%744.26039	%744.260457	0.000134	0	0.990764025	
DNAJC3	%2291.143961	%2291.144028	0.000134	0	0.990764025	
CLU	%2586.5376	%2586.53766	0.00012	0	0.991259787	
TP53I3	%1652.213539	%1652.213596	0.000114	0	0.991481086	
PRKAR2A	%2023.127507	%2023.127562	0.00011	0	0.99163187	
GPC1	%2722.848398	%2722.848452	0.000108	0	0.99170829	
ENO1	%2054.244343	%2054.244396	0.000106	0	0.991785421	
CTBS	%1987.622075	%1987.622125	0.0001	0	0.992021287	
KPNB1	%3991.710906	%3991.710956	0.0001	0	0.992021287	
HSPB1	%964.72338	%964.72343	1E%04	0	0.992021287	
SFN	%1070.961116	%1070.961163	9.4E%05	0	0.992264343	
YWHAG	%1078.462822	%1078.462869	9.4E%05	0	0.992264343	
TGFBR3	%4154.322357	%4154.322404	9.4E%05	0	0.992264343	
EXTL2	%1509.152173	%1509.152219	9.2E%05	0	0.992347077	
WFDC8	%1415.133791	%1415.133837	9.2E%05	0	0.992347077	
PEBP4	%1277.638437	%1277.638483	9.2E%05	0	0.992347077	
GANAB	%4579.779613	%4579.779658	9E%05	0	0.992430716	
FUCA1	%2440.830873	%2440.830918	9E%05	0	0.992430716	
GLO1	%898.684054	%898.684098	8.8E%05	0	0.992515289	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
IDH1	%2148.814957	%2148.814999	8.4E%05	0	0.99268737	
RAB14	%906.933411	%906.933453	8.4E%05	0	0.99268737	
TPT1	%767.034396	%767.034437	8.2E%05	0	0.992774947	
TWSG1	%990.387434	%990.387475	8.2E%05	0	0.992774947	
DNAJB9	%1082.190467	%1082.190507	8E%05	0	0.992863599	
PI15	%1214.6853	%1214.685339	7.8E%05	0	0.992953366	
SLC1A1	%2564.797779	%2564.797818	7.8E%05	0	0.992953366	
USP14	%2152.875402	%2152.875441	7.8E%05	0	0.992953366	
fam3B	%1384.088208	%1384.088246	7.6E%05	0	0.993044292	
TSTA3	%1605.850053	%1605.850091	7.6E%05	0	0.993044292	
ARF1	%802.333419	%802.333457	7.6E%05	0	0.993044292	
SERPINB6	%2140.822637	%2140.822674	7.4E%05	0	0.993136422	
PGAM2	%1125.984114	%1125.984149	7E%05	0	0.993324497	
CPE	%2255.019745	%2255.019779	6.8E%05	0	0.99342055	
EEF1A1	%2041.953382	%2041.953416	6.8E%05	0	0.99342055	
PSMA6	%1114.32582	%1114.325854	6.8E%05	0	0.99342055	
GNPDA1	%1287.860311	%1287.860343	6.4E%05	0	0.993616992	
GSS	%2204.697017	%2204.697049	6.4E%05	0	0.993616992	
ACPP	%2126.030794	%2126.030824	6E%05	0	0.993819675	
MDH1	%1613.270002	%1613.270032	6E%05	0	0.993819675	
B4GALT1	%2163.332072	%2163.3321	5.6E%05	0	0.994029234	
TSG101	%1726.947063	%1726.947091	5.6E%05	0	0.994029234	
PPIA	%757.047452	%757.047479	5.4E%05	0	0.994136823	
FSTL1	%1390.251588	%1390.251614	5.2E%05	0	0.994246422	
WFDC9	%484.053815	%484.05384	5E%05	0	0.994358151	
CD151	%1221.702784	%1221.702808	4.8E%05	0	0.994472138	
PGM1	%2775.812536	%2775.812558	4.4E%05	0	0.994707471	
FKBP4	%2244.135203	%2244.135224	4.2E%05	0	0.994829153	
PCMT1	%1290.088827	%1290.088848	4.2E%05	0	0.994829153	
HINT1	%580.02349	%580.023511	4.2E%05	0	0.994829153	
GM2A	%1026.987446	%1026.987467	4.2E%05	0	0.994829153	
PPP1R7	%1599.821356	%1599.821376	4E%05	0	0.994953769	
GDF15	%1712.022682	%1712.022701	3.8E%05	0	0.99508154	
CD9	%1042.243326	%1042.243344	3.6E%05	0	0.995212721	
FAM3C	%978.945772	%978.94579	3.6E%05	0	0.995212721	
PPP2CA	%1404.950926	%1404.950944	3.6E%05	0	0.995212721	
TTR	%787.241153	%787.241171	3.6E%05	0	0.995212721	
PPT1	%1498.798881	%1498.798898	3.4E%05	0	0.9953476	
TNFSF10	%1407.15312	%1407.153137	3.4E%05	0	0.9953476	
TAGLN2	%907.149038	%907.149055	3.4E%05	0	0.9953476	
CPM	%2172.298164	%2172.29818	3.2E%05	0	0.995486507	
DDT	%577.492783	%577.492799	3.2E%05	0	0.995486507	
UGDH	%2200.074687	%2200.074702	3E%05	0	0.995629828	
NME3	%751.632504	%751.632519	3E%05	0	0.995629828	
RAB27A	%1047.525532	%1047.525547	3E%05	0	0.995629828	
SH3BGRL2	%468.874796	%468.87481	2.8E%05	0	0.995778011	
GNG12	%817.92306	%817.923074	2.8E%05	0	0.995778011	
RUVBL1	%2020.85136	%2020.851374	2.8E%05	0	0.995778011	
s100A11	%497.122242	%497.122256	2.8E%05	0	0.995778011	
UBE2L3	%718.559454	%718.559467	2.6E%05	0	0.995931589	
LCP1	%2873.199449	%2873.199462	2.6E%05	0	0.995931589	
HEBP2	%1011.788849	%1011.788861	2.4E%05	0	0.996091196	
MDH2	%1639.877347	%1639.877359	2.4E%05	0	0.996091196	
PTN	%769.043888	%769.0439	2.4E%05	0	0.996091196	
VAT1	%1981.04834	%1981.048351	2.2E%05	0	0.996257603	
BPNT1	%1443.223403	%1443.223413	2E%05	0	0.996431764	
AKR1A1	%1504.24592	%1504.245928	1.6E%05	0	0.99680847	
ANXA4	%1495.327972	%1495.32798	1.6E%05	0	0.99680847	
GNB1	%1523.547018	%1523.547026	1.6E%05	0	0.99680847	
RHOA	%812.291481	%812.291489	1.6E%05	0	0.99680847	

Gene	lnL	lnL	2ΔlnL	branch_w	P0value	k
SERPINA6	%2120.213601	%2120.213609	1.6E%05	0	0.99680847	
CNP	%1957.91178	%1957.911787	1.4E%05	0	0.997014596	
GNB2L1	%1451.515365	%1451.515372	1.4E%05	0	0.997014596	
PRDX1	%898.432195	%898.432202	1.4E%05	0	0.997014596	
CLIC1	%1149.184406	%1149.184413	1.4E%05	0	0.997014596	
ANG	%874.590466	%874.590472	1.2E%05	0	0.997236052	
ANXA5	%1412.503119	%1412.503125	1.2E%05	0	0.997236052	
YWHAB	%1085.130045	%1085.130051	1.2E%05	0	0.997236052	
SERPINF1	%2281.708508	%2281.708514	1.2E%05	0	0.997236052	
CD14	%1923.046905	%1923.04691	1E%05	0	0.997476872	
TXN	%469.042743	%469.042748	1E%05	0	0.997476872	
HIST2H2BE	%531.300038	%531.300043	1E%05	0	0.997476872	
IGJ	%899.495129	%899.495134	1E%05	0	0.997476872	
MSMB	%701.259151	%701.259156	1E%05	0	0.997476872	
NAPA	%1260.183813	%1260.183818	1E%05	0	0.997476872	
NIF3L1	%1933.002717	%1933.002722	1E%05	0	0.997476872	
ARF6	%713.214285	%713.214289	8E%06	0	0.997743245	
B2M	%642.341008	%642.341012	8E%06	0	0.997743245	
CREG1	%1115.99544	%1115.995444	8E%06	0	0.997743245	
GALNT6	%2889.678921	%2889.678925	8E%06	0	0.997743245	
CACYBP	%1005.809009	%1005.809012	6E%06	0	0.998045592	
RAC1	%947.657584	%947.657587	6E%06	0	0.998045592	
TIMP3	%905.358987	%905.35899	6E%06	0	0.998045592	
APOA2	%562.199223	%562.199225	4E%06	0	0.998404232	
DCD	%649.029894	%649.029896	4E%06	0	0.998404232	
HRSP12	%647.632213	%647.632215	4E%06	0	0.998404232	
CAPZA2	%1219.831477	%1219.831478	2E%06	0	0.998871621	
tor1B	%1562.057247	%1562.057248	2E%06	0	0.998871621	
SPINK2	%513.689213	%513.689214	2E%06	0	0.998871621	
PSMA7	%1181.051965	%1181.051966	2E%06	0	0.998871621	
DBI	%658.285382	%658.285382	0	0	1	
GSTO1	%1164.091221	%1164.091221	0	0	1	
PRDX6	%1048.738405	%1048.738405	0	0	1	
RAB10	%817.552679	%817.552679	0	0	1	
TGFB3	%1782.020919	%1782.020919	0	0	1	
YWHAQ	%1126.692118	%1126.692118	0	0	1	
ACTN1	%4234.824992	%4234.824424	%0.001136	0	#NUM!	
AGR2	%795.143618	%795.143604	%2.8E%05	0	#NUM!	
AGT	%2693.348228	%2693.347885	%0.000686	0	#NUM!	
ALDOC	%1676.507636	%1676.507381	%0.00051	0	#NUM!	
ANTXR2	%2363.387127	%2363.386975	%0.000304	0	#NUM!	
APOD	%1109.090356	%1109.090219	%0.000274	0	#NUM!	
BAIAP2	%2820.906445	%2717.615836	%206.581218	0	#NUM!	
CAPZB	%2006.143723	%2006.143722	%2E%06	0	#NUM!	
CD47	%1467.859864	%1467.859855	%1.8E%05	0	#NUM!	
CDC42	%983.518283	%983.518253	%6E%05	0	#NUM!	
COL9A1	%4610.317983	%4610.317264	%0.001438	0	#NUM!	
COPB2	%4428.345153	%4073.869565	%708.951176	0	#NUM!	
CUL3	%3550.462457	%3336.2129	%428.499114	0	#NUM!	
CYB561	%1914.481517	%1914.481443	%0.000148	0	#NUM!	
CYB5R2	%1633.830791	%1468.071615	%331.518352	0	#NUM!	
DDAH1	%1302.501844	%1302.501766	%0.000156	0	#NUM!	
DPP4	%4107.232383	%3557.466155	%1099.532456	0	#NUM!	
DPP7	%2836.207864	%2587.92499	%496.565748	0	#NUM!	
EFHD2	%1219.582333	%1219.582317	%3.2E%05	0	#NUM!	
F11R	%1624.957849	%1624.957845	%8E%06	0	#NUM!	
FMOD	%1738.22922	%1738.229197	%4.6E%05	0	#NUM!	
FTH1	%832.161239	%832.161227	%2.4E%05	0	#NUM!	
GALNT7	%2933.806908	%2933.806887	%4.2E%05	0	#NUM!	
GFRA2	%2174.043633	%2076.652961	%194.781344	0	#NUM!	

Gene	lnL	lnL	2ΔlnL	branch_w	PQvalue	k
GMPPA	%2275.587955	%2236.272855	%78.6302	0	#NUM!	
GNS	%2820.042424	%2820.04242	%8E%06	0	#NUM!	
GPX3	%1102.627534	%1102.627376	%0.000316	0	#NUM!	
HPRT1	%1071.034448	%1071.034308	%0.00028	0	#NUM!	
KRT1	%3124.510237	%3124.510033	%0.000408	0	#NUM!	
LAP3	%3061.117587	%3061.117302	%0.00057	0	#NUM!	
LDHA	%1655.528388	%1655.528383	%1E%05	0	#NUM!	
LDHB	%1500.35107	%1500.351062	%1.6E%05	0	#NUM!	
LSAMP	%1597.019837	%1597.019817	%4E%05	0	#NUM!	
MPI	%1971.567561	%1971.567545	%3.2E%05	0	#NUM!	
NEU1	%2052.725119	%2052.725115	%8E%06	0	#NUM!	
PFN1	%648.281844	%648.281843	%2E%06	0	#NUM!	
PFN2	%782.864895	%782.864791	%0.000208	0	#NUM!	
PPIB	%977.200603	%977.200601	%4E%06	0	#NUM!	
PPP1CC	%1481.731222	%1397.753996	%167.954452	0	#NUM!	
PRKAR1A	%1752.821862	%1752.821859	%6E%06	0	#NUM!	
PSMA1	%1253.110928	%1253.110909	%3.8E%05	0	#NUM!	
PSMA2	%1089.873234	%1089.87322	%2.8E%05	0	#NUM!	
PSMB8	%1421.940574	%1421.940377	%0.000394	0	#NUM!	
PSMD14	%1271.536875	%1271.536856	%3.8E%05	0	#NUM!	
RAB13	%919.80199	%919.801989	%2E%06	0	#NUM!	
Rab18	%1027.789387	%1027.789381	%1.2E%05	0	#NUM!	
RAB1A	%880.866004	%880.865653	%0.000702	0	#NUM!	
RAB1B	%984.578696	%984.578571	%0.00025	0	#NUM!	
RAB5C	%1147.4385	%1147.438483	%3.4E%05	0	#NUM!	
RBP4	%999.91605	%887.287897	%225.256306	0	#NUM!	
RNASE4	%749.658613	%749.65861	%6E%06	0	#NUM!	
RUVBL2	%2412.566854	%2138.776605	%547.580498	0	#NUM!	
sez6L2	%4434.817196	%4433.524511	%2.58537	395.5084	#NUM!	
SOD1	%861.691894	%861.691883	%2.2E%05	0	#NUM!	
SPINT3	%506.712218	%506.712212	%1.2E%05	0	#NUM!	
TSN	%997.593312	%997.593298	%2.8E%05	0	#NUM!	
VAMP2	%492.558883	%492.558874	%1.8E%05	0	#NUM!	
VAMP8	%450.203331	%450.203314	%3.4E%05	0	#NUM!	
YWHAE	%1079.034222	%1079.034221	%2E%06	0	#NUM!	
YWHAZ	%1005.291348	%991.250673	%28.08135	0	#NUM!	

Stem-African Ape

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPG2	&2059.92872	&2132.9454	146.03336	0.02325	1.27658E&33	
MYH9	&817.343655	&876.338133	117.988956	0	1.74356E&27	
FCGBP	&6824.11874	&6854.73281	61.228142	0.14715	5.08298E&15	
PTPRS	&9650.427351	&9679.117405	57.380108	0.00894	3.59222E&14	
FLNB	&12657.90394	&12684.75997	53.712056	0.02035	2.32134E&13	
THBS2	&838.305995	&860.173869	43.735748	0.02504	3.75844E&11	
SORL1	&10867.92137	&10888.56884	41.294954	0.02041	1.30906E&10	
col12A1	&14644.73757	&14665.1539	40.83265	0.06476	1.65839E&10	
PLXNB2	&9383.125486	&9402.813419	39.375866	0.05749	3.49591E&10	
FASN	&13845.70104	&13865.24898	39.095892	0.11781	4.03492E&10	
EEF2	&4122.120079	&4140.843701	37.447244	0	9.39193E&10	
CLSTN1	&4930.294559	&4948.169034	35.74895	0.03605	2.24453E&09	
RELN	&16740.06117	&16757.85855	35.594768	0.08016	2.42939E&09	
ACTN4	&4157.079722	&4174.207445	34.255446	0	4.83321E&09	
PFKP	&4124.887273	&4141.637663	33.50078	0	7.12354E&09	
SEMA7A	&318.610081	&335.013576	32.80699	0	1.01778E&08	
COL18A1	&9613.21785	&9628.959336	31.482972	0.18447	2.01197E&08	
PLOD3	&732.288784	&747.7179	30.858232	0.03726	2.77582E&08	
MYO1C	&5453.237009	&5467.663182	28.852346	0.01745	7.81112E&08	
TKT	&3006.248785	&3020.548016	28.598462	0.02174	8.90529E&08	
GPC1	&2722.377882	&2736.428683	28.101602	0.02754	1.15111E&07	
PTPRF	&9058.542483	&9072.290328	27.49569	0	1.57445E&07	
AGRN	&10949.36028	&10962.95356	27.18656	0.15669	1.84738E&07	
PTPRD	&9070.118936	&9083.678162	27.118452	0	1.91363E&07	
ODZ2	&12811.63069	&12825.1061	26.950822	0.02658	2.08698E&07	
PYGB	&4726.109646	&4739.266997	26.314702	0.0181	2.90072E&07	
MUC6	&13540.81676	&13553.97344	26.31335	0.25472	2.90275E&07	
CNTNAP2	&7123.638625	&7136.513759	25.750268	0.07656	3.88573E&07	
GSN	&873.484556	&886.099534	25.229956	0.02525	5.08857E&07	
NAGLU	&596.896284	&609.284853	24.777138	0.04617	6.43563E&07	
DDB1	&5174.974342	&5187.110467	24.27225	0	8.36353E&07	
THBS1	&5464.264581	&5476.200642	23.872122	0.01464	1.02952E&06	
PSME4	&502.372722	&514.264916	23.784388	0.0589	1.07753E&06	
RUVBL2	&138.420962	&149.820434	22.798944	0	1.79865E&06	
GAA	&4985.791635	&4997.129742	22.676214	0.07085	1.91727E&06	
PPP5C	&321.429767	&332.405336	21.951138	0.02569	2.79681E&06	
IGF2R	&12690.01924	&12700.96316	21.887832	0.26013	2.89061E&06	
ACE	&6850.149369	&6861.092215	21.885692	0.09069	2.89384E&06	
MAN2B1	&5062.197196	&5073.004475	21.614558	0.05253	3.33312E&06	
ACTN1	&4233.76055	&4244.510655	21.50021	0	3.5379E&06	
SERPINI1	&1932.049738	&1942.765901	21.432326	0	3.66539E&06	
ATRN	&7589.239933	&7599.84915	21.218434	0.06679	4.09804E&06	
SI	&9016.351532	&9026.830616	20.958168	0.17656	4.69422E&06	
STXBP2	&3028.070779	&3038.420342	20.699126	0.00765	5.37405E&06	
FN1	&12062.936	&12072.98106	20.09012	0.10648	7.38773E&06	
CANT1	&220.212973	&230.106618	19.78729	0	8.65563E&06	
MGAM	&9728.588136	&9738.313141	19.45001	0.16271	1.03267E&05	
LAMC1	&7895.408451	&7905.095693	19.374484	0.071	1.07433E&05	
PACSIN2	&691.317125	&700.954963	19.275676	0	1.13139E&05	
sez6L2	&4432.622669	&4442.155162	19.064986	0.04393	1.26342E&05	
SLIT2	&7466.715364	&7476.035554	18.64038	0	1.57842E&05	
CLTC	&7273.643037	&7282.756486	18.226898	0	1.9609E&05	
NRCAM	&6120.431846	&6129.501915	18.140138	0	2.0523E&05	
PITPNA	&1221.163317	&1230.233377	18.14012	0	2.05231E&05	
TPP2	&6054.722706	&6063.757333	18.069254	0	2.13014E&05	
IQGAP1	&7510.481726	&7519.423995	17.884538	0.03948	2.3472E&05	
KPNB1	&3991.224395	&4000.004336	17.559882	0	2.784E&05	
ITIH5	&5266.795195	&5275.573716	17.557042	0.1229	2.78816E&05	
ANXA2	&1663.131686	&1671.866558	17.469744	0	2.91917E&05	
GDI2	&124.272458	&132.90628	17.267644	0	3.24669E&05	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
APP	&788.565026	&797.059013	16.987974	0	3.76173E&05	
RTN4RL1	&265.77915	&274.192225	16.82615	0.04798	4.09649E&05	
GALNT6	&887.640582	&896.046935	16.812706	0	4.12561E&05	
THBS4	&698.35985	&706.474643	16.229586	0.04203	5.61109E&05	
SLC1A1	&562.940874	&570.975398	16.069048	0	6.10742E&05	
IDE	&639.924199	&647.909369	15.97034	0	6.43427E&05	
CCT5	&475.825293	&483.805754	15.960922	0	6.46636E&05	
CPO	&172.30087	&180.280507	15.959274	0.0705	6.47199E&05	
CAPN1	&437.271046	&445.2297	15.917308	0	6.61708E&05	
ALDOA	&009.493691	&017.45136	15.915338	0	6.62397E&05	
ALDOC	&674.955062	&682.90919	15.908256	0	6.64881E&05	
PFAS	&779.237405	&786.953469	15.432128	0.15134	8.55219E&05	
DPP7	&587.661789	&595.310531	15.297484	0.07279	9.18388E&05	
SELENBP1	&613.124729	&620.719868	15.190278	0.04084	9.72026E&05	
GNMT	&451.575683	&459.121677	15.091988	0.06862	0.000102397	
GLG1	&644.987725	&652.466565	14.95768	0.11025	0.00010995	
BAIAP2	&716.785981	&724.242385	14.912808	0	0.000112596	
HSPA8	&010.867894	&018.310733	14.885678	0	0.000114227	
GPRC5C	&502.5475	&509.973048	14.851096	0.03518	0.00011634	
CAB39L	&526.000409	&533.391375	14.781932	0	0.000120686	
LCP1	&872.864637	&880.212566	14.695858	0	0.000126324	
PROM2	&693.364527	&700.61991	14.510766	0.12117	0.000139361	
CNTN3	&074.66518	&081.764024	14.197688	0.10148	0.000164573	
OLFM1	&197.245612	&204.340129	14.189034	0	0.000165331	
TGFB1	&740.179678	&747.196535	14.033714	0.0392	0.000179562	
TCP1	&481.629226	&488.625291	13.99213	0.04507	0.000183577	
HSPA1L	&828.147276	&835.074237	13.853922	0.07656	0.000197584	
LGMN	&358.924385	&365.829876	13.810982	0.04131	0.000202151	
ACLY	&465.876591	&472.750026	13.74687	0.07927	0.000209169	
ANXA6	&524.434734	&531.297546	13.725624	0	0.000211548	
PSMA1	&252.186385	&258.938098	13.503426	0	0.000238128	
MMP2	&194.276056	&200.968648	13.385184	0	0.00025362	
CD81	&098.694611	&105.224149	13.059076	0	0.000301818	
GALNS	&943.198712	&949.679653	12.961882	0	0.000317897	
CCT4	&398.018292	&404.47619	12.915796	0	0.000325821	
ADAMTSL1	&529.677843	&536.108834	12.861982	0.08795	0.000335325	
RUVBL1	&020.851407	&027.228971	12.755128	0	0.000355034	
TOLLIP	&330.534409	&336.729033	12.389248	0	0.000431813	
STEAP2	&248.016829	&254.187909	12.34216	0	0.000442842	
KRT8	&763.491353	&769.647602	12.312498	0.00259	0.000449935	
OLFM4	&760.304526	&766.446787	12.284522	0.05527	0.00045673	
COL6A2	&172.983291	&179.092763	12.218944	0.07556	0.000473067	
DNAJC3	&290.418635	&296.468655	12.10004	0	0.000504207	
YWHAB	&085.130045	&091.107467	11.954844	0	0.000545055	
HSPA5	&989.743933	&995.656477	11.825088	0	0.00058438	
LPL	&389.159334	&395.024319	11.72997	0.05374	0.000615016	
PURA	&246.335175	&252.188869	11.707388	0	0.000622524	
CCT3	&974.542931	&980.364025	11.642188	0.05202	0.000644727	
CACNA2D1	&979.996634	&985.802158	11.611048	0	0.000655612	
GPI	&904.44902	&910.234765	11.57149	0	0.000669707	
GANAB	&579.41235	&585.151834	11.478968	0.12465	0.000703882	
PSAP	&460.751829	&466.47688	11.450102	0	0.000714901	
ST14	&409.97842	&415.638622	11.320404	0.14419	0.0007666	
FUCA1	&439.598604	&445.227113	11.257018	0.06722	0.000793225	
MAN2A1	&436.588287	&442.208963	11.241352	0.12263	0.000799949	
CCT8	&456.559085	&462.13269	11.14721	0	0.000841582	
DPP4	&555.257161	&560.816399	11.118476	0	0.00085472	
FBP1	&664.066075	&669.610871	11.089592	0	0.000868136	
PGM1	&774.884478	&780.413209	11.057462	0	0.00088331	
Hyou1	&706.578033	&712.060489	10.964912	0.0581	0.000928534	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
MLPH	&874.244817	&879.697326	10.905018	0.1566	0.000959041	
LIFR	&5259.436355	&5264.853146	10.833582	0.15887	0.000996756	
ARSA	&2672.708269	&2678.107538	10.798538	0.09598	0.001015803	
NME3	&751.17622	&756.540321	10.728202	0	0.001055149	
PGLS	&1262.478398	&1267.826703	10.69661	0	0.00107332	
RAB3B	&1024.038841	&1029.378566	10.67945	0	0.001083323	
PGAM2	&1125.555591	&1130.876356	10.64153	0	0.001105762	
PRCP	&2720.089238	&2725.311298	10.44412	0.05616	0.001230405	
PRKAR1A	&1752.564741	&1757.779404	10.429326	0	0.0012403	
MAN2B2	&5889.354064	&5894.565787	10.423446	0.21136	0.001244255	
KLK3	&1479.130289	&1484.279451	10.298324	0	0.001331511	
RRBP1	&4917.372399	&4922.413058	10.081318	0.05786	0.001497802	
YWHAG	&1078.462822	&1083.50129	10.076936	0	0.001501368	
GRHPR	&1676.947007	&1681.969266	10.044518	0.09551	0.00152802	
IQGAP2	&7133.58046	&7138.599133	10.037346	0	0.001533981	
COLEC12	&3645.931315	&3650.944376	10.026122	0	0.001543356	
NUCB2	&2063.036708	&2067.976402	9.879388	0	0.001671405	
IL1RAP	&3278.006502	&3282.91027	9.807536	0	0.001737982	
LAMP1	&2234.917985	&2239.815843	9.795716	0	0.001749189	
LDHA	&1654.67064	&1659.550486	9.759692	0	0.001783798	
ARF1	&802.333419	&807.169042	9.671246	0	0.001871743	
RAB11B	&959.630271	&964.455613	9.650684	0	0.001892811	
PSMD2	&4157.773194	&4162.570852	9.595316	0	0.001950744	
TMEFF2	&1661.787864	&1666.575642	9.575556	0	0.001971851	
LAMB2	&9314.839273	&9319.626716	9.574886	0.25628	0.001972571	
GMPPA	&2235.466396	&2240.133345	9.333898	0.0689	0.002249533	
CRYZ	&1747.383257	&1751.936088	9.105662	0	0.002548195	
MSLN	&3967.778355	&3972.213057	8.869404	0.30248	0.002899898	
LTA4H	&2792.970018	&2797.388699	8.837362	0.0701	0.002951254	
RAB3D	&1031.509888	&1035.919792	8.819808	0	0.00297978	
SERPINF1	&2280.455061	&2284.857884	8.805646	0	0.003002998	
ANXA7	&2297.959691	&2302.346144	8.772906	0.07145	0.00305738	
SYT7	&2154.298803	&2158.684735	8.771864	0	0.003059127	
GNB2	&1550.697917	&1555.048061	8.700288	0	0.003181598	
GNB2L1	&1451.515393	&1455.856633	8.68248	0	0.003212835	
PKM2	&962.365392	&966.690097	8.64941	0	0.003271673	
ACRBP	&3029.289659	&3033.571757	8.564196	0.19606	0.003428383	
RAB5B	&1048.89757	&1053.171227	8.547314	0	0.003460324	
LAP3	&3058.508429	&3062.752302	8.487746	0	0.003575465	
SOD3	&1097.752796	&1101.988171	8.47075	0	0.003609026	
GUSB	&811.982874	&816.214516	8.463284	0.172	0.00362387	
APEH	&360.607432	&364.808704	8.402544	0	0.003746963	
NUCB1	&215.180478	&219.372353	8.38375	0	0.003785905	
TSN	&997.593312	&1001.767187	8.34775	0	0.003861652	
EPHA5	&4894.960951	&4899.128804	8.335706	0.0711	0.003887337	
DNASE2	&1919.00223	&1923.13012	8.25578	0	0.004062245	
EEF1A1	&2041.953382	&2046.077813	8.248862	0	0.004077756	
CAPNS1	&1634.028888	&1638.129862	8.201948	0.05643	0.004184544	
PGM2	&782.374652	&786.441675	8.134046	0.05778	0.00434417	
SORT1	&973.954371	&978.018294	8.127846	0.07551	0.00435905	
AMBP	&1760.980175	&1765.037069	8.113788	0	0.004392983	
VCP	&670.714806	&674.751277	8.072942	0	0.004493111	
SEMA3F	&869.883118	&873.892912	8.019588	0.10137	0.00462741	
ALB	&213.586863	&217.581933	7.99014	0	0.004703278	
NEU1	&2052.581163	&2056.565695	7.969064	0.08308	0.004758354	
PHGDH	&552.149974	&556.113561	7.927174	0	0.00486978	
CRISP1	&1445.543512	&1449.486362	7.8857	0	0.004982719	
GNPTG	&1708.304156	&1712.230487	7.852662	0.12566	0.005074593	
EFHD2	&1218.168459	&1222.090428	7.843938	0	0.00509914	
ENPP3	&4423.32363	&4427.226831	7.806402	0.08981	0.005206146	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CTSF	&2581.068265	&2584.95991	7.78329	0.10974	0.005273168	
USP14	&2152.192787	&2156.017291	7.649008	0	0.005680355	
TGM4	&677.250254	&681.065888	7.631268	0.19144	0.005736496	
IDUA	&710.034114	&713.828532	7.588836	0.2681	0.005873086	
PPP1R7	&1599.368379	&1603.156689	7.57662	0	0.005913021	
GPR56	&512.534556	&516.321614	7.574116	0.16942	0.005921241	
PRDX4	&1290.41216	&1294.171879	7.519438	0	0.006103672	
MPI	&1970.397507	&1974.130091	7.465168	0	0.006290416	
TIMP3	&905.118694	&908.826873	7.416358	0	0.006463351	
CDH1	&4612.107527	&4615.797733	7.380412	0.12344	0.006593806	
HSPB1	&963.337349	&967.020949	7.3672	0	0.006642428	
CTSD	&2194.742814	&2198.420947	7.356266	0.08583	0.006682944	
ANXA5	&1411.405531	&1415.077675	7.344288	0	0.006727617	
APLP2	&675.528397	&679.148576	7.240358	0.06937	0.007128277	
PDIA3	&2417.309268	&2420.896903	7.17527	0	0.007391532	
PTPRJ	&7429.262981	&7432.807687	7.089412	0.30348	0.007754068	
TGFBR3	&4154.016549	&4157.555151	7.077204	0.08726	0.007807073	
RAB13	&919.801983	&923.336076	7.068186	0	0.007846466	
TGFB3	&1781.892092	&1785.417737	7.05129	0	0.007920819	
ENO1	&2054.145493	&2057.654388	7.01779	0	0.008070378	
CLU	&2586.435644	&2589.923135	6.974982	0.15742	0.008265705	
ELSPBP1	&1097.060974	&1100.539495	6.957042	0	0.008348995	
CNDP2	&2405.49604	&2408.912566	6.833052	0.12204	0.008948623	
PPT1	&1498.074338	&1501.490374	6.832072	0	0.008953534	
SYT1	&1899.502802	&1902.891829	6.778054	0	0.009228545	
RAB1B	&983.953973	&987.327917	6.747888	0	0.009385872	
PROS1	&324.396761	&327.729204	6.664886	0	0.009833095	
GFRA2	&2075.943564	&2079.263126	6.639124	0	0.009976298	
VCL	&5089.412904	&5092.730195	6.634582	0	0.010001766	
MINPP1	&2558.129996	&2561.421563	6.583134	0	0.010294948	
MDH2	&1639.266817	&1642.531815	6.529996	0	0.01060702	
ALDH7A1	&687.071256	&690.331359	6.520206	0.13034	0.010665565	
ABP1	&4017.846152	&4021.066341	6.440378	0.2177	0.011155491	
APOH	&1788.300158	&1791.501625	6.402934	0.13124	0.011393193	
GOT1	&2039.4032	&2042.583285	6.36017	0.14299	0.011671036	
COL9A1	&4610.043777	&4613.194672	6.30179	0.19549	0.012061612	
FBLN2	&5915.515817	&5918.658749	6.285864	0.27457	0.012170473	
ARHGDIA	&1707.229577	&1710.347609	6.236064	0.08309	0.012517436	
SEMA3C	&591.707456	&594.804374	6.193836	0.0707	0.012819601	
GNS	&2819.977347	&2823.066736	6.178778	0.09365	0.012929154	
RBP4	&887.062251	&890.136986	6.14947	0	0.013145149	
GGH	&1666.325872	&1669.378361	6.104978	0.20483	0.013480163	
CD151	&1221.169742	&1224.210361	6.081238	0.158	0.013662499	
GPR115	&4130.270264	&4133.298791	6.057054	0.25904	0.013850855	
TSTA3	&1605.608328	&1608.636536	6.056416	0.17898	0.01385586	
GALNT7	&2933.243984	&2936.262879	6.03779	0	0.014002803	
KRT10	&3014.325665	&3017.28852	5.92571	0.14909	0.014921525	
RAB1A	&880.36056	&883.234902	5.748684	0	0.016501013	
SERPINB5	&1776.060308	&1778.911119	5.701622	0	0.016949243	
AHCY	&2344.7055	&2347.55275	5.6945	0.11251	0.01701816	0.019827586
DSC2	&4622.821587	&4625.667781	5.692388	0.1949	0.017038653	0.019913793
MMP7	&1412.551815	&1415.387622	5.671614	0	0.017241586	0.02
TUBB1	&2182.507273	&2185.341751	5.668956	0.0758	0.01726773	0.020086207
HSPA4	&3746.365204	&3749.192793	5.655178	0	0.017403908	0.020172414
DPEP3	&2750.330632	&2753.148698	5.636132	0.10012	0.017593981	0.020258621
RNASE1	&844.132782	&846.939485	5.613406	0	0.017823586	0.020344828
BTD	&2766.566284	&2769.371873	5.611178	0.19758	0.017846262	0.020431034
C1RL	&2663.767718	&2666.56817	5.600904	0.18222	0.017951213	0.020517241
VAMP2	&492.558883	&495.342823	5.56788	0	0.018292896	0.020603448
ACP5	&1619.902464	&1622.683944	5.56296	0	0.018344372	0.020689655

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SERPINB6	&2140.735878	&2143.514857	5.557958	0.09612	0.018396861	0.020775862
CCT2	&2334.105903	&2336.878574	5.545342	0	0.018529935	0.020862069
PAM	&4585.594271	&4588.360045	5.531548	0.18615	0.018676574	0.020948276
GSTZ1	&1095.083342	&1097.834177	5.50167	0	0.018998322	0.021034483
TSG101	&1726.763376	&1729.502947	5.479142	0	0.019244703	0.02112069
PPIC	&1090.459729	&1093.159483	5.399508	0	0.020142429	0.021206897
GC	&2486.531617	&2489.228377	5.39352	0.14782	0.020211659	0.021293103
PLOD2	&3514.219105	&3516.911276	5.384342	0	0.020318249	0.02137931
TSNAX	&1309.976539	&1312.656192	5.359306	0	0.020611975	0.021465517
BGN	&1722.068363	&1724.661884	5.187042	0	0.022755916	0.021551724
FSTL1	&1390.080251	&1392.659542	5.158582	0	0.023131776	
LSAMP	&1596.655793	&1599.233257	5.154928	0.10989	0.023180497	
ACTR1A	&1747.712288	&1750.281708	5.13884	0	0.023396276	
SMPD1	&3206.613589	&3209.138709	5.05024	0.15467	0.024622528	
GAPDHS	&2136.758645	&2139.276691	5.036092	0.16534	0.024824432	
LIPG	&2621.461926	&2623.969829	5.015806	0.09135	0.025116934	
BASP1	&922.50288	&924.998746	4.991732	0.10549	0.025468704	
PTGDS	&982.730375	&985.223692	4.986634	0.06879	0.025543851	
FUT3	&2253.903443	&2256.394739	4.982592	0.08017	0.025603595	
CKB	&1605.135279	&1607.625364	4.98017	0.06544	0.025639464	0.022413793
GGT1	&3050.251093	&3052.738682	4.975178	0.05714	0.025713558	
SERPINC1	&2499.893996	&2502.378732	4.969472	0	0.025798522	
BPNT1	&1442.54839	&1445.026499	4.956218	0	0.025997005	
PGC	&1950.006653	&1952.484077	4.954848	0.11841	0.026017612	
MPST	&1728.332431	&1730.809388	4.953914	0	0.02603167	
IL1R1	&2816.915405	&2819.384874	4.938938	0	0.026258165	
CALR	&1871.844568	&1874.309546	4.929956	0	0.02639499	
ALDH9A1	&2588.174666	&2590.63939	4.929448	0	0.02640275	
PSAT1	&1799.148728	&1801.602568	4.90768	0.10714	0.026737531	
APOB	&23798.53154	&23800.9367	4.81033	0.53146	0.028289627	
NAPA	&1260.183833	&1262.540692	4.713718	0	0.029922869	
PRSS22	&1602.900006	&1605.243691	4.68737	0.17242	0.030385121	
ANTXR2	&2362.808428	&2365.14125	4.665644	0	0.030771881	
HEBP2	&1011.115059	&1013.421362	4.612606	0	0.031737767	
CD109	&7432.48383	&7434.781424	4.595188	0.27682	0.032061826	
EDIL3	&2208.41311	&2210.691053	4.555886	0	0.032805786	
HEXB	&2926.908944	&2929.18047	4.543052	0.13095	0.033052611	
MATN2	&4673.642252	&4675.899963	4.515422	0.23112	0.033590599	
DSC3	&4389.324477	&4391.543734	4.438514	0.22578	0.035136818	
HDHD2	&1220.597603	&1222.814171	4.433136	0	0.035247689	
PSMA5	&1038.294519	&1040.505657	4.422276	0	0.035472691	
KLK11	&1493.605589	&1495.787802	4.364426	0.2029	0.036696844	
CRTAC1	&3032.559136	&3034.740819	4.363366	0.02902	0.036719683	
GP2	&2924.643378	&2926.820773	4.35479	0.10736	0.036905009	
IDI1	&1551.715891	&1553.853046	4.27431	0.31274	0.03869267	
HIST2H2BE	&531.300085	&533.385506	4.170842	0	0.041125357	
NEO1	&6916.580666	&6918.658704	4.156076	0.23604	0.041485408	
CAPG	&1646.98438	&1649.046402	4.124044	0.01876	0.042277902	
CNP	&1957.911457	&1959.969907	4.1169	0.09376	0.042456809	
CAT	&2660.732303	&2662.750831	4.037056	0.20473	0.044511407	
CA6	&1743.855364	&1745.785664	3.8606	0	0.049432648	
ALDH1A1	&2397.580075	&2399.507234	3.854318	0.11676	0.049618095	
SERPINA5	&2277.629077	&2279.551061	3.843968	0.12717	0.049925237	0.025258621
TMC5	&5451.186181	&5453.08513	3.797898	0.22524	0.051316967	
PLA1A	&2498.426721	&2500.259001	3.66456	0.12714	0.055581317	
DCXR	&1306.260815	&1308.085566	3.649502	0.1664	0.056085979	
YWHAQ	&1125.664288	&1127.476158	3.62374	0	0.056960688	
PTN	&768.837701	&770.646185	3.616968	0	0.057193017	
PSMA4	&1161.933721	&1163.730679	3.593916	0	0.057991438	
CD47	&1467.42646	&1469.213894	3.574868	0	0.058660111	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SLC35F2	&1867.760199	&1869.546719	3.57304	0	0.058724711	
DEFB129	&915.313705	&917.095927	3.564444	0.13654	0.059029506	
GSR	&2856.920037	&2858.70203	3.563986	0.15208	0.059045793	
BCAN	&4543.698951	&4545.469489	3.541076	0.27568	0.059866613	
HINT1	&579.977086	&581.694597	3.435022	0.1325	0.063827735	
LIPA	&2212.12137	&2213.829514	3.416288	0.14854	0.064556018	
ORM1	&1197.297809	&1198.992774	3.38993	0	0.065595734	
ACYP1	&476.597295	&478.26367	3.33275	0	0.067913234	
GPR64	&4793.60854	&4795.244086	3.271092	0.27203	0.070510674	
LTF	&4531.851896	&4533.48147	3.259148	0.44298	0.071026021	
WFDC8	&1412.726094	&1414.336169	3.22015	999	0.072736964	
ADAM10	&3311.571197	&3313.175683	3.208972	0	0.073235483	
MANBA	&4390.432237	&4392.027137	3.1898	0.32923	0.074099077	
SERPINA6	&2120.178864	&2121.763656	3.169584	0.30157	0.075021553	
TIMP2	&997.116113	&998.653952	3.075678	0	0.079471451	
KAL1	&3350.846662	&3352.375672	3.05802	0.22911	0.080339512	
ADAMTS1	&4874.323605	&4875.842796	3.038382	0.23663	0.081316931	
ALCAM	&2704.945644	&2706.452078	3.012868	0	0.082606013	
CACYBP	&1005.340086	&1006.839311	2.99845	0	0.083344218	
CYB5R2	&1467.856587	&1469.355113	2.997052	0.13676	0.083416174	
MME	&3524.403687	&3525.892374	2.977374	0	0.084436165	
LMAN2	&1581.145399	&1582.630008	2.969218	0	0.084862868	
CFL1	&744.221741	&745.692842	2.942202	0	0.086293021	
RDX	&2860.547303	&2862.017949	2.941292	0	0.086341646	
FKBP4	&2243.552233	&2245.022642	2.940818	0	0.086366985	
KRT5	&2976.892059	&2978.355539	2.92696	0.21901	0.087111382	
IDH1	&2148.174666	&2149.633976	2.91862	0	0.08756272	
CYB561	&1914.351872	&1915.789743	2.875742	0.22604	0.089923519	
HEXA	&2619.612071	&2621.049649	2.875156	0.2707	0.089956257	
VAT1	&1981.015242	&1982.452467	2.87445	0.2091	0.089995717	
GNPDA1	&1287.733794	&1289.170647	2.873706	0	0.090037321	
GDF15	&1711.184598	&1712.618952	2.868708	0	0.090317348	
PPIA	&756.898019	&758.327808	2.859578	0	0.090831325	
CTSZ	&1651.372668	&1652.80191	2.858484	0.10376	0.090893125	
CTSH	&1641.378625	&1642.795109	2.832968	0.16507	0.092347548	
SIL1	&2462.217881	&2463.606096	2.77643	0.24137	0.095661185	
PRDX2	&981.035977	&982.419314	2.766674	0	0.096245957	
NUTF2	&660.807179	&662.174305	2.734252	0	0.098217479	
FH	&2428.404492	&2429.767315	2.725646	0.14201	0.09874816	
tor1B	&1561.839637	&1563.193352	2.70743	0	0.099881786	
TPI1	&1185.603296	&1186.945218	2.683844	0	0.101370766	
CUL3	&3336.120839	&3337.459853	2.678028	0	0.101741647	
UGDH	&2199.96265	&2201.297789	2.670278	0	0.102238164	
FUCA2	&2251.736562	&2253.071205	2.669286	0.21492	0.102301909	
TWSG1	&990.312338	&991.643557	2.662438	0	0.102743145	
GPC4	&2541.929916	&2543.243772	2.627712	0	0.105012942	
UBE2L3	&718.263105	&719.564902	2.603594	0	0.10662168	
LDHB	&1500.35107	&1501.648419	2.594698	0	0.107221876	
PSMA2	&1089.44353	&1090.727824	2.568588	0	0.109004989	
LCN1	&1024.673789	&1025.955186	2.562794	0.1816	0.109405076	
APOD	&1108.310494	&1109.591533	2.562078	999	0.109454629	
LZTFL1	&1304.19636	&1305.4683	2.54388	0.17555	0.110722401	
RAD23B	&1919.336586	&1920.60337	2.533568	0	0.111447954	
Rab18	&1027.648713	&1028.914372	2.531318	0	0.111606959	
CAPZB	&2005.248309	&2006.504761	2.512904	0	0.11291768	
BPIL1	&2383.459394	&2384.697994	2.4772	0.35997	0.115507721	
LDLR	&4410.665389	&4411.895212	2.459646	0.3656	0.116805104	
PPP1CC	&1397.753986	&1398.983155	2.458338	0	0.116902418	
NCSTN	&3555.541965	&3556.756737	2.429544	0.24091	0.11906753	
NPC2	&720.531143	&721.738649	2.415012	0	0.120177049	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SMS	&1889.913131	&1891.114196	2.40213	0	0.121170167	
CD44	&3893.268668	&3894.457317	2.377298	0.32544	0.123110318	
CTSB	&1793.662598	&1794.849795	2.374394	0.26084	0.123339452	
RAB5C	&147.234175	&148.412927	2.357504	0	0.12468154	
CREG1	&117.82773	&118.99858	2.3417	0	0.125952035	
ANXA1	&595.186574	&596.341849	2.31055	0	0.128498575	
AKR7A2	&2000.203371	&2001.357664	2.308586	0.22434	0.128661044	
ENPP5	&242.462457	&243.615393	2.305872	0.23171	0.128885932	
CLIC1	&148.7496	&149.897351	2.295502	0	0.129749255	
ANXA4	&1495.018789	&1496.160841	2.284104	0	0.130705605	
AGR2	&794.723638	&795.85389	2.260504	0	0.132710864	
RALB	&1037.220528	&1038.350777	2.260498	0.16555	0.132711378	
PRKCSH	&2724.023926	&2725.15041	2.252968	0.2558	0.133358405	
DDAH1	&1302.283777	&1303.400101	2.232648	0	0.135122097	
GM2A	&1026.567425	&1027.681811	2.228772	0.11272	0.135461472	
LEFTY2	&2007.726355	&2008.837573	2.222436	0.19418	0.136018296	
COPB2	&4073.320754	&4074.420346	2.199184	0.25501	0.138083817	
HPX	&2735.455519	&2736.541245	2.171452	0.32811	0.140593431	
CCT7	&2534.541097	&2535.620718	2.159242	0	0.141714583	
SFN	&1070.889398	&1071.968105	2.157414	0	0.141883298	
SLC15A2	&496.851659	&497.908218	2.113118	0.32694	0.14604149	
CPM	&2172.270252	&2173.32633	2.112156	0.17883	0.146133306	
GSS	&2204.32845	&2205.384112	2.111324	0	0.146212767	
PRSS8	&1907.463462	&1908.518873	2.110822	0.25522	0.146260735	
CAMP	&1001.890271	&1002.940068	2.099594	0.25519	0.147338257	
DAG1	&4330.038554	&4331.064081	2.051054	0.38581	0.15210086	
TFRC	&4085.493538	&4086.512094	2.037112	0.3461	0.153500838	
IL1RL1	&848.025527	&849.043191	2.035328	0.43344	0.153681029	
ACO1	&4249.066646	&4250.082491	2.03169	0.2483	0.154049225	
B4GALT1	&2163.300544	&2164.31482	2.028552	0.18898	0.154367621	
CPE	&2254.801344	&2255.8058	2.008912	0.22134	0.15637743	
B4GALT4	&1760.051629	&1761.050102	1.996946	0	0.157616505	
ANXA11	&4324.082025	&4325.074021	1.983992	0.20109	0.158970489	
SLC44A4	&3576.349363	&3577.340068	1.98141	0.38992	0.159241945	
Crisp2	&1476.98122	&1477.971914	1.981388	0.21022	0.15924426	
ADAM7	&4046.701565	&4047.676573	1.950016	0.3715	0.162585127	
VPS28	&1274.573219	&1275.542794	1.93915	0.08744	0.163760855	
CPVL	&2495.103208	&2496.040071	1.873726	0.29429	0.171048946	
XPNPEP1	&2970.881614	&2971.794847	1.826466	0.19761	0.176545535	
MAMDC2	&3253.748394	&3254.6409	1.785012	0	0.181535084	
PAICS	&2100.308259	&2101.195085	1.773652	0.20964	0.18293076	
PSMB4	&1249.696541	&1250.574854	1.756626	0.20867	0.185045915	
SCGB2A1	&558.510572	&559.361292	1.70144	999	0.192099764	
DNASE1	&1529.615655	&1530.456003	1.680696	0.30915	0.194831996	
PSMB7	&1343.597176	&1344.437189	1.680026	0.21213	0.194920998	
PSCA	&648.443435	&649.263805	1.64074	0.27397	0.200223967	
PRDX1	&98.1982	&99.004302	1.612204	0.22145	0.204182264	
GRN	&3084.499664	&3085.284348	1.569368	0.36793	0.210298819	
P4HB	&2492.414121	&2493.197951	1.56766	0	0.210547164	
ANG	&873.954364	&874.730283	1.551838	999	0.212864307	
NAGA	&2039.208422	&2039.98101	1.545176	0.27983	0.213849009	
CTBS	&1985.793625	&1986.55753	1.52781	999	0.216441422	
PSMB6	&1148.433435	&1149.19273	1.51859	0.23271	0.217832993	
CP	&5168.484039	&5169.237255	1.506432	0.42807	0.21968434	
GNB1	&1523.476773	&1524.224142	1.494738	0	0.221482785	
AGT	&2693.075663	&2693.808792	1.466258	0.39714	0.225937026	
SDCBP	&1416.927519	&1417.655138	1.455238	0.20264	0.227689327	
RAB27A	&1047.383463	&1048.104437	1.441948	0	0.229824372	
A4GALT	&1746.159142	&1746.856406	1.394528	0.06392	0.237641915	
PEBP4	&1277.512121	&1278.197486	1.37073	0.20511	0.241686499	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SEMG2	&578.367598	&579.047323	1.35945	0.5545	0.243632824	
PGD	&2494.852027	&2495.531191	1.358328	0.0731	0.243827464	
AKR1B1	&1486.358618	&1487.037668	1.3581	0.2992	0.24386704	
LYZ	&799.213167	&799.880508	1.334682	999	0.24797399	
MMP14	&2638.93192	&2639.585595	1.30735	0.3053	0.252875013	
PGK1	&1900.649083	&1901.296571	1.294976	0	0.255132958	
FMOD	&1734.737234	&1735.380363	1.286258	0.35262	0.2567387	
CRISP3	&1300.601818	&1301.243545	1.283454	0.20733	0.257257809	
CTSO	&1609.270992	&1609.908879	1.275774	0.31548	0.25868627	
TFPI2	&1254.861487	&1255.498904	1.274834	999	0.25886178	
PSMB2	&1080.317949	&1080.939027	1.242156	999	0.265055944	
ACAT2	&2217.933461	&2218.535528	1.204134	0.31639	0.272496988	
TTR	&787.007337	&787.607229	1.199784	0.27259	0.273364854	
LCN2	&1102.473727	&1103.071782	1.19611	0.34894	0.274100552	
B2M	&641.315259	&641.873264	1.11601	999	0.290779229	
A1BG	&2641.601292	&2642.151501	1.100418	0.40311	0.294174389	
LGALS3	&1333.655788	&1334.204851	1.098126	999	0.294677737	
SCPEP1	&2265.124481	&2265.647537	1.046112	0.29933	0.306404231	
apoa1BP	&1426.111385	&1426.616335	1.0099	0.39578	0.314926797	
GBA	&3378.770134	&3379.274024	1.00778	999	0.31543527	
LRG1	&1930.307614	&1930.802112	0.988996	0.47678	0.319987885	
RNASET2	&1453.014597	&1453.495971	0.962748	0.2279	0.326495491	
VTN	&2593.373328	&2593.850329	0.954002	0.50617	0.32870271	
NELL1	&4125.819235	&4126.295587	0.952704	0.4337	0.329031971	
F11R	&1624.788904	&1625.262394	0.94698	0.50607	0.330489205	
TEX101	&1484.408345	&1484.868245	0.9198	0.31686	0.337527491	
PRKAR2A	&2021.85056	&2022.291669	0.882218	15.69073	0.347594906	
TF	&4065.827043	&4066.25835	0.862614	1.61017	0.353008215	
PRKACA	&1826.840399	&1827.257577	0.834356	0	0.361015963	
LGALS3BP	&3226.634425	&3227.044667	0.820484	0.3655	0.365038694	
ALAD	&1834.752317	&1835.14847	0.792306	0.40073	0.373403751	
PI15	&1214.442548	&1214.829278	0.77346	0	0.379148797	
IDS	&2682.746309	&2683.125627	0.758636	0.28901	0.38375572	
NIF3L1	&1932.061351	&1932.435589	0.748476	999	0.386959168	
TNFSF10	&1407.148606	&1407.518636	0.74006	0.41387	0.389641659	
ACR	&2431.658493	&2432.024342	0.731698	0.5388	0.392333354	
SDC1	&1666.675031	&1667.037715	0.725368	0.53279	0.394388733	
ACPP	&2125.321242	&2125.669153	0.695822	2.25135	0.404191134	
WFDC2	&657.01895	&657.363422	0.688944	999	0.406523798	
GSTT1	&1141.737986	&1142.075392	0.674812	5.77186	0.411378938	
ZPBP	&1823.868511	&1824.199818	0.662614	0.44344	0.415638617	
SPINK2	&513.429861	&513.758077	0.656432	999	0.417822415	
CAP1	&2294.673603	&2295.001277	0.655348	0.52884	0.418207094	
EGF	&6295.380351	&6295.702201	0.6437	0.69429	0.422374141	
SERPINA4	&2416.732457	&2417.039151	0.613388	0.46429	0.433515013	
FOLH1	&3750.791859	&3751.086952	0.590186	0.32435	0.442347203	
RNASE4	&749.6421	&749.936937	0.589674	0.30918	0.442545209	
CLN5	&2182.28143	&2182.564107	0.565354	0	0.452111042	
SMPDL3B	&2536.471803	&2536.752596	0.561586	999	0.453621924	
FAM3C	&977.277354	&977.557556	0.560404	13.49634	0.454097511	
APOE	&1813.680632	&1813.954893	0.548522	0.26556	0.458922234	
GSTM3	&1075.996763	&1076.266593	0.53966	999	0.462573668	
GLA	&2064.979292	&2065.248811	0.539038	999	0.462831684	
GPX3	&1102.527122	&1102.796271	0.538298	0.33269	0.463138948	
ANXA3	&1634.956291	&1635.222131	0.53168	0.34363	0.465901408	
SERPINA1	&2320.31519	&2320.576474	0.522568	1.78202	0.469748297	
LNPEP	&4994.094059	&4994.347315	0.506512	0.5846	0.476652695	
PLA2G7	&2164.415525	&2164.662542	0.494034	0.36138	0.482133327	
GAPDH	&1560.632338	&1560.876183	0.48769	999	0.484959556	
ASAH1	&2202.879635	&2203.074059	0.388848	0.54501	0.532905564	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
MDH1	&1612.94215	&1613.133429	0.382558	0.40042	0.536237408	
NRP1	&4385.255801	&4385.442082	0.372562	0.46763	0.54161106	
APOA2	&561.862183	&562.035712	0.347058	999	0.555783268	
LDHC	&1561.428678	&1561.601752	0.346148	0	0.556301795	
PSMA6	&1114.162679	&1114.326445	0.327532	0	0.567115962	
CD38	&1612.091534	&1612.245451	0.307834	1.80173	0.579012381	
PCMT1	&1289.646303	&1289.793159	0.293712	0.45961	0.587851554	
smpdl3A	&2309.518032	&2309.66313	0.290196	0.56012	0.590094956	
SPINT1	&2729.108277	&2729.248997	0.28144	22.65533	0.595758939	
GSTP1	&1059.963616	&1060.104048	0.280864	0.5758	0.596135479	
C9	&132.718629	&132.852977	0.268696	1.3154	0.604207851	
PSMB8	&1421.767998	&1421.89657	0.257144	0.63823	0.612089089	
CAB39	&1445.087421	&1445.199072	0.223302	0.50582	0.636535396	
SEMG1	&120.973623	&121.081607	0.215968	1.64717	0.642129424	
AZGP1	&1711.600981	&1711.707912	0.213862	0.70276	0.643757102	
SPACA3	&1235.804006	&1235.908003	0.207994	0.71711	0.64834425	
pla2g2A	&857.409334	&857.497037	0.175406	0.57978	0.675351345	
TALDO1	&1587.987176	&1588.074702	0.175052	0.58788	0.675660417	
SORD	&1998.767011	&1998.851878	0.169734	0.63824	0.680348319	
PODXL2	&2866.235996	&2866.320579	0.169166	1.53212	0.680854076	
PDCD6IP	&896.509186	&896.591593	0.164814	0.59312	0.684762509	
TP53I3	&1651.361113	&1651.436763	0.1513	0.69677	0.697296115	
ANPEP	&5013.221215	&5013.28396	0.12549	0.78012	0.723154774	
fam3B	&1383.856312	&1383.917388	0.122152	1.48781	0.726712092	
DBI	&658.144873	&658.204575	0.119404	0.60699	0.729681801	
EFEMP1	&2219.489311	&2219.545732	0.112842	0.65566	0.736931471	
IGKC	&592.8178	&592.868775	0.10195	0.75703	0.749501989	
CD59	&866.364187	&866.407615	0.086856	1.42002	0.768212811	
EXTL2	&1508.606866	&1508.647102	0.080472	0.70015	0.776658787	
ECM1	&2915.814129	&2915.850299	0.07234	1.19573	0.787959723	
CFB	&3282.628893	&3282.66398	0.070174	0.85102	0.791083605	
GLO1	&897.692393	&897.725178	0.06557	0.70155	0.797899568	
APCS	&1273.357463	&1273.38949	0.064054	0.83161	0.800199503	
EEF1G	&2358.179634	&2358.210358	0.061448	0.73068	0.804221784	
QPCT	&1826.963944	&1826.991986	0.056084	0.72665	0.812795964	
MSMB	&701.113341	&701.141143	0.055604	0.7428	0.813583985	
KIF5B	&4446.821053	&4446.847711	0.053316	0.75876	0.817390489	
CA4	&1908.165417	&1908.185522	0.04021	0.86855	0.841070545	
SLPI	&797.325985	&797.345743	0.039516	0.8442	0.842429899	
PIP	&979.770047	&979.787541	0.034988	1.24421	0.851620807	
CD14	&1922.906322	&1922.92052	0.028396	0.81061	0.866181191	
SDCBP2	&1529.011795	&1529.024456	0.025322	999	0.873567336	
DNAJB9	&1081.827867	&1081.836305	0.016876	0.87343	0.896639484	
ACRV1	&1556.763769	&1556.771283	0.015028	1.17425	0.902432769	
RAB27B	&1001.19175	&1001.1978	0.0121	0.86283	0.912409375	
AGA	&1771.193798	&1771.198105	0.008614	1.11242	0.926053206	
KRT9	&261.53008	&261.531874	0.003588	0.948	0.952235346	
tmpRSS2	&227.673114	&227.674726	0.003224	0.96682	0.954720224	
FDPS	&2085.71673	&2085.718145	0.00283	0.94252	0.957574353	
CD63	&1057.696785	&1057.698007	0.002444	999	0.960571179	
SERPINA3	&2836.445559	&2836.446323	0.001528	0.97085	0.96881892	
LAMP2	&1922.585441	&1922.585889	0.000896	0.92631	0.976120281	
TPT1	&767.034396	&767.034828	0.000864	0	0.976550456	
SOD1	&861.579618	&861.580012	0.000788	1.03517	0.977605254	
RPLP0	&1380.982875	&1380.983182	0.000614	0	0.980231223	
PIGR	&4428.020301	&4428.020551	0.0005	1.01342	0.982160245	
PPIB	&977.200578	&977.200782	0.000408	0	0.983884618	
GCHFR	&390.365953	&390.366071	0.000236	0	0.987743147	
DCD	&649.010326	&649.010425	0.000198	0.98268	0.98877314	
IGJ	&899.495048	&899.495138	0.00018	0	0.989295576	

Gene	lnL&free	lnL&fixed	2&lnL	branch_w	P&value	k
CST6	&707.924372	&707.924459	0.000174	0	0.989475485	
RALA	&1071.344672	&1071.344724	0.000104	0	0.991863283	
CD9	&1042.243318	&1042.243365	9.4E&05	0	0.992264343	
PPP2CA	&1404.950923	&1404.950963	8E&05	0	0.992863599	
WFDC9	&484.053812	&484.05384	5.6E&05	0	0.994029234	
PFN2	&782.864767	&782.864791	4.8E&05	0	0.994472138	
CAPZA1	&1243.865903	&1243.865917	2.8E&05	0	0.995778011	
SH3BGRL2	&468.874796	&468.87481	2.8E&05	0	0.995778011	
GNG12	&817.92306	&817.923074	2.8E&05	0	0.995778011	
GSTO1	&1164.091191	&1164.091204	2.6E&05	0	0.995931589	
CA2	&1301.212787	&1301.212799	2.4E&05	0	0.996091196	
GNAI3	&1543.818883	&1543.818894	2.2E&05	0	0.996257603	
RAC1	&947.657573	&947.657583	2E&05	0	0.996431764	
ARF6	&713.214283	&713.214289	1.2E&05	0	0.997236052	
TAGLN2	&907.14904	&907.149046	1.2E&05	0	0.997236052	
SPINT3	&506.712207	&506.712212	1E&05	0	0.997476872	
TXN	&469.042743	&469.042748	1E&05	0	0.997476872	
VAMP8	&450.203314	&450.203319	1E&05	0	0.997476872	
s100A11	&497.122245	&497.122248	6E&06	0	0.998045592	
PFN1	&648.281839	&648.28184	2E&06	0	0.998871621	
PRDX5	&1042.862129	&1042.862129	0	0	1	
PRDX6	&1048.738405	&1048.738405	0	0	1	
AKR1A1	&1505.584116	&1504.021959	&3.124314	7.96026	#NUM!	
CAPZA2	&1219.831478	&1219.831471	&1.4E&05	0	#NUM!	
DDR1	&4228.540127	&4214.167179	&28.745896	17.94427	#NUM!	
GLB1	&3874.695966	&3851.395698	&46.600536	117.38162	#NUM!	
HPRT1	&1071.034443	&1071.034308	&0.00027	0	#NUM!	
HRSP12	&647.632232	&647.632225	&1.4E&05	0	#NUM!	
KRT1	&3125.435423	&3124.257924	&2.354998	164.37593	#NUM!	
PPP2R4	&2046.30499	&2046.304873	&0.000234	0	#NUM!	
PSMA3	&1388.168284	&1298.641757	&179.053054	0	#NUM!	
PSMA7	&1181.052427	&1181.052277	&0.0003	0	#NUM!	
PSMD14	&1309.730655	&1271.537133	&76.387044	0	#NUM!	
RAB10	&817.552682	&817.55268	&4E&06	0	#NUM!	
RAB14	&933.121946	&906.933453	&52.376986	0	#NUM!	
RAP1B	&777.425012	&777.425005	&1.4E&05	0	#NUM!	
RHOA	&812.291506	&812.291494	&2.4E&05	0	#NUM!	
SDK2	&10146.10462	&10141.31886	&9.571512	6.25843	#NUM!	
YWHAE	&1079.034222	&1079.034221	&2E&06	0	#NUM!	
YWHAZ	&991.250973	&991.250673	&0.0006	0	#NUM!	

Stem-Hominoid

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
HSPG2	&32056.40681	&32108.11081	103.407998	0	2.72771E&24	
PTPRD	&9072.312352	&9090.378809	36.132914	0	1.84307E&09	
TOLLIP	&1330.012248	&1339.056778	18.08906	0	2.10809E&05	
SORL1	&10870.13651	&10878.97022	17.667422	0.09995	2.63094E&05	
SEMA3F	&867.978449	&875.79816	15.639422	0	7.66401E&05	
SIL1	&458.773155	&466.46979	15.39327	0	8.72987E&05	
TEX101	&1478.303963	&1485.281096	13.954266	0	0.000187312	
ODZ2	&12811.19963	&12818.15603	13.912802	0	0.00019149	
AGRN	&10948.61678	&10955.18351	13.133458	0.0575	0.000290069	
GLG1	&5645.349006	&5651.662869	12.627726	0	0.000380067	
NRCAM	&6120.898928	&6127.15497	12.512084	0	0.000404328	
NEU1	&2051.108078	&2056.948667	11.681178	0	0.000631355	
RTN4RL1	&2265.870294	&2271.57738	11.414172	0.05384	0.00072886	
RUVBL2	&2138.58275	&2144.264929	11.364358	0	0.00074867	
ADAMTS1	&4874.83099	&4880.41269	11.1634	0.05227	0.000834269	
COLEC12	&8645.778714	&8651.348494	11.13956	0	0.000845059	
NME3	&751.16707	&756.664442	10.994744	0	0.000913706	
ACLY	&5465.225864	&5470.367632	10.283536	0	0.001342225	
MYO1C	&5454.043793	&5459.135896	10.184206	0.0977	0.001416487	
CACNA2D1	&4980.044108	&4984.998534	9.908852	0	0.001644857	0.001669449
GUSB	&811.481467	&816.42807	9.893206	0.12264	0.001658901	0.001752922
PDCD6IP	&899.276669	&904.199267	9.845196	0	0.001702758	0.001836394
DDR1	&4202.064051	&4206.938055	9.748008	0	0.001795171	0.001919866
LAMA5	&19256.68866	&19261.45096	9.524608	0.15682	0.002027349	0.002003339
ACTN1	&4234.111179	&4238.580567	8.938776	0	0.002791797	0.002086811
CAPNS1	&1633.423469	&1637.813172	8.779406	0	0.003046504	0.002170284
KRT1	&124.35415	&128.609395	8.51049	0.06704	0.00353105	0.002253756
IQGAP1	&7510.011096	&7514.255147	8.488102	0	0.003574765	0.002337229
HSPA8	&8010.867894	&8015.099113	8.462438	0	0.003625556	0.002420701
GANAB	&4578.21844	&4582.448909	8.460938	0	0.003628547	0.002504174
P4HB	&2492.621798	&2496.821956	8.400316	0.06032	0.003751558	
CNTNAP2	&7123.819396	&7127.977153	8.315514	0.05313	0.003930788	
GPI	&2904.929587	&2909.059461	8.259748	0	0.004053375	
SEMA7A	&322.9251	&327.022789	8.195378	0.06501	0.004199724	
DSC2	&4620.86939	&4624.962757	8.186734	0	0.004219782	
col12A1	&14645.49565	&14649.49784	8.004374	0.05622	0.004666449	
ANXA6	&525.38514	&529.36776	7.96524	0	0.004768417	
smpdl3A	&307.4376	&311.35521	7.83522	0	0.005123792	
VCL	&5089.305951	&5093.201516	7.79113	0	0.005250335	
GSTZ1	&1094.411337	&1098.306174	7.789674	0	0.005254568	
ADAMTSL1	&8528.523363	&8532.359061	7.671396	0	0.005610304	
GSTP1	&1061.603259	&1065.423308	7.640098	0.05803	0.005708482	
ANTXR2	&2362.304606	&2366.005261	7.40131	0	0.00651764	
sez6L2	&4432.382275	&4435.975201	7.185852	0	0.007348065	
PDIA3	&2417.456333	&2420.986477	7.060288	0	0.007881133	
MSMB	&696.807709	&700.309299	7.00318	0	0.008136505	
HSPA4	&3746.253139	&3749.713179	6.92008	0	0.008523316	
ADAM7	&4044.416408	&4047.861265	6.889714	0	0.008669314	
HSPA5	&2989.962423	&2993.404438	6.88403	0	0.008696925	
PSMB7	&1343.388998	&1346.826108	6.87422	0	0.008744791	0.004173623
ALCAM	&2704.617506	&2707.985444	6.735876	0	0.009449282	
GMPPA	&2234.897493	&2238.248852	6.702718	0	0.009626605	
SFN	&1070.809382	&1074.143501	6.668238	0	0.009814617	
CA4	&1906.191745	&1909.496045	6.6086	0.14337	0.010148742	
COL6A2	&6171.979746	&6175.265065	6.570638	0	0.010367478	
CP	&5167.011181	&5170.283457	6.544552	0	0.010520582	
FUCA1	&2439.377587	&2442.631298	6.507422	0	0.010742514	
MYH9	&8819.142969	&8822.39174	6.497542	0.04239	0.010802373	
PSAT1	&1798.331973	&1801.451593	6.23924	0	0.012495008	
Hyou1	&4706.118622	&4709.203222	6.1692	0	0.012999338	0.005008347

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CLN5	&2181.089834	&2184.111384	6.0431	0.08205	0.013960749	
APOH	&1787.418215	&1790.405893	5.975356	0	0.014507153	
MDH2	&1639.280489	&1642.256413	5.951848	0	0.014701866	
HIST2H2BE	&531.300085	&534.176844	5.753518	0	0.016455671	
LAMP1	&2235.058546	&2237.929236	5.74138	0	0.016569769	
PDCD6	&1145.977625	&1148.848081	5.740912	0	0.016574184	
OLFM1	&2197.510381	&2200.360057	5.699352	0	0.016971178	
THBS4	&4698.364877	&4701.188546	5.647338	0	0.017481891	
GOT1	&2038.86738	&2041.677403	5.620046	0	0.017756183	
PTGDS	&981.896291	&984.663966	5.53535	0	0.018636038	
LRG1	&1929.046902	&1931.796743	5.499682	0	0.019019932	
RAP1B	&777.425012	&780.136594	5.423164	0	0.019871319	
FUT3	&2251.684975	&2254.36044	5.35093	0	0.020711221	
APOE	&1811.739679	&1814.413394	5.34743	0	0.020752838	
IL1RAP	&278.586	&281.230999	5.289998	0.09428	0.021448245	
IL1R1	&2817.208727	&2819.797247	5.17704	0.08044	0.022887282	
LPL	&2388.746468	&2391.31244	5.131944	0	0.023489405	
DPP7	&2586.717963	&2589.268633	5.10134	0	0.023907368	
FASN	&13844.43508	&13846.9662	5.06225	0.24867	0.024452472	
GBA	&3377.709624	&3380.158959	4.89867	0	0.026877388	
LDHB	&1500.35107	&1502.769884	4.837628	0	0.02784517	
CNP	&1957.904043	&1960.321424	4.834762	0.08403	0.02789149	
MDH1	&1612.689545	&1615.095383	4.811676	0	0.02826754	
SOD1	&857.650737	&860.017988	4.734502	999	0.029563406	
MME	&3524.16949	&3526.532978	4.726976	0	0.029693047	
GGT1	&3050.105022	&3052.466286	4.722528	0.04598	0.029769946	
CCT8	&2457.039407	&2459.352795	4.626776	0	0.031476658	
B2M	&640.681202	&642.984871	4.607338	0	0.031835415	
ALDH9A1	&2588.152069	&2590.434406	4.564674	0	0.032637885	
MAMDC2	&3253.321467	&3255.566804	4.490674	0	0.034080239	0.007512521
NUCB1	&2215.979492	&2218.221151	4.483318	0	0.034227211	
MAN2B2	&5888.932746	&5891.172286	4.47908	0.10002	0.034312187	
FLNB	&12658.84271	&12661.06576	4.446088	0.08236	0.034981294	
CALR	&1871.828872	&1874.020007	4.38227	0	0.036314603	
PLA1A	&2498.099066	&2500.261685	4.325238	0.08124	0.037551163	
CTSD	&2194.750783	&2196.905239	4.308912	0.08647	0.037913202	
ACP5	&1619.973357	&1622.126277	4.30584	0	0.037981734	
GPD1L	&1727.648905	&1729.789481	4.281152	0	0.038537221	
HSPA1L	&3827.462445	&3829.596345	4.2678	0	0.038841187	
HEBP2	&1011.135768	&1013.266614	4.261692	0	0.038981077	
KRT8	&2765.362992	&2767.472534	4.219084	0.12588	0.039971734	
SMPDL3B	&2536.458477	&2538.561861	4.206768	0.19374	0.040262982	
TGFBR3	&4154.319903	&4156.42097	4.202134	0.17865	0.040373143	
EPHA5	&4894.684103	&4896.779975	4.191744	0	0.040621288	
GLA	&2065.274916	&2067.364031	4.17823	0.10765	0.040946443	
LGMN	&2360.092558	&2362.167797	4.150478	0.09192	0.041622773	
FH	&2427.991869	&2430.048231	4.112724	0	0.042561758	
LTA4H	&2792.917461	&2794.967178	4.099434	0	0.042897572	
COPB2	&4073.474782	&4075.52089	4.092216	0	0.043081124	
ECM1	&2915.206819	&2917.232971	4.052304	0	0.044111102	
ASRGL1	&1616.918467	&1618.917425	3.997916	0	0.045556559	
FOLH1	&749.71396	&751.703826	3.979732	0	0.04605089	
LIPG	&2621.687376	&2623.665234	3.955716	0.13886	0.046712442	
STXBP2	&3026.895402	&3028.859829	3.928854	0.22391	0.047464279	
UGCGL1	&7216.17562	&7218.105765	3.86029	0.10341	0.049441782	
APEH	&360.971701	&362.890371	3.83734	0	0.050122981	0.009682805
PFKP	&4126.809541	&4128.71735	3.815618	0	0.05077687	
CAB39L	&1526.351775	&1528.248205	3.79286	0	0.05147163	
PPP5C	&2321.254338	&2323.148151	3.787626	0	0.051632831	
NPEPPS	&4005.271053	&4007.147202	3.752298	0	0.052734963	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
SLIT2	&7468.258291	&7470.128894	3.741206	0	0.053086116	
WFDC2	&657.830098	&659.682505	3.704814	0.01983	0.054255718	
APOA2	&558.432033	&560.27604	3.688014	999	0.054804836	
FDPS	&2086.573485	&2088.414399	3.681828	0.10214	0.05500851	
ANXA11	&4322.735687	&4324.570673	3.669972	0	0.055401115	
SERPINB5	&1776.275802	&1778.07609	3.600576	0	0.057759555	
ACRBP	&3029.657777	&3031.453141	3.590728	0.10074	0.058102785	
FKBP4	&2243.43529	&2245.212282	3.553984	0	0.059402663	
HEXA	&2618.942298	&2620.719207	3.553818	0	0.059408605	
AKR7A2	&1999.030908	&2000.793167	3.524518	0	0.060467405	
PPIC	&1090.777503	&1092.517634	3.480262	0	0.062104906	
PSME4	&3502.592882	&3504.332554	3.479344	0.13007	0.062139369	
PSMB1	&1154.89423	&1156.621007	3.453554	0	0.063115919	
PSMB5	&1222.736156	&1224.433704	3.395096	0	0.065390557	
GPC4	&2541.890855	&2543.583882	3.386054	0	0.065750128	
NPC2	&720.354961	&722.008787	3.307652	0	0.068957954	
SLC15A2	&3496.631877	&3498.262061	3.260368	0.13826	0.070973197	
TKT	&3006.103348	&3007.730813	3.25493	0	0.071208978	
PSMA3	&1296.113181	&1297.740433	3.254504	0	0.071227483	
KRT5	&2977.443506	&2979.039981	3.19295	0	0.073956439	
ARF6	&713.214475	&714.778904	3.128858	0	0.076917604	
PACSIN2	&2694.269272	&2695.833432	3.12832	0.07925	0.076942994	
LCP1	&2873.117557	&2874.680916	3.126718	0	0.077018649	
PGAM2	&1125.833665	&1127.369938	3.072546	0	0.079624679	
LGALS3BP	&3226.950311	&3228.476017	3.051412	0.14304	0.080666982	
PROS1	&3325.842667	&3327.345759	3.006184	0.12012	0.082947354	
RUVBL1	&2020.851407	&2022.351061	2.999308	0	0.083300089	
C3	&3543.592437	&3545.079493	2.974112	0.39161	0.084606546	
ATRN	&7590.977645	&7592.45794	2.96059	0	0.085316804	
LEFTY2	&2008.742452	&2010.216087	2.94727	0.07822	0.086022761	
FUCA2	&2251.092389	&2252.564845	2.944912	0	0.086148391	
DNAJC3	&2290.907974	&2292.364976	2.914004	0.13089	0.087813614	
GNB2L1	&1451.515393	&1452.968891	2.906996	0	0.088196011	
RRBP1	&4917.754017	&4919.185095	2.862156	0.16471	0.090685875	
NUTF2	&660.760014	&662.161578	2.803128	0	0.0940806	
TUBB1	&2182.079439	&2183.47605	2.793222	0	0.094663718	
VAMP2	&492.558883	&493.952964	2.788162	0	0.094963091	
GALC	&3333.309857	&3334.700782	2.78185	0	0.095337985	
IDH1	&2147.91485	&2149.304076	2.778452	0	0.095540472	
PRDX2	&980.734766	&982.122644	2.775756	0	0.09570146	
MAN2B1	&5063.285535	&5064.665655	2.76024	0.11023	0.096633739	
SERPINA3	&2835.595591	&2836.969482	2.747782	0.15847	0.097389442	
RAB10	&817.552669	&818.913979	2.72262	0	0.098935499	
MPST	&1728.550436	&1729.903854	2.706836	0	0.099918991	
TPT1	&766.336891	&767.677823	2.681864	0	0.101496863	
CUL3	&3336.118751	&3337.457162	2.676822	0	0.101818738	
NAGA	&2038.959581	&2040.27002	2.620878	0	0.10546607	
TWSG1	&990.311175	&991.613816	2.605282	0	0.10650821	
CACYBP	&1005.37158	&1006.661656	2.580152	0	0.10821127	
MATN2	&4673.069391	&4674.357512	2.576242	0	0.108478929	
PSCA	&648.444962	&649.733059	2.576194	0	0.108482219	
PGK2	&1983.413161	&1984.684455	2.542588	0.20928	0.110813021	
CST1	&1078.82719	&1080.094932	2.535484	0.17923	0.11131275	
CPAMD8	&10032.86933	&10034.13535	2.53204	0.29155	0.111555909	
AGT	&2688.619359	&2689.868414	2.49811	999	0.113983015	
GNB2	&1550.937983	&1552.182858	2.48975	0	0.114589925	
PPP1R7	&1599.692344	&1600.925066	2.465444	0	0.116374814	
C1RL	&2663.826056	&2665.056963	2.461814	0.15254	0.116644004	
HRSP12	&647.171563	&648.401714	2.460302	0	0.116756332	
KIF5B	&4448.475233	&4449.679117	2.407768	0.13002	0.1207344	

Gene	lnL&free	lnL&fixed	2Δlnl	branch_w	P&value	k
TGFB3	&1781.980162	&1783.177018	2.393712	0	0.121824051	
ACTR1A	&1747.712288	&1748.890496	2.356416	0	0.124768547	
CTSZ	&1650.878259	&1652.056051	2.355584	0	0.124835127	
BCAN	&4543.796021	&4544.955038	2.318034	0.13536	0.127881564	
GNAI3	&1543.818883	&1544.975185	2.312604	0	0.128328906	
TP53I3	&1651.779013	&1652.93408	2.310134	0	0.128532969	
apoa1BP	&1425.726843	&1426.877616	2.301546	0	0.1292453	
RAB11B	&959.630271	&960.780629	2.300716	0	0.129314377	
VAMP8	&450.203331	&451.351337	2.296012	0	0.129706646	
C9	&3133.109976	&3134.254291	2.28863	999	0.130324913	
TSN	&997.593312	&998.731548	2.276472	0	0.131350362	
SPOCK3	&2096.585678	&2097.722651	2.273946	0.15333	0.131564541	
SERPINB6	&2140.319196	&2141.451238	2.264084	0.30436	0.132404479	
STEAP2	&2249.365792	&2250.49712	2.262656	0.04196	0.132526596	
FTH1	&832.004684	&833.127793	2.246218	0	0.133941406	
PIGR	&4428.819519	&4429.94025	2.241462	0.31404	0.134353895	
TTR	&786.404571	&787.51973	2.230318	0	0.135325993	
AGR2	&794.722325	&795.836167	2.227684	0	0.135556907	
CAPG	&1646.947193	&1648.056187	2.217988	0.13141	0.136410729	
PPP1CC	&1397.753986	&1398.857959	2.207946	0	0.137301373	
PPP2CA	&1404.837712	&1405.938971	2.202518	0	0.137785504	
PLOD2	&3514.59599	&3515.69638	2.20078	0.23162	0.137940923	
Rab18	&1027.660989	&1028.742082	2.162186	0	0.141443342	
RPLP0	&1380.877595	&1381.950881	2.146572	0	0.142888611	
RHOA	&812.291506	&813.359105	2.135198	0	0.143951874	
CD47	&1467.610072	&1468.672004	2.123864	0	0.145020267	
CD59	&865.97226	&867.033781	2.123042	999	0.145098099	
ACE2	&4533.497526	&4534.549154	2.103256	0.14739	0.146985843	
HDHD2	&1221.051789	&1222.102244	2.10091	0	0.147211502	
APOD	&1108.4633	&1109.501838	2.077076	999	0.14952637	
LIFR	&5259.578182	&5260.613104	2.069844	0.21874	0.150236888	
Crisp2	&1475.386107	&1476.417474	2.062734	999	0.150939144	
CA2	&1300.731377	&1301.762509	2.062264	0	0.150985697	
EFEMP1	&2220.531918	&2221.561672	2.059508	0	0.151259002	
PSMB8	&1421.319516	&1422.341928	2.044824	0	0.152724646	
RAD23B	&1919.335414	&1920.356158	2.041488	0.26716	0.153059858	
PITPNA	&1222.64575	&1223.666236	2.040972	0	0.153111782	
LAP3	&3060.721872	&3061.737842	2.03194	0.10308	0.154023891	
ENPP3	&4424.178893	&4425.193727	2.029668	0.28115	0.154254301	
CA6	&1744.758365	&1745.768507	2.020284	0.14671	0.15521011	
ABP1	&4017.246819	&4018.254415	2.015192	0	0.155731569	
AKR1A1	&1504.026258	&1505.023354	1.994192	0	0.157903258	
TPI1	&1185.646575	&1186.627665	1.96218	0	0.161280363	
TMC5	&5451.461313	&5452.438691	1.954756	0.34043	0.162075267	
LAMC1	&7895.107241	&7896.072302	1.930122	0	0.164745098	
FSTL1	&1390.17605	&1391.140642	1.929184	0	0.164847747	
BGN	&1722.313418	&1723.266321	1.905806	0.03837	0.16742988	
PPIB	&977.115853	&978.063959	1.896212	0	0.16850293	
SDC1	&1664.81159	&1665.758778	1.894376	999	0.168709177	
B4GALT4	&1760.551434	&1761.497633	1.892398	0.32968	0.168931699	
IDS	&2682.286835	&2683.220149	1.866628	0	0.171861779	
TMEM8	&4067.20396	&4068.135624	1.863328	0.13551	0.172241192	
CCT4	&2398.481334	&2399.402527	1.842386	0	0.174671551	
GLB1L	&242.251257	&243.159896	1.817278	0.27728	0.177637626	
MMP14	&2639.56753	&2640.475432	1.815804	0	0.177813551	
CDH1	&4608.271101	&4609.17825	1.814298	999	0.177993503	
LMAN2	&1581.150578	&1582.052991	1.804826	0	0.179130148	
RALB	&1037.272606	&1038.168951	1.79269	0	0.180598757	
IDE	&4641.20719	&4642.096227	1.778074	0	0.182386006	
KLK3	&1480.308231	&1481.196769	1.777076	214.93196	0.182508787	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
LIPA	&2210.488258	&2211.375064	1.773612	4.309	0.182935697	
ANXA4	&1495.058836	&1495.941184	1.764696	0	0.184039855	
TPP2	&6056.469521	&6057.346858	1.754674	0	0.185290223	
SERPINA6	&2120.026666	&2120.900622	1.747912	0.15141	0.186139438	
CLSTN1	&4930.438303	&4931.303065	1.729524	0.10606	0.188471699	
MGAM	&9728.064507	&9728.927208	1.725402	0.43547	0.188999171	
TGM4	&3677.993771	&3678.84331	1.699078	0.35345	0.192408599	
GGH	&1666.693914	&1667.538195	1.688562	0.16667	0.193790638	
PRKAR1A	&1752.776097	&1753.613243	1.674292	0	0.195684641	
SERPINA5	&2277.796282	&2278.62764	1.662716	0.24649	0.197237014	
YWHAG	&1078.462822	&1079.293751	1.661858	0	0.197352647	
ALB	&3215.546615	&3216.375158	1.657086	0.3605	0.197997226	
PAM	&4585.317489	&4586.144077	1.653176	0	0.198527211	
pla2g2A	&857.206428	&858.020827	1.628798	0.173	0.201869383	
SLC35F2	&1867.756254	&1868.567116	1.621724	0	0.202851568	
GDF15	&1711.419552	&1712.209164	1.579224	0	0.208872505	
PRDX4	&1292.08802	&1292.872732	1.569424	0	0.210290683	
PHGDH	&2552.63768	&2553.411826	1.548292	0	0.213387765	
NIF3L1	&1932.997904	&1933.766809	1.53781	0.39928	0.214944077	
CAP1	&2295.370425	&2296.138641	1.536432	0	0.215149677	
BTD	&2766.98932	&2767.755164	1.531688	0.3055	0.215859283	
GPR115	&4130.499258	&4131.257711	1.516906	0.20814	0.218088309	
ST14	&4408.723926	&4409.470848	1.493844	0.32578	0.221620998	
GALNS	&2944.373231	&2945.117923	1.489384	0.23784	0.22231206	
APLP2	&3675.3379	&3676.078949	1.482098	0	0.223446559	
TIMP2	&997.144658	&997.878711	1.468106	0	0.225644762	
PAICS	&2099.947963	&2100.661269	1.426612	0	0.232318159	
LTF	&4529.673042	&4530.383072	1.42006	2.86776	0.233393528	
ACTN4	&4157.51932	&4158.226332	1.414024	0	0.234389533	
GC	&2487.097369	&2487.800239	1.40574	0.20969	0.235764867	
NP	&1452.102079	&1452.802318	1.400478	0	0.236643554	
CNTN3	&5074.403397	&5075.094728	1.382662	0	0.239648232	
APP	&3790.979591	&3791.670579	1.381976	0	0.239764849	
F11R	&1624.88813	&1625.571017	1.365774	0.22436	0.242539298	
MAN2A1	&5436.970954	&5437.645223	1.348538	0.17417	0.245533868	
CCT2	&2334.139993	&2334.80972	1.339454	0	0.247130279	
FAM12A	&791.733298	&792.401653	1.33671	0	0.247615001	
ACAT2	&216.8809	&217.547919	1.334038	999	0.248088122	
CTSB	&1794.344975	&1795.008583	1.327216	0.14596	0.249301099	
PLOD3	&3733.182265	&3733.838151	1.311772	0	0.252074076	
BPIL1	&2383.304126	&2383.949737	1.291222	0	0.255822874	
IL6ST	&4250.078785	&4250.718247	1.278924	0.18681	0.258099195	
DPP4	&555.90004	&556.535622	1.271164	999	0.259548428	
XPNPEP1	&2971.851032	&2972.480888	1.259712	0	0.261705612	
AZGP1	&1711.816525	&1712.435877	1.238704	0.30163	0.265720971	
PFAS	&6779.144495	&6779.750045	1.2111	0.38487	0.271114379	
SPACA3	&1234.95375	&1235.550516	1.193532	999	0.274618266	
THBS2	&5839.130176	&5839.722532	1.184712	0	0.27639881	
TSTA3	&1605.580365	&1606.154967	1.149204	0	0.283715842	
FN1	&12062.68788	&12063.2532	1.130628	0.26147	0.287641425	
CPM	&2172.012328	&2172.565469	1.106282	0	0.29289159	
ALDH1A1	&2397.444032	&2397.992554	1.097044	0	0.294915739	
MINPP1	&2559.336885	&2559.876911	1.080052	0.33072	0.298685924	
SERPINF1	&2281.707943	&2282.247852	1.079818	0.13131	0.298738274	
SMS	&1890.051339	&1890.588587	1.074496	0	0.29993211	
MLPH	&8876.604559	&8877.138299	1.06748	0.31116	0.301515349	
SEMA3C	&8591.571891	&8592.102445	1.061108	0.22801	0.302962612	
IL1RL1	&8847.340844	&8847.866543	1.051398	999	0.305185335	
PRKAR2A	&2021.589629	&2022.107434	1.03561	30.76235	0.308844672	
FMOD	&1738.103908	&1738.616467	1.025118	0	0.311308074	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
CD81	&1098.940209	&1099.451599	1.02278	0	0.311860492	
APOB	&23798.14217	&23798.63607	0.987798	0.69055	0.320281159	
VAT1	&1979.069452	&1979.558019	0.977134	999	0.322907401	
HPX	&2735.741947	&2736.225308	0.966722	0.34478	0.325499065	
ORM1	&1197.087844	&1197.56861	0.961532	725.55277	0.326801193	
LCN1	&1023.505683	&1023.98512	0.958874	999	0.327470736	
SPINT1	&2729.988489	&2730.459252	0.941526	0.35858	0.331885702	
THBS1	&5463.010103	&5463.47954	0.938874	0.29824	0.332567588	
CAMP	&1002.956971	&1003.423901	0.93386	999	0.333861911	
AKR1B1	&1486.588626	&1487.046177	0.915102	0	0.338764322	
SYT7	&2154.823913	&2155.276274	0.904722	0	0.341518717	
SORT1	&8973.965411	&8974.410595	0.890368	0	0.345377603	
LNPEP	&4992.07581	&4992.487759	0.823898	2.75478	0.364042942	
DCD	&648.733988	&649.145905	0.823834	0.28524	0.364061574	
CTSF	&2580.492563	&2580.900883	0.81664	999	0.366164386	
CD109	&7432.591846	&7432.990922	0.798152	0.39648	0.371646466	
PAEP	&996.182074	&996.572265	0.780382	999	0.377024336	
PRKCSH	&2722.40006	&2722.787759	0.775398	999	0.378552301	
ASAH1	&2202.921528	&2203.302596	0.762136	0.37149	0.382660892	
LAMB2	&9314.866365	&9315.245273	0.757816	0.3253	0.384012865	
COMP	&3818.136179	&3818.511766	0.751174	0.2203	0.38610479	
DNASE2	&1920.28249	&1920.641024	0.717068	999	0.397107346	
SEMG2	&3579.007105	&3579.364506	0.714802	2.42674	0.397854259	
GRHPR	&1677.360192	&1677.707335	0.694286	0	0.404710368	
ITIH5	&5267.20688	&5267.553478	0.693196	0.38661	0.405079425	
GAPDHS	&2136.531868	&2136.876671	0.689606	0	0.406298427	
PTPRS	&9652.797172	&9653.138414	0.682484	0	0.408732678	
CPE	&2253.448404	&2253.786556	0.676304	999	0.410862341	
Park7	&839.595737	&839.932912	0.67435	999	0.411539098	
BAIAP2	&2717.454226	&2717.788658	0.668864	0	0.413447949	
DAG1	&4329.470539	&4329.800902	0.660726	999	0.416303755	
NEO1	&6916.573082	&6916.902167	0.65817	0	0.417206746	
GSR	&2856.269515	&2856.597137	0.655244	0.51574	0.418244029	
CCT7	&2532.423868	&2532.751261	0.654786	65.20519	0.418406739	
SDCBP	&1416.66252	&1416.988709	0.652378	0	0.419263763	
tmpRSS2	&3228.411356	&3228.731425	0.640138	0.45928	0.42366083	
SPINT3	&506.413224	&506.732749	0.63905	999	0.424055015	
MSLN	&3967.387766	&3967.706839	0.638146	308.69857	0.424382956	
PRDX6	&1046.826306	&1047.144692	0.636772	10.60621	0.424882126	
IDI1	&1550.89829	&1551.216138	0.635696	999	0.425273649	
PSMA7	&1180.955743	&1181.272569	0.633652	0	0.426018892	
CTSO	&1608.700115	&1609.010236	0.620242	999	0.430957371	
ALAD	&1834.653419	&1834.962328	0.617818	0	0.431859288	
CD14	&1922.453395	&1922.761058	0.615326	999	0.432789495	
LAMP2	&1922.073814	&1922.380517	0.613406	999	0.433508266	
IMPA1	&1610.972772	&1611.277053	0.608562	999	0.435329757	
CRISP3	&1300.697888	&1300.979095	0.562414	0.10888	0.453289237	
UGDH	&2197.739424	&2198.018593	0.558338	19.07624	0.454930664	
CYB5R2	&1468.068068	&1468.345755	0.555374	0.32162	0.456130157	
ALDH7A1	&2686.942715	&2687.207342	0.529254	0	0.466920662	
MANBA	&4390.416528	&4390.679354	0.525652	0.41053	0.468440607	
PODXL2	&2867.82695	&2868.086529	0.519158	0	0.471201076	
LCN2	&1101.995823	&1102.248038	0.50443	180.29835	0.477560059	
OS9	&131.039462	&131.28944	0.499956	999	0.479519456	
RNASE4	&749.641808	&749.890863	0.49811	0.31379	0.480331751	
RAB1A	&880.629337	&880.874008	0.489342	0	0.48422097	
QPCT	&1827.265602	&1827.505666	0.480128	0.35665	0.488364344	
ACPP	&2125.735737	&2125.974577	0.47768	999	0.489475065	
GAS6	&3533.450568	&3533.684725	0.468314	0.23044	0.493763832	
LYZ	&799.783025	&800.016412	0.466774	999	0.494475035	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
GNPDA1	&1287.779669	&1288.010681	0.462024	0	0.49667957	
CFB	&3283.979304	&3284.206277	0.453946	0.43767	0.500466994	
DNASE1	&1527.451687	&1527.678151	0.452928	3.82713	0.500947764	
CFL1	&744.232028	&744.458211	0.452366	0	0.501213515	
ALDOA	&2009.952401	&2010.17818	0.451558	0	0.501596012	
CNDP2	&2404.260858	&2404.486222	0.450728	999	0.501989441	
LIPI	&2582.874266	&2583.098833	0.449134	999	0.502746491	
KRT10	&3012.846183	&3013.068485	0.444604	0.61852	0.50490863	
EGF	&6295.422528	&6295.640514	0.435972	0.48342	0.509073034	
GP2	&2925.423564	&2925.641311	0.435494	0.54847	0.509305367	
ESD	&1288.472463	&1288.688904	0.432882	0.37702	0.510578173	
SLC44A4	&3576.719095	&3576.926766	0.415342	0.4722	0.519270494	
VCP	&3670.885888	&3671.089727	0.407678	0	0.52315042	
ACR	&2431.070541	&2431.271284	0.401486	10.36061	0.526322821	
ORM2	&1234.84941	&1235.048063	0.397306	999	0.52848384	
PGLS	&1263.39282	&1263.589795	0.39395	0.2911	0.530230387	
IDUA	&3710.016025	&3710.208894	0.385738	0.16984	0.534548241	
ANXA7	&2298.59233	&2298.781657	0.378654	0.4066	0.538324474	
SERPING1	&2615.352065	&2615.540651	0.377172	0.44651	0.539120634	
WFDC9	&483.84583	&484.032289	0.372918	0.41432	0.541417989	
ANXA1	&1594.050747	&1594.231232	0.36097	999	0.547968015	
LDHC	&1561.37981	&1561.555407	0.351194	0.38203	0.553438013	
RDX	&2860.302374	&2860.47628	0.347812	999	0.555354325	
SCPEP1	&2264.824731	&2264.995551	0.34164	0.56726	0.558884109	
CAPN1	&3436.042196	&3436.211105	0.337818	0.3357	0.56109143	
C19orf10	&834.363307	&834.526844	0.327074	372.19206	0.567387124	
TFPI2	&1255.902489	&1256.064455	0.323932	0.4222	0.569254184	
IGFBP2	&1366.909339	&1367.068128	0.317578	0	0.573066827	
GALNT6	&2889.411378	&2889.568301	0.313846	0.36871	0.57532966	
CAT	&2660.503143	&2660.659441	0.312596	999	0.576091528	
GSN	&3874.714622	&3874.866882	0.30452	0	0.581062564	
CD151	&1220.600235	&1220.750364	0.300258	999	0.583720723	
RAB3D	&1030.524496	&1030.668793	0.288594	999	0.59112294	
RNASET2	&1452.190009	&1452.334207	0.288396	999	0.591250249	
WFDC8	&1414.710071	&1414.85298	0.285818	2.2677	0.592913003	
EEF2	&4122.24226	&4122.366107	0.247694	0	0.618703504	
RNASE1	&845.786763	&845.905409	0.237292	0.50076	0.626168853	
RAB27A	&1047.224526	&1047.340482	0.231912	0.46639	0.630109719	
fam3B	&1383.72706	&1383.84238	0.23064	1.68273	0.631049684	
GPC1	&2721.744473	&2721.85934	0.229734	999	0.631721134	
SLPI	&797.469714	&797.579666	0.219904	0.44051	0.639113075	
PGCP	&2255.011142	&2255.120086	0.217888	0.46891	0.64065389	
ACRV1	&1557.251169	&1557.354946	0.207554	0.26059	0.648691346	
KRT9	&3261.843732	&3261.944967	0.20247	287.54116	0.652734477	
VTN	&2593.069515	&2593.164927	0.190824	999	0.662231693	
DDT	&576.801995	&576.895286	0.186582	0.55206	0.665776746	
PLA2G7	&2164.408327	&2164.50047	0.184286	0.44753	0.667715502	
CLTC	&7273.995531	&7274.080665	0.170268	0.23651	0.679873737	
PTPRJ	&7429.260013	&7429.339909	0.159792	0.75419	0.689348089	
QSCN6	&3085.279854	&3085.358425	0.157142	0.70153	0.691801556	
GPRC5C	&2499.739535	&2499.81695	0.15483	1.96137	0.693961718	
LGALS3	&1334.465392	&1334.540127	0.14947	0.68571	0.699042361	
TFRC	&4085.258921	&4085.331258	0.144674	0.60108	0.703677939	
ACE	&6849.711752	&6849.776672	0.12984	999	0.71859799	
SEMG1	&3121.115445	&3121.177675	0.12446	0.78678	0.724246714	
AGA	&1771.450092	&1771.511691	0.123198	999	0.725591554	
GAPDH	&1562.746316	&1562.807832	0.123032	0	0.725769026	
SPON2	&1579.710345	&1579.769467	0.118244	0.32723	0.730946872	
SOD3	&1098.254117	&1098.311291	0.114348	999	0.735247281	
CTSH	&1640.781941	&1640.837184	0.110486	0.64426	0.739591509	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
NCSTN	&3554.364348	&3554.41913	0.109564	1.82336	0.740641063	
IGKC	&593.210104	&593.26355	0.106892	0.65844	0.74371068	
CRYZ	&1749.705934	&1749.75794	0.104012	0.64247	0.747067185	
VPS28	&1274.605259	&1274.657103	0.103688	0	0.747447989	
PRSS8	&1906.801607	&1906.852748	0.102282	2.32309	0.749108142	
ARSA	&2673.168009	&2673.219137	0.102256	0.58507	0.74913896	
GPR64	&4793.512673	&4793.563191	0.101036	0.73211	0.750589918	
PROM2	&4693.882166	&4693.931874	0.099416	134.60814	0.752531586	
EEF1G	&2358.728786	&2358.777503	0.097434	0.5268	0.754930939	
SMPD1	&3205.337984	&3205.380089	0.08421	1.48154	0.771671197	
SEPP1	&1952.753016	&1952.792133	0.078234	0.68836	0.779705059	
OLFM4	&2762.404343	&2762.4429	0.077114	1.875	0.781247208	
ANXA3	&1634.838742	&1634.873824	0.070164	0.58196	0.791098146	
TF	&4068.616715	&4068.651584	0.069738	0.80168	0.791718634	
AHCY	&2344.930615	&2344.961384	0.061538	0.3183	0.804081377	
ANPEP	&5015.47298	&5015.503568	0.061176	0.464	0.804646787	
CD38	&1612.368953	&1612.397813	0.05772	0.73353	0.810136555	
SERPINA1	&2322.025452	&2322.048162	0.04542	0.78283	0.831233611	
PGC	&1950.023703	&1950.044897	0.042388	0	0.836881944	
NELL1	&4125.9882	&4126.008542	0.040684	0.63547	0.840149111	
PSMD2	&4158.224264	&4158.234466	0.020404	0	0.886414515	
DPEP3	&2751.163972	&2751.174146	0.020348	160.94868	0.886569438	
SLC1A1	&2563.216718	&2563.225959	0.018482	1.2561	0.891861978	
SORD	&1998.579844	&1998.587143	0.014598	1.21515	0.903831879	
FBP1	&1664.965042	&1664.971088	0.012092	0	0.912438219	
COL9A1	&4609.866751	&4609.871902	0.010302	1.18173	0.919154535	
EFHD2	&1219.578015	&1219.582846	0.009662	0	0.921697673	
PSAP	&2461.68938	&2461.693555	0.00835	0.73615	0.927191976	
IGJ	&899.486539	&899.489775	0.006472	0.90391	0.935880362	
PYGB	&4728.448313	&4728.451077	0.005528	0	0.940731478	
APCS	&1273.340454	&1273.343173	0.005438	1.10997	0.941215045	
DDB1	&5175.568315	&5175.570811	0.004992	0	0.943673063	
SERPINA4	&2416.822594	&2416.824438	0.003688	0	0.951575111	
PGD	&2494.86989	&2494.871115	0.00245	0	0.96052285	
TCP1	&2481.71028	&2481.71143	0.0023	0	0.961749464	
ZPBP	&1823.463437	&1823.464534	0.002194	1.06498	0.962640626	
ANXA2	&1663.301304	&1663.302338	0.002068	0	0.963728488	
CAPZB	&2003.53085	&2003.531876	0.002052	1.0199	0.963868979	
MMP2	&3195.19982	&3195.200845	0.00205	0	0.963886579	
ENO1	&2054.244315	&2054.24508	0.00153	0	0.968798531	
LSAMP	&1597.019759	&1597.020302	0.001086	0	0.97371086	
NUCB2	&2066.585478	&2066.586014	0.001072	0	0.9738808	
CANT1	&2223.109215	&2223.109728	0.001026	0	0.974447142	
CRISP1	&1448.644421	&1448.644866	0.00089	0	0.976200346	
MFAP4	&1278.242166	&1278.242539	0.000746	0	0.978210088	
CCT5	&2476.099963	&2476.100324	0.000722	0	0.978563375	
GLO1	&898.683931	&898.68429	0.000718	0	0.978622825	
SDCBP2	&1529.14264	&1529.142999	0.000718	0	0.978622825	
CAB39	&1447.437038	&1447.437367	0.000658	0	0.9795353	
EDIL3	&2208.964801	&2208.96512	0.000638	0	0.979848646	
PSMA6	&1114.3257	&1114.326018	0.000636	0	0.97988025	
DDAH1	&1302.501685	&1302.501994	0.000618	0	0.980166947	
AMBP	&1761.760621	&1761.760915	0.000588	0	0.980654224	
DCXR	&1306.331931	&1306.332223	0.000584	0	0.980720125	
RAB27B	&1001.97614	&1001.976429	0.000578	0	0.980819402	
TGFB1	&1740.483061	&1740.483337	0.000552	0	0.981255682	
SYT1	&1899.670356	&1899.670624	0.000536	0	0.981529287	
GNMT	&1451.576293	&1451.57655	0.000514	0	0.981912255	
PSMD14	&1271.536848	&1271.537098	0.0005	0	0.982160245	
TNFSF10	&1406.820566	&1406.820799	0.000466	1.02986	0.982777377	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PGM1	&2775.81248	&2775.812712	0.000464	0	0.98281437	
PRDX5	&1042.861753	&1042.861951	0.000396	0	0.984123346	
CKB	&1605.378908	&1605.379093	0.00037	0	0.98465333	
PSMB2	&1082.809967	&1082.810146	0.000358	0	0.984904216	
CLIC1	&1149.184036	&1149.184204	0.000336	0	0.985375353	
GNS	&2820.042364	&2820.042528	0.000328	0	0.985550486	
TSNAX	&1310.494041	&1310.494196	0.00031	0	0.985952518	
IGFBP5	&1175.618587	&1175.618723	0.000272	0	0.986841547	
NBL1	&996.243295	&996.243429	0.000268	0	0.98693865	
PIP	&979.905796	&979.905928	0.000264	0	0.987036481	
MARCKS	&1424.86227	&1424.862386	0.000232	0	0.987847454	
SERPINI1	&1936.734249	&1936.734352	0.000206	0	0.988548595	
GALNT7	&2933.806817	&2933.806915	0.000196	0	0.988829981	
USP14	&2152.875387	&2152.875485	0.000196	0	0.988829981	
KPNB1	&3991.710902	&3991.710999	0.000194	0	0.988887113	
BASP1	&922.687622	&922.687708	0.000172	0	0.989536142	
PSMA1	&1253.11084	&1253.110924	0.000168	0	0.989658524	
GDI2	&2125.47388	&2125.473963	0.000166	0	0.989720261	
TALDO1	&1588.910403	&1588.910482	0.000158	0	0.989971011	
EEF1A1	&2041.953382	&2041.953456	0.000148	0	0.990293555	
ARF1	&802.333419	&802.33349	0.000142	0	0.990492333	
EXTL2	&1509.152161	&1509.152231	0.00014	0	0.990559523	
GSS	&2204.696869	&2204.696939	0.00014	0	0.990559523	
HEXB	&2927.742458	&2927.742527	0.000138	0	0.990627194	
CST6	&707.924382	&707.92445	0.000136	0	0.990695358	
RAB5B	&1050.846189	&1050.846257	0.000136	0	0.990695358	
GM2A	&1026.987412	&1026.987479	0.000134	0	0.990764025	
PKM2	&2963.629459	&2963.629526	0.000134	0	0.990764025	
DEFB129	&916.675777	&916.675842	0.00013	0	0.990902913	
HINT1	&580.023479	&580.023542	0.000126	0	0.991043956	
CD9	&1042.243314	&1042.243374	0.00012	0	0.991259787	
TSG101	&1726.947059	&1726.947119	0.00012	0	0.991259787	
CPVL	&2495.25868	&2495.258739	0.000118	0	0.991332926	
GNB1	&1523.547033	&1523.547092	0.000118	0	0.991332926	
PCMT1	&1290.088816	&1290.088871	0.00011	0	0.99163187	
ACO1	&4249.264306	&4249.26436	0.000108	0	0.99170829	
GSTM3	&1077.412518	&1077.412571	0.000106	0	0.991785421	
RAB14	&906.933411	&906.933464	0.000106	0	0.991785421	
PSMB6	&1148.769222	&1148.769274	0.000104	0	0.991863283	
MMP7	&1413.80642	&1413.806471	0.000102	0	0.991941898	
IQGAP2	&7134.44596	&7134.446011	0.000102	0.98524	0.991941898	
PRCP	&2722.61297	&2722.61302	1E&04	0	0.992021287	
PGK1	&1900.768995	&1900.769043	9.6E&05	0	0.992182485	
RAB3B	&1024.365539	&1024.365585	9.2E&05	0	0.992347077	
PSMA5	&1038.294519	&1038.294565	9.2E&05	0	0.992347077	
FAM3C	&978.945764	&978.945809	9E&05	0	0.992430716	
LZTFL1	&1304.347111	&1304.347155	8.8E&05	0	0.992515289	
tor1B	&1562.057236	&1562.057279	8.6E&05	0	0.992600829	
DNAJB9	&1082.190466	&1082.190508	8.4E&05	0	0.99268737	
TAGLN2	&907.149034	&907.149075	8.2E&05	0	0.992774947	
LDHA	&1655.528365	&1655.528405	8E&05	0	0.992863599	
RAB5C	&1147.438485	&1147.438525	8E&05	0	0.992863599	
CD63	&1057.698308	&1057.698347	7.8E&05	0	0.992953366	
GNPTG	&1708.304086	&1708.304125	7.8E&05	0	0.992953366	
PSMB4	&1249.978414	&1249.978452	7.6E&05	0	0.993044292	
TMEFF2	&1662.60365	&1662.603688	7.6E&05	0	0.993044292	
FAM12B	&709.496256	&709.496292	7.2E&05	0	0.993229806	
PSMA4	&1162.065776	&1162.06581	6.8E&05	0	0.99342055	
RAB2A	&862.788137	&862.788171	6.8E&05	0	0.99342055	
YWHAB	&1085.130045	&1085.130077	6.4E&05	0	0.993616992	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	P&value	k
PPIA	&757.04745	&757.04748	6E&05	0	0.993819675	
PPT1	&1498.798812	&1498.798841	5.8E&05	0	0.993923551	
PURA	&1247.663241	&1247.66327	5.8E&05	0	0.993923551	
RAB13	&919.801983	&919.802011	5.6E&05	0	0.994029234	
BPNT1	&1443.223395	&1443.223422	5.4E&05	0	0.994136823	
PFN2	&782.864765	&782.864791	5.2E&05	0	0.994246422	
GNG12	&317.923056	&317.92308	4.8E&05	0	0.994472138	
SCGB2A1	&560.015018	&560.015042	4.8E&05	0	0.994472138	
CAPZA1	&1243.865901	&1243.865922	4.2E&05	0	0.994829153	
GSTO1	&1164.091209	&1164.091229	4E&05	0	0.994953769	
TIMP3	&905.359003	&905.359022	3.8E&05	0	0.99508154	
CTBS	&1987.622096	&1987.622114	3.6E&05	0	0.995212721	
SPINK2	&513.689197	&513.689213	3.2E&05	0	0.995486507	
UBE2L3	&718.559453	&718.559468	3E&05	0	0.995629828	
YWHAQ	&1126.692108	&1126.692123	3E&05	0	0.995629828	
SH3BGRL2	&468.874796	&468.87481	2.8E&05	0	0.995778011	
TXN	&469.042739	&469.042751	2.4E&05	0	0.996091196	
YWHAE	&1079.03422	&1079.034229	1.8E&05	0	0.996614873	
GCHFR	&390.366005	&390.366013	1.6E&05	0	0.99680847	
ACYP1	&477.581384	&477.58139	1.2E&05	0	0.997236052	
RAC1	&947.657586	&947.657591	1E&05	0	0.997476872	
GSTT1	&1142.872246	&1142.872249	6E&06	0	0.998045592	
PFN1	&648.28184	&648.281841	2E&06	0	0.998871621	
YWHAZ	&991.250676	&991.250677	2E&06	0	0.998871621	
CAPZA2	&1219.831477	&1219.831477	0	0	1	
RALA	&1071.344706	&1071.344706	0	0	1	
ADAM10	&311.838687	&311.838639	&9.6E&05	0	#NUM!	
B4GALT1	&2163.846135	&2163.588074	&0.516122	6.61451	#NUM!	
CCT3	&2975.977828	&2975.977789	&7.8E&05	0	#NUM!	
CD44	&3894.617103	&3893.750367	&1.733472	334.2725	#NUM!	
CLU	&2587.721945	&2586.91637	&1.61115	62.38994	#NUM!	
CPO	&2176.418542	&2176.418513	&5.8E&05	0	#NUM!	
CREG1	&1291.795778	&1115.995481	&351.600594	0	#NUM!	
CYB561	&1914.814223	&1914.675719	&0.277008	999	#NUM!	
GAA	&4987.857151	&4987.565232	&0.583838	30.48989	#NUM!	
GLB1	&3848.958699	&3848.792188	&0.333022	999	#NUM!	
GPX3	&1106.719909	&1104.371909	&4.696	33.41154	#NUM!	
GRN	&3084.500272	&3084.500021	&0.000502	0	#NUM!	
HPRT1	&1071.034428	&1071.034319	&0.000218	0	#NUM!	
KAL1	&3352.698558	&3351.524206	&2.348704	30.38976	#NUM!	
KLK11	&1494.090447	&1494.089233	&0.002428	0	#NUM!	
MPI	&1971.740955	&1971.444652	&0.592606	8.48774	#NUM!	
NAGLU	&3600.101489	&3598.246811	&3.709356	109.26662	#NUM!	
NRP1	&4386.525645	&4385.770376	&1.510538	11.84917	#NUM!	
PEBP4	&1278.40152	&1277.646766	&1.509508	37.66081	#NUM!	
PGM2	&3784.104036	&3784.047769	&0.112534	4.27371	#NUM!	
PI15	&1214.82888	&1214.685355	&0.28705	0	#NUM!	
PLXNB2	&9390.907374	&9388.977077	&3.860594	19.67803	#NUM!	
PPP2R4	&2046.972484	&2046.793173	&0.358622	0	#NUM!	
PRDX1	&898.432201	&898.4322	&2E&06	0	#NUM!	
PSMA2	&1128.425968	&1089.873227	&77.105482	0	#NUM!	
PTN	&769.043929	&769.043926	&6E&06	0	#NUM!	
PTPRF	&9060.437157	&9060.201135	&0.472044	39.5271	#NUM!	
RAB1B	&984.578676	&984.578608	&0.000136	0	#NUM!	
RELN	&16751.46317	&16745.96093	&11.004492	20.7097	#NUM!	
s100A11	&497.122298	&497.122282	&3.2E&05	0	#NUM!	
SELENBP1	&2613.433991	&2613.404888	&0.058206	79.3288	#NUM!	
SERPINC1	&2501.019372	&2501.0192	&0.000344	0	#NUM!	
UBE2N	&635.715109	&635.715016	&0.000186	0	#NUM!	

Control Branch Estimate – LRT

Human

Gene	Free lnL	Fixed lnL	2ΔlnL	branch_w	Pvalue	k
JAG2	-6294.309467	-6315.355034	42.091134	0.01214	8.71173E-11	0.000780031
CARD11	-5917.232279	-5936.242049	38.01954	0.01561	7.00397E-10	
NCOR2	-12227.24599	-12243.33558	32.179184	0.05217	1.40589E-08	
SPTB	-11267.91534	-11282.93796	30.04523	0.08104	4.22086E-08	
RBBP6	-8238.580309	-8251.339034	25.51745	0.02778	4.384E-07	
RALGDS	-4384.69157	-4396.925829	24.468518	0	7.5534E-07	
LRPPRC	-7698.16609	-7709.598292	22.864404	0	1.73842E-06	
SLIT1	-7420.159224	-7431.348588	22.378728	0.02807	2.2384E-06	
MRGPRE	-1600.890334	-1611.803598	21.826528	0	2.98445E-06	
EPHB3	-4498.808065	-4509.718656	21.821182	0	2.99278E-06	
GRIK3	-4315.399281	-4325.908536	21.01851	0.02606	4.54868E-06	
APC2	-11996.37679	-12006.83339	20.9132	0.1021	4.80572E-06	
SIPA1	-4987.144649	-4997.371023	20.452748	0	6.11217E-06	
COL5A2	-6697.633538	-6707.28424	19.301404	0	1.11624E-05	
PLCH2	-7498.457593	-7507.556635	18.198084	0.14157	1.99079E-05	
COL20A1	-6580.359476	-6589.420113	18.121274	0.16805	2.07273E-05	
SQSTM1	-2439.264198	-2448.08777	17.647144	0.03643	2.65914E-05	
CLCN4	-3596.855786	-3605.193675	16.675778	0	4.43436E-05	
PNKP	-2842.954651	-2851.197533	16.485764	0.03532	4.90167E-05	
FZR1	-2351.335332	-2359.507544	16.344424	0	5.28113E-05	
TNS3	-7655.187922	-7663.296432	16.21702	0.07818	5.64844E-05	
DNAI2	-3180.876008	-3188.909017	16.066018	0.0798	6.1172E-05	
MAP4K4	-6064.034436	-6071.999578	15.930284	0	6.57187E-05	
CDC37	-1706.942366	-1714.455146	15.02556	0	0.000106065	
C19orf68	-3319.257217	-3326.68181	14.849186	0.06482	0.000116458	
TBC1D9	-5834.083947	-5841.401746	14.635598	0	0.000130427	
C4orf31	-2782.531257	-2789.64239	14.222266	0	0.000162437	
RNF216	-4383.863948	-4390.928283	14.12867	0	0.000170722	
SEMA4B	-3997.758441	-4004.719947	13.923012	0.20101	0.000190452	
MAT2A	-1791.911247	-1798.793718	13.764942	0	0.000207166	
B4GALT5	-1750.956945	-1757.669283	13.424676	0	0.000248336	
RHOB	-856.477374	-863.180662	13.406576	0	0.000250744	
GCGR	-2922.105247	-2928.616807	13.02312	0.04538	0.000307669	
PCDHB5	-4601.692924	-4608.170045	12.954242	0.13652	0.000319197	
SLC24A4	-2704.591798	-2710.98405	12.784504	0.05226	0.000349502	
PRMT6	-1671.652394	-1677.954762	12.604736	0	0.000384771	
MAP4K5	-5015.981328	-5022.157959	12.353262	0	0.000440217	
MBTPS2	-2423.491701	-2429.572687	12.161972	0	0.000487738	
GFOD2	-1869.084713	-1875.151314	12.133202	0	0.00049532	
PLCB1	-5509.514153	-5515.568032	12.107758	0	0.000502125	
MEGF10	-5514.985371	-5520.980155	11.989568	0.14714	0.000534992	
SFRP1	-1509.071059	-1515.048002	11.953886	0.06314	0.000545335	
ITGB8	-3616.778401	-3622.70112	11.845438	0	0.000578028	
VPS13D	-20747.05963	-20752.93705	11.754852	0.24218	0.000606848	
SCN1B	-1018.578166	-1024.37962	11.602908	0	0.000658488	
PCDH7	-5421.035447	-5426.822783	11.574672	0.04026	0.000668562	
PITPNM1	-6236.479764	-6242.234039	11.50855	0.0996	0.000692768	
ANO1	-4809.008501	-4814.725492	11.433982	0.11798	0.00072113	
EPB41L1	-4096.646982	-4102.350063	11.406162	0.0554	0.000732009	
SHPRH	-8159.354088	-8165.042156	11.376136	0.16987	0.000743937	
SULF2	-4179.670412	-4185.293228	11.245632	0.09981	0.000798106	
GCK	-2423.997651	-2429.56446	11.133618	0	0.000847771	
TBC1D17	-3152.167704	-3157.721298	11.107188	0.11111	0.000859938	
ROR2	-4588.639619	-4594.076337	10.873436	0.12934	0.000975534	
PLB1	-7860.047253	-7865.456806	10.819106	0.17849	0.00100458	
DGAT1	-2574.137197	-2579.535519	10.796644	0	0.001016843	
TBXA2R	-1671.185027	-1676.550486	10.730918	0.04187	0.001053602	
OVOL2	-1301.725758	-1307.066194	10.680872	0	0.00108249	
BCL9L	-7013.222343	-7018.560468	10.67625	0.13991	0.001085198	
MAP3K7	-2660.631102	-2665.963872	10.66554	0	0.0010915	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
SLC4A4	%4931.004958	%4936.327488	10.64506	0	0.001103653	
RAE1	%1759.570235	%1764.826655	10.51284	0	0.001185479	
RAP1GAP2	%3635.794671	%3641.040694	10.492046	0.04711	0.001198895	
PLK2	%3090.317365	%3095.459043	10.283356	0	0.001342356	
RD3	%982.439424	%987.579938	10.281028	0.0446	0.00134405	
ASB1	%1624.850294	%1629.886588	10.072588	0	0.001504915	
ANKRD52	%5052.777624	%5057.812278	10.069308	0.06566	0.001507596	
GOLGA6C	%5058.436874	%5063.445114	10.01648	0.2843	0.001551457	
PNPLA7	%6802.603638	%6807.516755	9.826234	0.26618	0.001720402	
SDHA	%3588.397156	%3593.302279	9.810246	0	0.001735423	
PIAS1	%2899.282588	%2904.139482	9.713788	0	0.001828907	
SMC2	%5402.128586	%5406.901755	9.546338	0	0.002003487	
OR5AS1	%1661.59818	%1666.340972	9.485584	0	0.002070927	
ZNF335	%6610.576176	%6615.241258	9.330164	0.17329	0.002254122	
DCAF12L2	%2618.227844	%2622.885933	9.316178	0.08971	0.002271393	
EPT1	%1771.49599	%1776.061143	9.130306	0	0.002514097	
SUMF1	%1880.682444	%1885.246578	9.128268	0.06966	0.002516899	
HSPBP1	%1503.106431	%1507.649461	9.08606	0	0.002575652	
ALOX15	%3885.324981	%3889.854413	9.058864	0.10672	0.002614243	
SLC25A23	%2100.704301	%2105.206017	9.003432	0	0.002694731	
TSPAN15	%1376.782216	%1381.265211	8.96599	0	0.002750516	
FBXL12	%1532.526452	%1536.992659	8.932414	0	0.002801538	
TGM1	%4090.164333	%4094.583322	8.837978	0.10978	0.002950258	
ECEL1	%3727.328148	%3731.725056	8.793816	0.11465	0.003022533	
ZNF569	%3121.583383	%3125.974417	8.782068	0	0.003042061	
NCKAP1L	%5397.117902	%5401.483191	8.730578	0.11546	0.003129173	
RNF208	%1198.479032	%1202.840802	8.72354	0	0.003141275	
ZNF324B	%3117.199874	%3121.551889	8.70403	0.10175	0.003175073	
SUV39H1	%1814.111869	%1818.463745	8.703752	0	0.003175557	
LAMA4	%8660.592912	%8664.943452	8.70108	0.16257	0.003180216	
CHRDL2	%2445.16753	%2449.508028	8.680996	0.06956	0.003215452	
ARHGAP4	%5883.351311	%5887.604411	8.5062	0.0595	0.003539384	
SYNPO2L	%4885.039447	%4889.200979	8.323064	0	0.003914484	
HIST1H3F	%761.424527	%765.555903	8.262752	0	0.004046674	
DCAF5	%4503.29364	%4507.418127	8.248974	0	0.004077504	
DSCR3	%1519.806034	%1523.919536	8.227004	0.07415	0.004127161	
ABHD4	%1660.455799	%1664.545301	8.179004	0	0.004237802	
ZC4H2	%923.282245	%927.262999	7.961508	0	0.004778259	
KIAA0947	%12219.00842	%12222.98402	7.951196	0.33253	0.004805561	
ZC3H12D	%2708.368136	%2712.337281	7.93829	0.15892	0.004839955	
ADAM9	%3865.273917	%3869.237889	7.927944	0	0.004867708	
GP1BA	%4198.747555	%4202.689841	7.884572	0.14378	0.004985828	
GPT2	%2463.830374	%2467.750315	7.839882	0	0.005110594	
SDAD1	%3554.621949	%3558.519351	7.794804	0	0.005239669	
KIDINS220	%8391.371654	%8395.262424	7.78154	0	0.005278278	
SEMA6B	%4181.396911	%4185.264452	7.735082	0.09551	0.00541581	
CLK4	%2165.182505	%2168.969796	7.574582	0	0.005919711	
PRPF4B	%4588.660254	%4592.357282	7.394056	0.0725	0.006543976	
WDR63	%4324.004435	%4327.682707	7.356544	0.14465	0.00668191	
ZCCHC17	%1050.374557	%1054.051147	7.35318	0	0.006694424	
TMCC3	%2204.32564	%2207.990916	7.330552	0.07474	0.006779223	
ZNF625	%1427.568382	%1431.231841	7.326918	0.0875	0.006792943	
CYP4F11	%2992.682157	%2996.296619	7.228924	0.13362	0.007173819	
FAAH2	%2752.233819	%2755.844607	7.221576	0	0.007203244	
ZBTB38	%5739.803493	%5743.406651	7.206316	0.12572	0.007264746	
ALKBH3	%1305.46778	%1309.03718	7.1388	0	0.007543362	
LGALS7	%625.759122	%629.326793	7.135342	0	0.007557923	
VPS52	%3325.404053	%3328.920217	7.032328	0	0.008005122	
CHL1	%6212.607585	%6216.113191	7.011212	0.19033	0.008100083	
MLXIPL	%3536.637921	%3540.13098	6.986118	0.12876	0.008214432	0.009360374

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
KANK3	%4442.084644	%4445.506446	6.843604	0.18053	0.008895919	0.009438378
GPR179	%14281.29379	%14284.65037	6.713148	0.29731	0.009570463	0.009516381
PDZD7	%2714.570507	%2717.921089	6.701164	0	0.009634999	0.009594384
HELB	%5542.125914	%5545.468237	6.684646	0.20363	0.009724683	0.009672387
SLC35C1	%1829.497819	%1832.835033	6.674428	0.06431	0.00978059	0.00975039
DLEC1	%9086.013436	%9089.324446	6.62202	0.34088	0.010072553	0.009828393
THY1	%745.588387	%748.886322	6.59587	0	0.01022156	
FKRP	%2437.245959	%2440.534914	6.57791	0	0.010325206	
ADAM29	%4768.794647	%4772.025514	6.461734	0.18449	0.011022203	
CHMP5	%937.877506	%941.094312	6.433612	0	0.011198063	
CDK9	%1677.562915	%1680.768151	6.410472	0	0.011344925	
CPA5	%2349.041357	%2352.237075	6.391436	0.12519	0.011467223	
SV2B	%3190.749229	%3193.900003	6.301548	0.08816	0.012063259	
KCNB1	%3940.826399	%3943.973654	6.29451	0	0.012111249	
TEKT5	%2695.334827	%2698.3967	6.123746	0.19198	0.013337786	
SLC6A4	%3061.378597	%3064.436276	6.115358	0.18463	0.013401227	
RBCK1	%2218.619099	%2221.664909	6.09162	0	0.01358245	
GCOM1	%2848.782074	%2851.822659	6.08117	0.09153	0.013663025	
TBR1	%2895.591077	%2898.623424	6.064694	0	0.013791065	
DUSP1	%1011.279256	%1014.289549	6.020586	0	0.014139951	
SIX6	%1100.224406	%1103.208106	5.9674	0	0.014572752	
CEACAM6	%2792.880767	%2795.856762	5.95199	0.17964	0.014700682	
ACCN1	%2710.977466	%2713.930909	5.906886	0	0.015081809	0.011154446
ADNP2	%5611.187908	%5614.119197	5.862578	0	0.015466125	0.011232449
PPIG	%3510.137988	%3513.061537	5.847098	0	0.01560276	0.011310452
SEC14L5	%3456.495687	%3459.415272	5.83917	0.15072	0.015673218	0.011388456
CHST2	%2516.214411	%2519.107669	5.786516	0	0.016149564	0.011466459
NUP88	%3816.599313	%3819.492179	5.785732	0.15118	0.016156768	0.011544462
ADH1A	%2352.66335	%2355.52271	5.71872	0.09841	0.016784963	
SCG3	%2151.488002	%2154.335122	5.69424	0	0.017020682	
TNFSF9	%1175.145037	%1177.964422	5.63877	0.09638	0.017567527	
DENND4B	%7194.452058	%7197.261012	5.617908	0.13943	0.017777857	
CNTFR	%1738.554024	%1741.353455	5.598862	0.09305	0.017972148	
PER3	%6656.631317	%6659.415025	5.567416	0.36338	0.018297744	
GUCA1B	%890.171812	%892.916615	5.489606	0	0.019129854	
DCAF7	%1558.854472	%1561.577741	5.446538	0	0.019607145	
KCNG2	%1852.606949	%1855.312091	5.410284	0.03221	0.020018459	
NXT1	%642.059909	%644.756137	5.392456	0	0.020223987	
DNAJC17	%1457.909828	%1460.584289	5.348922	0	0.020735087	
C19orf47	%2053.974436	%2056.624899	5.300926	0	0.02131409	
CNTN6	%5057.83508	%5060.481653	5.293146	0.15	0.02140951	
ZNF235	%3660.649767	%3663.287565	5.275596	0.14871	0.021626383	
FAM120A	%5421.435648	%5424.07012	5.268944	0	0.021709178	
TNFAIP8L3	%1464.30402	%1466.937526	5.267012	0	0.021733287	
PRSS55	%2131.638519	%2134.258353	5.239668	0.18115	0.022077487	
PRKCD	%3135.974559	%3138.587659	5.2262	0.08401	0.02224909	
TTLL9	%2361.261837	%2363.871968	5.220262	0.15323	0.022325187	
RPS12	%639.68747	%642.284274	5.193608	0	0.022670104	
IL10RA	%3126.143197	%3128.73714	5.187886	0.22783	0.022744867	
OR51F2	%1553.565702	%1556.157007	5.18261	999	0.022814029	
STX2	%1321.503358	%1324.077942	5.149168	0	0.023257514	
AGPAT2	%1422.224505	%1424.79667	5.14433	0.08927	0.023322409	
MAGEA8	%1512.371439	%1514.933679	5.12448	0	0.023590638	
RC3H1	%5132.529154	%5135.089198	5.120088	0.1115	0.023650417	
KLRG2	%2204.779534	%2207.332978	5.106888	0.14897	0.023831029	
CASP8	%2452.586108	%2455.135326	5.098436	0	0.023947427	
DDB2	%2011.224	%2013.75888	5.06976	0	0.024346754	
NDP	%595.147685	%597.680208	5.065046	0	0.024413057	
GSC	%1065.297847	%1067.828879	5.062064	0.06466	0.024455097	
HLF	%1269.629001	%1272.141031	5.02406	0	0.024997491	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
TMEM121	%1354.624482	%1357.126641	5.004318	0.06394	0.025284163	
NR2C2	%2829.727489	%2832.229471	5.003964	0	0.025289335	
CDC20	%2289.954552	%2292.43921	4.969316	0	0.025800849	
KIAA0562	%4760.426024	%4762.890394	4.92874	0.24548	0.02641357	
RABEP1	%3980.734476	%3983.196425	4.923898	0.17385	0.02648769	
PNPT1	%3659.50524	%3661.966974	4.923468	0.15576	0.026494283	
ACOT12	%2906.95138	%2909.390897	4.879034	0.16105	0.027184829	
ZNF570	%2394.267639	%2396.705757	4.876236	0	0.027228934	
C21orf59	%1401.312574	%1403.745137	4.865126	0.09869	0.027404797	
ARV1	%1316.36415	%1318.786251	4.844202	0	0.027739224	
CENPT	%3151.631791	%3154.034944	4.806306	999	0.028355767	
GJA4	%1636.85368	%1639.249831	4.792302	0.09806	0.028587196	
MOCS3	%2331.926257	%2334.297694	4.742874	0	0.029419884	
ZFP37	%3098.12633	%3100.479849	4.707038	193.36647	0.030039366	
WISP3	%1792.461747	%1794.814786	4.706078	0.18157	0.030056147	
ZMYND17	%2328.053635	%2330.392596	4.677922	0.17875	0.030552685	
ASCC3	%10025.67686	%10028.00155	4.649378	0.21136	0.031064802	
TACR2	%1978.396068	%1980.718147	4.644158	0.24053	0.03115942	
PLEKHB2	%1115.484988	%1117.798333	4.62669	0	0.031478236	
MED19	%1132.811498	%1135.091969	4.560942	0	0.032709078	
ZC3H13	%7602.039383	%7604.311193	4.54362	0.16738	0.033041646	
CMBL	%1195.371016	%1197.637596	4.53316	0	0.033244178	
C1QTNF7	%1370.712712	%1372.965214	4.505004	0	0.033795817	
ISYNA1	%2711.4572	%2713.679406	4.444412	0.1426	0.035015646	
GPR176	%2457.059983	%2459.24223	4.364494	0.11128	0.03669538	
ME2	%2646.27449	%2648.439821	4.330662	0.11246	0.037431685	
ADAMTS8	%4012.672244	%4014.836409	4.32833	0.27034	0.037483004	
METAP1D	%1549.938698	%1552.085413	4.29343	0.11273	0.038259906	
PRRC1	%2120.341832	%2122.481918	4.280172	0.11583	0.038559446	
KDM5D	%8474.566259	%8476.699305	4.266092	0.38478	0.038880252	
BROX	%1818.441594	%1820.553271	4.223354	0.11446	0.039871274	
USP7	%4825.010202	%4827.110751	4.201098	0.11529	0.040397814	
DACT2	%4065.044315	%4067.136751	4.184872	0.31498	0.040786293	
ZNF275	%2173.710734	%2175.786298	4.151128	0.10577	0.041606798	
RFX7	%6744.09695	%6746.168338	4.142776	0.23113	0.041812547	
GPR39	%2381.250458	%2383.303011	4.105106	0.15392	0.042753911	
TSSK4	%1832.62866	%1834.674787	4.092254	0.10784	0.043080156	
COPS4	%1959.825584	%1961.864741	4.078314	0.11861	0.04343698	
C20orf160	%2426.376763	%2428.414342	4.075158	0	0.043518196	
TMEM43	%2110.144477	%2112.172216	4.055478	0.11869	0.044028252	
GLYAT	%1577.31339	%1579.337244	4.047708	0.12015	0.04423136	
RNF34	%1774.181677	%1776.187443	4.011532	0	0.045190071	
CAPN7	%3743.398902	%3745.395604	3.993404	0.17702	0.045678694	
ZNF157	%2378.923944	%2380.919056	3.990224	0.12206	0.04576498	
C11orf84	%2730.770539	%2732.72197	3.902862	0.1745	0.048203925	
KLHDC4	%2858.165511	%2860.094925	3.858828	0.25953	0.049484884	
ZNF528	%3226.603882	%3228.527744	3.847724	0.26026	0.049813544	0.017706708
STAT5B	%3676.170084	%3678.064192	3.788216	0.12765	0.051614633	0.017784711
RESP18	%1249.505989	%1251.397056	3.782134	999	0.051802553	0.017862715
RAB17	%1171.3083	%1173.184693	3.752786	0.22186	0.052719571	
MIER1	%1903.160719	%1905.025112	3.728786	0	0.053482252	
CD2AP	%3055.096559	%3056.950998	3.708878	0.2562	0.054123762	
MSL2	%2520.952103	%2522.802549	3.700892	0	0.054383387	
PIP4K2C	%1757.571574	%1759.41605	3.688952	0.13231	0.054774022	
PCDHA3	%4896.663832	%4898.500644	3.673624	0.12937	0.055279865	
YLPM1	%9690.256714	%9692.083186	3.652944	0.25342	0.055970195	
LDB3	%3931.500842	%3933.326588	3.651492	0	0.056019007	
CCDC73	%5509.477441	%5511.297702	3.640522	0.28658	0.056389252	
ARHGEF25	%2845.692211	%2847.502637	3.620852	0.13501	0.057059645	
PTTG2	%1128.609285	%1130.413553	3.608536	0.13389	0.057483702	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
HRH3	%2194.303914	%2196.101509	3.59519	0.09579	0.057947004	
C11orf20	%1249.57929	%1251.375287	3.591994	0	0.05805854	
FAM167A	%1035.122666	%1036.909364	3.573396	0.17595	0.058712125	
GNAO1	%2115.173281	%2116.944474	3.542386	0	0.059819353	
ABCB11	%6822.358278	%6824.122307	3.528058	0.38869	0.060338422	
RCN2	%1491.199061	%1492.961273	3.524424	0	0.060470833	
STUB1	%1347.877786	%1349.633303	3.511034	0	0.060961398	
LAIR1	%1742.000284	%1743.752745	3.504922	0.21334	0.061186727	
ZNF592	%5979.225333	%5980.95176	3.452854	0.1418	0.063142652	
ZNF574	%4509.203923	%4510.915253	3.42266	0.14184	0.064307317	
UNC13C	%10553.97582	%10555.68198	3.412322	0.35949	0.06471133	
GNPAT	%3338.401019	%3340.081037	3.360036	0.21426	0.066796608	
TMEM61	%1208.73832	%1210.417383	3.358126	0	0.066874129	
CCDC132	%4370.033345	%4371.709431	3.352172	0.1847	0.0671164	
NPY1R	%1729.927902	%1731.58583	3.315856	0.14601	0.068614579	
MDM4	%2142.534285	%2144.178999	3.289428	0.12877	0.069727309	
CYTH1	%1782.921618	%1784.564791	3.286346	0	0.069858327	
CDK13	%6756.551912	%6758.185347	3.26687	0.14957	0.070692381	
COQ3	%1948.41737	%1950.050104	3.265468	999	0.070752832	
CDC23	%2708.114353	%2709.72676	3.224814	0.15011	0.072530036	
ZFP57	%2763.580853	%2765.154006	3.146306	999	0.076099057	
DBX1	%2071.82081	%2073.393398	3.145176	0.13993	0.076151785	
ORC2	%2609.511964	%2611.074262	3.124596	0.19683	0.077118985	
TBCB	%1153.056132	%1154.616402	3.12054	0	0.077311159	
LTK	%4352.386998	%4353.941663	3.10933	0.17888	0.077844977	
PMFBP1	%5170.032262	%5171.58457	3.104616	0.38756	0.07807064	
TMED4	%1062.24842	%1063.800508	3.104176	0	0.078091739	
NR1D2	%2650.239441	%2651.79087	3.102858	0.19879	0.078154977	
S100A4	%429.462564	%431.011969	3.09881	0	0.078349546	
ABCD3	%3242.455918	%3243.996926	3.082016	0	0.079162346	
UBLCP1	%1381.3107	%1382.84875	3.0761	0	0.07945083	
HIST1H2AJ	%620.351488	%621.855889	3.008802	0	0.082813476	
MRPL43	%1378.417739	%1379.92027	3.005062	0	0.083004801	
RGS18	%1077.886436	%1079.387868	3.002864	0	0.083117466	
DDTL	%773.616085	%775.117118	3.002066	0	0.083158411	
SUSD3	%1285.803076	%1287.290882	2.975612	0.12717	0.084528152	
RPL26	%712.405319	%713.888508	2.966378	0	0.085011997	
DIRC2	%2215.707323	%2217.179706	2.944766	0.16411	0.086156176	
PADI1	%3540.743125	%3542.21222	2.93819	0.27422	0.08650762	
RBP7	%646.112962	%647.556179	2.886434	0	0.089328444	
HIST1H3G	%641.629555	%643.066003	2.872896	0	0.09008264	
MARK2	%3519.922517	%3521.347584	2.850134	0	0.091366321	
AGGF1	%3399.432915	%3400.831635	2.79744	999	0.094414945	
HNRPLL	%2492.535923	%2493.930784	2.789722	0	0.094870685	
MAGEB3	%1940.715061	%1942.100188	2.770254	999	0.096030922	
EBI3	%1154.006764	%1155.383327	2.753126	0	0.097064489	
PNMA1	%1586.624506	%1587.99337	2.737728	0	0.098004017	
NPY5R	%1990.230878	%1991.599373	2.73699	0	0.098049296	
CWC22	%4319.253885	%4320.6208	2.73383	0.30302	0.098243429	
EXPH5	%10701.14773	%10702.51448	2.733512	0.44524	0.098262988	
DERL1	%1106.154167	%1107.513582	2.71883	0	0.099170684	
POU2F2	%2165.729979	%2167.08838	2.716802	0	0.09929678	
TSPAN8	%1576.406449	%1577.760964	2.70903	0.15012	0.099781647	
CCDC115	%881.21492	%882.568444	2.707048	0	0.099905711	
ZBP1	%2566.363019	%2567.710945	2.695852	0.32938	0.100609695	
PPM1E	%3396.178817	%3397.525547	2.69346	0	0.100760802	
WSB2	%1866.424284	%1867.76227	2.675972	0	0.10187311	
TJP2	%6016.434657	%6017.771671	2.674028	0.33056	0.101997583	
DEF8	%2631.800489	%2633.125344	2.64971	0.17761	0.103568789	
LHFPL2	%1093.113696	%1094.434326	2.64126	0	0.104120936	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
ARCN1	%2281.851079	%2283.167852	2.633546	0	0.104627807	
PAX9	%1574.336248	%1575.650367	2.628238	0	0.104978154	
HSPB2	%813.49775	%814.807634	2.619768	0	0.10553987	
ELF4	%3310.886367	%3312.194164	2.615594	0.14983	0.105817894	
SPIB	%1095.60844	%1096.911366	2.605852	0.14698	0.106469924	
LRRTM3	%2556.56374	%2557.861907	2.596334	0	0.10711122	
PRKRIP1	%906.128128	%907.42047	2.584684	0	0.107901941	
ABHD10	%1500.480331	%1501.769233	2.577804	0	0.108371915	
TMEM208	%764.142591	%765.429325	2.573468	0	0.108669263	
CAPN11	%3810.104021	%3811.381975	2.555908	999	0.109882667	
NPFFR1	%2089.41524	%2090.689053	2.547626	0.27753	0.11046012	
TFEC	%1628.156421	%1629.425939	2.539036	0	0.111062576	
MSRB2	%998.846962	%1000.110663	2.527402	0	0.111884294	
FAM131A	%1321.354391	%1322.616615	2.524448	0	0.112094	
RBBP7	%2093.445797	%2094.705982	2.52037	0	0.112384213	
LPAR3	%1796.934687	%1798.188056	2.506738	0.23529	0.113360362	
DNAJC5G	%1131.212935	%1132.457351	2.488832	999	0.114656786	
PPP1R12A	%4527.358627	%4528.601354	2.485454	0.15326	0.114903188	
RGS8	%885.247336	%886.489203	2.483734	0.15214	0.115028874	
PLS3	%2742.932225	%2744.17286	2.48127	0	0.115209191	
UPF2	%5623.5589	%5624.787963	2.458126	0.1559	0.116918199	
SNRPA1	%1117.342391	%1118.56859	2.452398	0	0.117345478	
DDHD2	%3298.419508	%3299.645479	2.451942	0	0.117379567	
PDK3	%1819.564695	%1820.785859	2.442328	0	0.118100837	
HNRNPD	%1491.330243	%1492.550866	2.441246	0	0.118182318	
ZNF652	%2780.453262	%2781.668776	2.431028	0.15636	0.118954866	
DMGDH	%4203.815444	%4205.021797	2.412706	0.30431	0.120354162	
ANGEL2	%2366.273444	%2367.478959	2.41103	0	0.120483069	
SH3D21	%4135.23088	%4136.434376	2.406992	0.43642	0.120794275	
ACSM1	%3134.396307	%3135.597557	2.4025	0.30625	0.121141516	
SOCS4	%1990.074289	%1991.267331	2.386084	0.15558	0.122419949	
EXD1	%2904.651783	%2905.841947	2.380328	999	0.122871746	
PLP1	%1162.116293	%1163.304468	2.37635	0	0.123185066	
GPR89A	%1485.508071	%1486.689196	2.36225	0	0.12430279	
TTF1	%5078.339964	%5079.51628	2.352632	0.37088	0.125071679	
CAPS2	%2949.98322	%2951.159491	2.352542	0.25592	0.125078898	
FGF2	%1339.286176	%1340.453774	2.335196	0	0.12647907	
C4orf7	%517.288919	%518.445246	2.312654	0	0.128324779	
FBL	%1605.707938	%1606.85428	2.292684	0	0.129984971	
ROBO4	%5267.153983	%5268.296477	2.284988	0.45938	0.130631152	
LHFPL5	%930.232252	%931.371977	2.27945	0	0.131098357	
SLC7A14	%3656.530939	%3657.665967	2.270056	0.25427	0.131895136	
ATAD5	%9296.067923	%9297.198347	2.260848	0.4476	0.132681389	
GIMAP2	%1823.522341	%1824.641069	2.237456	0.25615	0.134702439	
C11orf40	%1330.423343	%1331.539241	2.231796	999	0.135196615	
MBD6	%4426.18323	%4427.29628	2.2261	0.20654	0.135695983	
ENOPH1	%1178.058797	%1179.161594	2.205594	0	0.137510917	
CES5A	%3265.962353	%3267.05958	2.194454	0.38381	0.138508281	
LAPTM4B	%2137.164623	%2138.252341	2.175436	0.17499	0.140229769	
HMGCR	%4421.102634	%4422.186202	2.167136	0.17525	0.140988594	
MAP2	%8749.80403	%8750.886269	2.164478	0.32376	0.141232575	
FAM126B	%2587.553567	%2588.635243	2.163352	0	0.141336075	
AHSA1	%1500.732916	%1501.813958	2.162084	0	0.14145273	
IFI44	%2282.481488	%2283.556416	2.149856	0.34383	0.142583262	
SOAT2	%2726.288078	%2727.35662	2.137084	0.17779	0.143774953	
PFDN6	%550.715284	%551.782219	2.13387	0	0.144076597	
ASH2L	%2900.959772	%2902.025996	2.132448	0.26543	0.144210284	
G6PC	%1733.806286	%1734.865835	2.119098	0.17985	0.145472197	
MBLAC2	%1291.541856	%1292.601326	2.11894	0.26616	0.145487206	
SLC45A2	%2718.341244	%2719.377465	2.072442	0.39235	0.149981205	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
TMEM92	%872.009801	%873.032231	2.04486	0.18823	0.152721033	
POGK	%2869.515591	%2870.53434	2.037498	0.18508	0.153461882	
RABGGTA	%2637.725162	%2638.701085	1.951846	0.28147	0.162388065	
FAM64A	%1281.020082	%1281.99525	1.950336	999	0.162550648	
ASPH	%3783.693034	%3784.665796	1.945524	0.28167	0.16307	
FMO6P	%713.028718	%713.98756	1.917684	0.23431	0.1661122	
ZNF561	%3224.300452	%3225.258998	1.917092	0.37007	0.166177591	
CCL24	%713.060204	%714.018528	1.916648	0.23441	0.166226654	
TTYH1	%2168.06299	%2169.007083	1.888186	0.31179	0.169406665	
NSUN3	%1619.478314	%1620.421518	1.886408	0.28696	0.169607621	
APOBEC1	%1254.752469	%1255.694373	1.883808	999	0.169901974	
SMR3B	%486.078918	%487.015827	1.873818	0	0.171038439	
FAM165B	%284.580306	%285.501344	1.842076	0	0.174707822	
PTPRCAP	%1095.711145	%1096.626004	1.829718	0.20133	0.176160858	
LETM2	%2521.673364	%2522.582403	1.818078	999	0.177542228	
UGT1A3	%2747.920659	%2748.81855	1.795782	0.39161	0.180223268	
GMNN	%1035.095007	%1035.991261	1.792508	0.24619	0.180620887	
SECTM1	%1274.887443	%1275.781589	1.788292	0.37069	0.181134404	
SLC5A3	%3196.40743	%3197.297681	1.780502	0.28388	0.182087696	
C9orf9	%840.386221	%841.26974	1.767038	0.06096	0.183749075	
ATG16L1	%2891.762896	%2892.645709	1.765626	0.20817	0.183924324	
GFRAL	%2056.058564	%2056.939787	1.762446	999	0.184319716	
CCDC69	%1442.224089	%1443.104818	1.761458	0.20776	0.184442762	
C4orf33	%1019.88122	%1020.753034	1.743628	999	0.186679791	
PRRG1	%979.291444	%980.157167	1.731446	0.20929	0.188226335	
OAS1	%2333.604153	%2334.451892	1.695478	999	0.192880419	
OR1A2	%1539.581173	%1540.405641	1.648936	0.21946	0.199103809	
ZFP64	%3245.509871	%3246.314181	1.60862	0.33145	0.204685896	
TMC8	%3630.99583	%3631.79019	1.58872	0.42575	0.207509105	
SLC16A8	%2346.077704	%2346.868321	1.581234	0.22593	0.208583035	
PM20D2	%2164.077828	%2164.861959	1.568262	0.2263	0.210459593	
ZNF20	%2601.684232	%2602.464096	1.559728	999	0.211705051	
LYG1	%1102.832283	%1103.590347	1.516128	0.21699	0.218206384	
MRPL21	%1127.886005	%1128.642833	1.513656	999	0.21858206	
COX5B	%678.309537	%679.065635	1.512196	999	0.218804302	
SMPD3	%3077.385606	%3078.138037	1.504862	0.14589	0.219924777	
MLLT6	%4823.822819	%4824.572287	1.498936	0.39307	0.220835148	
VSIG1	%2092.55652	%2093.305504	1.497968	999	0.220984283	
FAM111A	%3300.058278	%3300.801282	1.486008	3.0891	0.222836876	
STH	%711.808888	%712.544578	1.47138	999	0.225128087	
C10orf11	%975.668793	%976.403116	1.468646	0.23786	0.225559446	
ATAD2	%6457.586544	%6458.319559	1.46603	0.48214	0.225973116	
NPFF	%606.317769	%607.044132	1.452726	999	0.228091046	
OR6X1	%1670.833581	%1671.537655	1.408148	3.32697	0.235364079	
C11orf80	%3563.80095	%3564.502299	1.402698	0.52138	0.236272359	
ALDH1A3	%2496.754897	%2497.453019	1.396244	0.21908	0.237353461	
OR1N1	%1422.235171	%1422.930859	1.391376	999	0.238172864	
OR1N2	%1645.55232	%1646.237756	1.370872	0.42938	0.241662119	
CCDC68	%1602.613155	%1603.298001	1.369692	999	0.241864809	
CPT1B	%3719.615905	%3720.278521	1.325232	0.3049	0.249655224	
CEP78	%3500.865316	%3501.527149	1.323666	0.41487	0.249935177	
TOP3A	%5195.326675	%5195.982223	1.311096	2.89737	0.252196314	
LEPREL4	%1974.879768	%1975.53382	1.308104	0.30391	0.252738224	
MOAP1	%1703.526501	%1704.175477	1.297952	999	0.254587653	
WDR74	%1902.460245	%1903.107593	1.294696	999	0.255184338	
KPTN	%2402.784173	%2403.430067	1.291788	0.30948	0.255718706	
MARVELD3	%1940.809696	%1941.453745	1.288098	0.38538	0.256398761	
HIST1H2AL	%744.312769	%744.954583	1.283628	0	0.257225558	
TMEM105	%686.599624	%687.238641	1.278034	999	0.2582649	
CDT1	%2994.56027	%2995.198536	1.276532	0.39148	0.258544848	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
L3MBTL1	%3976.056051	%3976.691425	1.270748	0.26231	0.259626403	
DEFB110	%339.860535	%340.493278	1.265486	999	0.260615214	
IFI27L1	%553.588938	%554.214898	1.25192	999	0.263186084	
EFS	%2802.278514	%2802.895741	1.234454	0.36648	0.266542587	
KMO	%2494.275826	%2494.892363	1.233074	999	0.26681005	
ATP10D	%7192.179408	%7192.793361	1.227906	0.52583	0.267814658	
PYGO2	%1791.523303	%1792.137025	1.227444	0.27061	0.267904696	
CLEC4E	%1201.0335	%1201.639885	1.21277	999	0.270784224	
CHM	%3027.859479	%3028.445425	1.171892	999	0.279012826	
S1PR3	%1732.211221	%1732.789948	1.157454	0.20194	0.281994185	
OR5H6	%1746.153869	%1746.726057	1.144376	0.4801	0.284729552	
PCDHA1	%5052.774186	%5053.340731	1.13309	0.33679	0.287117195	
RTN4RL2	%1990.875835	%1991.418809	1.085948	0.18632	0.297370748	
CXCR5	%1773.875205	%1774.404549	1.058688	0.21796	0.303514613	
PSMD9	%1063.093022	%1063.620157	1.05427	999	0.304525713	
KRTAP4%7	%1359.212504	%1359.739414	1.05382	999	0.304628944	
KRT36	%2448.738085	%2449.248567	1.020964	0.52022	0.312290455	
SCT	%523.32595	%523.823951	0.996002	999	0.318279845	
DNAJC30	%1246.98277	%1247.47837	0.9912	999	0.319449261	
ZNF117	%3441.23908	%3441.731232	0.984304	999	0.321138523	
SDC2	%945.319905	%945.807675	0.97554	3.80162	0.323302394	
ADRA1B	%2498.352835	%2498.827697	0.949724	0.19774	0.329789561	
TNIP3	%2039.616887	%2040.078731	0.923688	0.3731	0.336508484	
CYLC1	%3426.182102	%3426.641931	0.919658	0.3744	0.337564786	
CACNG6	%1273.412997	%1273.869598	0.913202	999	0.339266259	
ZNF30	%3412.869594	%3413.316734	0.89428	0.53032	0.344320098	
BLNK	%2338.575592	%2339.017408	0.883632	0.38282	0.34720883	
TRAIP	%2304.883359	%2305.32436	0.882002	0.47644	0.347653934	
NT5M	%973.374645	%973.813393	0.877496	0.22969	0.348888423	
CA5A	%1403.828126	%1404.262865	0.869478	999	0.351099861	
C8orf39	%460.662939	%461.083433	0.840988	999	0.359114355	
GOLGA5	%3484.025483	%3484.442682	0.834398	0.53303	0.361003877	
MS4A7	%1299.761419	%1300.174726	0.826614	999	0.363253457	
GPRASP2	%4100.621457	%4101.033534	0.824154	2.43135	0.363968427	
GCDH	%2328.192919	%2328.604504	0.82317	0.2603	0.36425496	
CNPY1	%412.89422	%413.302442	0.816444	999	0.366221912	
WFDC11	%493.790202	%494.191682	0.80296	331.38799	0.370209849	
C17orf51	%1210.070461	%1210.467722	0.794522	999	0.372736265	
VCX2	%904.081246	%904.472852	0.783212	2.40479	0.376160593	
TTC29	%2306.779566	%2307.170597	0.782062	0.40549	0.376511248	
TIAF1	%617.317777	%617.705646	0.775738	999	0.378447789	
WFDC6	%441.479338	%441.86328	0.767884	999	0.380872451	
MYL6B	%1176.913887	%1177.294056	0.760338	0.27916	0.383222767	
USP1	%3480.304985	%3480.68045	0.75093	0.43511	0.386181947	
OR14A2	%1605.726417	%1606.097462	0.74209	0.43476	0.388992198	
SEC13	%1770.812726	%1771.183072	0.740692	0.38693	0.389439296	
FAM103A1	%518.952045	%519.321726	0.739362	0.27898	0.389865329	
PINX1	%1712.025225	%1712.393109	0.735768	0.4139	0.39101992	
TMEM194A	%2095.74847	%2096.11612	0.7353	999	0.391170628	
TSSK2	%1691.815766	%1692.175043	0.718554	17.83598	0.396618633	
MTIF3	%1539.138595	%1539.494799	0.712408	288.11553	0.398645571	
FOLR2	%1277.165096	%1277.520661	0.71113	0.44759	0.399068934	
C9orf142	%1043.224947	%1043.575658	0.701422	999	0.402306294	
IL17REL	%1708.600357	%1708.948443	0.696172	0.45668	0.404072955	
TAC4	%627.594911	%627.939971	0.69012	999	0.406123567	
BCCIP	%1571.301915	%1571.643366	0.682902	999	0.408589219	
GAL3ST4	%2425.397819	%2425.738042	0.680446	0.43124	0.409433188	
WDFY2	%1822.960304	%1823.295256	0.669904	0.43477	0.413085079	
RBM7	%1282.837387	%1283.169523	0.664272	0.30268	0.415055806	
AGAP10	%4366.793975	%4367.124347	0.660744	0.7089	0.416297406	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
SREK1	%2713.232794	%2713.562598	0.659608	0.26091	0.416698368	
IRF8	%2086.522953	%2086.852444	0.658982	0.30332	0.416919566	
IFNA2	%1005.649456	%1005.975155	0.651398	999	0.419613301	
CCRL1	%1662.586407	%1662.911348	0.649882	0.44063	0.420154871	
USP18	%2027.653401	%2027.976111	0.64542	0.30149	0.421754924	
NLGN3	%3583.499762	%3583.819187	0.63885	999	0.424127536	
ADAT2	%895.643293	%895.957765	0.628944	7.89283	0.427742926	
C14orf181	%762.006796	%762.320665	0.627738	999	0.428186246	
H2AFB3	%626.311264	%626.620144	0.61776	0.28522	0.431880904	
EPSTI1	%2231.252704	%2231.555494	0.60558	1.94606	0.436456889	
GALNT12	%3049.358437	%3049.658228	0.599582	999	0.438737556	
C1orf27	%2080.411648	%2080.709477	0.595658	999	0.440239508	
MAP4K3	%4019.706651	%4019.999803	0.586304	0.47708	0.443851908	
NUDCD1	%2710.037571	%2710.325248	0.575354	0.33262	0.448139189	
ERCC3	%3774.769136	%3775.049794	0.561316	999	0.453730492	
METTL6	%1402.764001	%1403.043105	0.558208	0.3378	0.454983169	
INTS6	%4109.900894	%4110.176978	0.552168	999	0.457433201	
CCNB1	%1926.12157	%1926.39387	0.5446	5.80552	0.460532565	
FBXO22	%1929.745821	%1930.006514	0.521386	4.60099	0.470251052	
CD69	%1045.183018	%1045.440649	0.515262	0.35336	0.472869806	
ERC1	%5074.825708	%5075.08021	0.509004	0.47092	0.475570335	
ZNF302	%2362.163431	%2362.408726	0.49059	0.624	0.483664237	
ITGB3BP	%887.075169	%887.318797	0.487256	999	0.4851539	
C1orf187	%1762.451477	%1762.693072	0.48319	0.36526	0.48698092	
POFUT2	%2134.778963	%2135.018367	0.478808	0.35839	0.48896274	
C14orf180	%1003.789303	%1004.028248	0.47789	56.22955	0.489379618	
MPHOSPH9	%4893.301448	%4893.534197	0.465498	0.36635	0.495065623	
C22orf41	%894.189136	%894.419949	0.461626	0.37014	0.496865039	
MRGPRD	%1879.490406	%1879.720638	0.460464	0.5417	0.497407202	
OR13J1	%1778.625395	%1778.854809	0.458828	38.1917	0.498172219	
C7orf60	%1789.514861	%1789.736145	0.442568	4.5764	0.505885588	
RAD21L1	%2719.795164	%2720.014124	0.43792	0.5143	0.508128095	
CEBPZ	%5167.204303	%5167.418609	0.428612	0.54003	0.512670806	
FAM55B	%2828.776157	%2828.986592	0.42087	1.62279	0.51650325	
PAFAH1B1	%1902.799262	%1903.005661	0.412798	0.39615	0.520552757	
SHMT2	%2376.262952	%2376.469079	0.412254	0.39588	0.520827675	
TRIM39	%2366.675284	%2366.87076	0.390952	0.40642	0.531799414	
KCNJ9	%1729.748997	%1729.938647	0.3793	0	0.537978103	
OR2J3	%1697.305546	%1697.492299	0.373506	1.9063	0.541099373	
CORO1C	%2135.218227	%2135.403571	0.370688	0.41613	0.542629488	
GUCY2F	%5371.630456	%5371.813629	0.366346	0.59318	0.545002779	
ZFYVE20	%3771.3801	%3771.553635	0.34707	0.57403	0.555776437	
LIPH	%2244.530426	%2244.694125	0.327398	0.43894	0.567195272	
CD300C	%1372.492467	%1372.649149	0.313364	0.55178	0.5756232	
AMBN	%2392.609948	%2392.757492	0.295088	0.45873	0.586978318	
ARHGAP19	%2378.709102	%2378.847341	0.276478	0.46567	0.599019007	
CCDC36	%3126.698571	%3126.829839	0.262536	0.68146	0.608383218	
PLXDC2	%2633.827429	%2633.954197	0.253536	0.62486	0.614596203	
ZNF192	%2772.272685	%2772.397459	0.249548	1.71142	0.617393524	
OR10G3	%1724.325854	%1724.44832	0.244932	0.63016	0.620666439	
PIGA	%2362.475326	%2362.595837	0.241022	999	0.623468945	
MAGEB17	%1974.994103	%1975.113073	0.23794	0.64831	0.62569793	
IRX6	%2442.963729	%2443.080844	0.23423	1.68518	0.628404932	
USP26	%5057.902179	%5058.018393	0.232428	0.69315	0.629729318	
JAM2	%1441.383491	%1441.494478	0.221974	884.46638	0.637539928	
FTSJ2	%1311.0085	%1311.118508	0.220016	0.6453	0.639027727	
FANCG	%3680.940894	%3681.049128	0.216468	0.57525	0.641744405	
IDO2	%2230.162805	%2230.258756	0.191902	0.66306	0.661338292	
CCDC157	%3832.251925	%3832.344796	0.185742	1.39981	0.666484398	
TXNDC11	%4977.243652	%4977.332032	0.17676	0.74432	0.674172559	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
DHTKD1	%4798.188689	%4798.274735	0.172092	0.78831	0.678259234	
PLAU	%2338.921143	%2339.004791	0.167296	0.59594	0.682526204	
MRPL55	%878.037483	%878.119351	0.163736	0.59356	0.685739907	
ZNF575	%1660.588824	%1660.667994	0.15834	0.6042	0.690689459	
CDCA2	%5452.722628	%5452.800468	0.15568	0.75561	0.693165388	
LAMC2	%5963.128391	%5963.206066	0.15535	0.75821	0.693474252	
FLT3	%4937.468203	%4937.543124	0.149842	1.49832	0.698686394	
LRRC27	%2939.374376	%2939.446268	0.143784	0.75358	0.704547811	
PNLIPRP3	%2314.033717	%2314.104562	0.14169	1.50106	0.706606671	
ICT1	%1154.9941	%1155.055494	0.122788	0.64166	0.726030132	
FCRL2	%3055.954779	%3056.015831	0.122104	1.26087	0.726763641	
C1orf101	%5590.400913	%5590.461178	0.12053	0.73172	0.728460371	
SMC5	%5110.848769	%5110.905342	0.113146	0.74257	0.736590499	
VPREB1	%805.776906	%805.831863	0.109914	0.65786	0.740242067	
TMEM232	%3271.356646	%3271.407845	0.102398	1.41466	0.7489707	
LRRC2	%1793.566516	%1793.61535	0.097668	1.42259	0.754646278	
ZNF540	%3153.339476	%3153.382593	0.086234	1.3702	0.76902058	
CHST4	%1995.75318	%1995.795248	0.084136	0.693	0.771768759	
TMEM139	%1120.522968	%1120.56221	0.078484	0.62617	0.779362456	
MFSD6L	%3312.111053	%3312.142414	0.062722	0.80235	0.802244311	
PLEKHA5	%4833.24576	%4833.275485	0.05945	1.30863	0.807367359	
IL19	%1203.431471	%1203.449572	0.036202	0.84576	0.849098946	
IL17RB	%2645.160585	%2645.173901	0.026632	0.81571	0.87036637	
TBRG1	%1916.430802	%1916.442341	0.023078	0.82814	0.879254411	
HEYL	%1750.819753	%1750.83035	0.021194	1.18385	0.8842517	
MPV17L	%1181.628982	%1181.638611	0.019258	0.84203	0.889629375	
CYP3A5	%2730.962274	%2730.970332	0.016116	0.85451	0.898980915	
CPB2	%2230.423424	%2230.430618	0.014388	1.14706	0.904522764	
FGGY	%2751.604273	%2751.610479	0.012412	0.9069	0.9112919	
OR6M1	%1728.940735	%1728.943945	0.00642	0.90572	0.936137917	
CCDC82	%2745.848714	%2745.851244	0.00506	1.08258	0.943291366	
HES5	%658.879368	%658.879938	0.00114	0	0.973065434	
HSD17B3	%1583.049715	%1583.050195	0.00096	0.96259	0.975282406	
TMEM178	%1347.049528	%1347.049997	0.000938	0	0.97556718	
MTG1	%1717.308309	%1717.308514	0.00041	0.97589	0.983845173	
DARC	%1863.918073	%1863.918271	0.000396	0.97585	0.984123346	
DHRS7	%1626.310393	%1626.310562	0.000338	0	0.985331897	
CA10	%1497.611745	%1497.611909	0.000328	0	0.985550486	
PSMD4	%1696.939869	%1696.940024	0.00031	0	0.985952518	
CDCA3	%1246.375569	%1246.375697	0.000256	0	0.987234392	
FXYD3	%495.779066	%495.779142	0.000152	0	0.990163268	
DLX6	%1107.77776	%1107.777834	0.000148	0	0.990293555	
GEMIN7	%641.842067	%641.842136	0.000138	0	0.990627194	
TUBB	%2154.245591	%2154.245653	0.000124	0	0.991115317	
C12orf5	%1454.660399	%1454.660454	0.00011	0	0.99163187	
EIF2C4	%3719.55317	%3719.553218	9.6E%05	0	0.992182485	
MED7	%980.949476	%980.949521	9E%05	0	0.992430716	
SDSL	%1768.817515	%1768.817558	8.6E%05	1.01101	0.992600829	
RNF11	%655.292812	%655.292847	7E%05	0	0.993324497	
MPZL2	%1008.25184	%1008.251873	6.6E%05	0	0.993518026	
DNAJC24	%685.156699	%685.156729	6E%05	0	0.993819675	
DRAP1	%964.9988	%964.998825	5E%05	0	0.994358151	
C9orf46	%559.674776	%559.6748	4.8E%05	0	0.994472138	
TAGLN	%885.165762	%885.165786	4.8E%05	0	0.994472138	
POLR2F	%562.780972	%562.780987	3E%05	0	0.995629828	
HM13	%1874.075827	%1874.07584	2.6E%05	0	0.995931589	
CISH	%1389.933197	%1389.93321	2.6E%05	0	0.995931589	
PPP2R2C	%2051.373847	%2051.373857	2E%05	0	0.996431764	
LHX2	%1796.59878	%1796.59879	2E%05	0	0.996431764	
ZNRD1	%572.059204	%572.059214	2E%05	0	0.996431764	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	Pvalue	k
C8orf40	%467.375964	%467.375973	1.8E%05	0	0.996614873	
GPHA2	%627.57699	%627.576998	1.6E%05	0	0.99680847	
MBNL2	%1567.260764	%1567.260772	1.6E%05	0	0.99680847	
NR1I3	%1719.752591	%1719.752599	1.6E%05	0	0.99680847	
ILKAP	%1841.49858	%1841.498587	1.4E%05	0	0.997014596	
GADD45A	%733.845789	%733.845796	1.4E%05	0	0.997014596	
DCAF4L1	%1947.942025	%1947.942032	1.4E%05	0	0.997014596	
TMEM106B	%1217.607899	%1217.607906	1.4E%05	0	0.997014596	
PPM1K	%1668.005822	%1668.005828	1.2E%05	0	0.997236052	
RPL23A	%869.3576	%869.357606	1.2E%05	0	0.997236052	
TMEM179	%904.101583	%904.101589	1.2E%05	0	0.997236052	
BET1	%508.096101	%508.096106	1E%05	0	0.997476872	
OAZ2	%820.725338	%820.725343	1E%05	0	0.997476872	
EPB49	%1818.382121	%1818.382126	1E%05	0	0.997476872	
HAUS2	%1109.529257	%1109.529261	8E%06	0	0.997743245	
GNG5P2	%353.079637	%353.07964	6E%06	0	0.998045592	
RPS23	%645.084004	%645.084007	6E%06	0	0.998045592	
PGAM1	%1123.194261	%1123.194264	6E%06	0	0.998045592	
GNAT2	%1603.340311	%1603.340313	4E%06	0	0.998404232	
NDUFA6	%805.108296	%805.108298	4E%06	0	0.998404232	
FOSB	%1438.019208	%1438.019209	2E%06	0	0.998871621	
ARL6IP1	%940.041495	%940.041496	2E%06	0	0.998871621	
LSM10	%586.604897	%586.604897	0	0	1	
WDR5B	%1588.901997	%1588.901997	0	0	1	
ATP5H	%762.138315	%762.138314	%2E%06	0	#NUM!	
C1orf43	%1161.442193	%1161.442174	%3.8E%05	0	#NUM!	
CAV1	%809.660489	%809.616076	%0.088826	0	#NUM!	
DCTN6	%847.906572	%847.906568	%8E%06	0	#NUM!	
DEFB103A	%336.132914	%336.132911	%6E%06	0	#NUM!	
EIF2C2	%4480.220739	%4040.738069	%878.96534	0	#NUM!	
LSM7	%502.257723	%453.512199	%97.491048	0	#NUM!	
MRPL20	%882.694106	%882.693995	%0.000222	0	#NUM!	
OLA1	%1684.858748	%1684.858735	%2.6E%05	0	#NUM!	
SLC22A17	%2376.769634	%2375.270992	%2.997284	7.11878	#NUM!	
SLC31A1	%859.479825	%859.479754	%0.000142	0	#NUM!	
SYNJ2BP	%724.646015	%647.257628	%154.776774	0	#NUM!	
TMEM18	%652.610843	%652.610835	%1.6E%05	0	#NUM!	
TMEM38B	%1446.3204	%1446.320217	%0.000366	0	#NUM!	
TMEM42	%680.798196	%680.488709	%0.618974	0	#NUM!	
WDR33	%6009.07471	%6006.095292	%5.958836	6.84237	#NUM!	
YTHDC1	%3094.0912	%3087.545809	%13.090782	0.92987	#NUM!	

Chimpanzee

Gene	Free lnL	Fixed lnL	branch_w	2ΔlnL	Pvalue	k
APC2	-11995.80066	-12022.36733	0.11836	53.133338	3.11658E-13	
NCOR2	-12227.23878	-12249.056	0.07968	43.634444	3.95811E-11	
VPS13D	-20748.22678	-20763.1976	0.11025	29.941642	4.45247E-08	
GRIK3	-4314.051878	-4325.999899	0.05978	23.896042	1.01681E-06	
CHL1	-6211.707024	-6222.261262	0.10072	21.108476	4.34004E-06	
FAM120A	-5418.288692	-5428.809193	0	21.041002	4.49559E-06	
PLCH2	-7498.542086	-7508.915811	0.12343	20.74745	5.24013E-06	
TOP3A	-5196.759018	-5207.113441	0.03616	20.708846	5.34684E-06	
SIPA1	-4987.153343	-4997.300102	0	20.293518	6.64252E-06	
HNRPLL	-2491.73189	-2501.789207	0	20.114634	7.29365E-06	
TBC1D9	-5834.012368	-5844.054812	0	20.084888	7.40797E-06	
RAP1GAP2	-3635.912285	-3645.648622	0.07278	19.472674	1.02049E-05	
ANO1	-4809.562093	-4819.143866	0.05024	19.163546	1.19983E-05	
IRF8	-2085.163167	-2094.102227	0	17.87812	2.35513E-05	
CARD11	-5918.671223	-5927.142495	0.03029	16.942544	3.85283E-05	
ZC3H13	-7600.004566	-7608.285389	0	16.561646	4.70939E-05	
CDT1	-2995.134517	-3003.388167	0.11822	16.5073	4.84631E-05	
ARHGAP4	-5880.784658	-5888.99241	0	16.415504	5.08675E-05	
SLIT1	-7420.423654	-7428.567574	0.08537	16.28784	5.4412E-05	
SMPD3	-3077.901126	-3086.044138	0.03447	16.286024	5.44642E-05	
ECEL1	-3727.819205	-3735.788718	0.07971	15.939026	6.54159E-05	
RALGDS	-4387.354867	-4395.303968	0.08805	15.898202	6.68422E-05	
ROR2	-4589.722916	-4597.531853	0.0363	15.617874	7.75184E-05	
ATP10D	-7190.098337	-7197.790175	0.04817	15.383676	8.7743E-05	
PLCB1	-5510.55559	-5517.918361	0.08391	14.725542	0.00012435	
CORO1C	-2135.592921	-2142.912615	0	14.639388	0.000130165	
GOLGA5	-3481.500307	-3488.634278	0	14.267942	0.000158542	
ARHGAP19	-2376.993393	-2383.894515	0	13.802244	0.000203094	
TBC1D17	-3152.669542	-3159.43403	0.07331	13.528976	0.000234908	
MAP4K4	-6064.512361	-6071.002216	0.15498	12.97971	0.000314885	
TTF1	-5075.160157	-5081.563574	0.16315	12.806834	0.000345356	
CDK9	-1677.474998	-1683.818924	0	12.687852	0.000368039	
STAT5B	-3676.193876	-3682.517542	0	12.647332	0.000376102	
CCDC82	-2741.027786	-2747.202106	0	12.34864	0.000441308	
KCNB1	-3940.673238	-3946.779859	0	12.213242	0.000474515	
DNAI2	-3180.647915	-3186.720036	0.04981	12.144242	0.000492397	
TNS3	-7655.514953	-7661.559858	0.10024	12.08981	0.000506981	
UNC13C	-10555.4018	-10561.40728	0.14371	12.010954	0.000528888	
ABCD3	-3241.373786	-3247.364119	0	11.980666	0.000537554	
EPHB3	-4498.045731	-4503.999409	0.08187	11.907356	0.000559127	
SFRP1	-1508.317613	-1514.223988	0	11.81275	0.000588265	
ZNF592	-5978.907767	-5984.693862	0.06068	11.57219	0.000669455	
SPTB	-11266.65652	-11272.43775	0.19836	11.562458	0.000672968	
TBXA2R	-1670.307241	-1676.017225	0	11.419968	0.000726589	
EIF2C2	-4034.238039	-4039.92761	0	11.379142	0.000742734	
PGAM1	-1122.726221	-1128.377399	0	11.302356	0.000774088	
RBBP6	-8240.560962	-8246.188468	0.16274	11.255012	0.000794083	
ABCB11	-6822.388497	-6827.988544	0.22053	11.200094	0.000817932	
LEPREL4	-1976.191706	-1981.78047	0.09822	11.177528	0.00082794	
CYTH1	-1782.855188	-1788.323116	0	10.935856	0.000943209	
YLPM1	-9690.564502	-9695.959469	0.10541	10.789934	0.001020535	
USP7	-4826.544816	-4831.932471	0	10.77531	0.00102863	
SDSL	-1768.205556	-1773.539134	0	10.667156	0.001090547	
ADAM29	-4768.864585	-4774.19766	0.28075	10.66615	0.00109114	
ZFP64	-3247.863833	-3253.13421	0	10.540754	0.001167708	
TJP2	-6016.747984	-6021.974788	0.16573	10.453608	0.001224101	
POGK	-2868.973982	-2874.1976	0	10.447236	0.001228331	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
BCL9L	%7012.626167	%7017.793906	0.19108	10.335478	0.001304973	
RFX7	%6743.815213	%6748.937527	0.064	10.244628	0.001370832	
PCDHA3	%4896.630749	%4901.733626	0.20511	10.205754	0.001400031	
ALDH1A3	%2495.770744	%2500.856873	0	10.172258	0.001425696	
ZNF335	%6610.042804	%6615.105148	0.22537	10.124688	0.001462964	
PNPLA7	%6799.87858	%6804.833077	0.41258	9.908994	0.00164473	
PSMD4	%1696.678702	%1701.585125	0	9.812846	0.001732971	
KCNJ9	%1724.99759	%1729.87489	0.15919	9.7546	0.001788746	
UPF2	%5623.724559	%5628.599527	0.06185	9.749936	0.00179329	
PLXDC2	%2634.174201	%2638.99867	0	9.648938	0.001894611	
RABGGTA	%2636.368381	%2641.183113	0	9.629464	0.001914805	
ADAMTS8	%4014.139329	%4018.913145	0.13234	9.547632	0.002002075	
CEACAM6	%2790.965698	%2795.69885	0	9.466304	0.002092806	
CACNG6	%1272.00119	%1276.63494	0	9.2675	0.002332559	
C4orf31	%2783.942704	%2788.572017	0.07167	9.258626	0.002343888	
FGGY	%2752.35241	%2756.925737	0	9.146654	0.002491733	
ADRA1B	%2495.442342	%2499.990591	0.24015	9.096498	0.002560994	
WDR33	%6005.286082	%6009.775187	0	8.97821	0.002732182	
FOLR2	%1277.330696	%1281.763401	0	8.86541	0.00290625	
USP1	%3478.985848	%3483.354936	0	8.738176	0.003116161	
JAG2	%6278.060405	%6282.407276	0.36304	8.693742	0.003193044	
CHST2	%2515.987853	%2520.321158	0	8.66661	0.003240935	
HRH3	%2188.650985	%2192.919672	0.266	8.537374	0.003479272	
PNPT1	%3658.044304	%3662.308425	0	8.528242	0.003496773	
DHTKD1	%4801.191216	%4805.433901	0.1599	8.48537	0.003580138	
MEGF10	%5514.61312	%5518.841144	0.18045	8.456048	0.003638315	
ABHD4	%1660.431974	%1664.65678	0	8.449612	0.003651213	
NCKAP1L	%5396.918326	%5401.138334	0.07275	8.440016	0.00367053	
GALNT12	%3048.991382	%3053.188439	0	8.394114	0.00376438	
KIDINS220	%8391.172248	%8395.356109	0.18538	8.367722	0.003819441	
PRKCD	%3135.308447	%3139.459057	0.10032	8.30122	0.003961846	
C11orf84	%2728.878557	%2733.017748	0	8.278382	0.004011986	
SLC22A17	%2376.461204	%2380.504281	0	8.086154	0.004460472	
SLC7A14	%3657.761392	%3661.783423	0.07648	8.044062	0.004565305	
MAP3K7	%2660.703636	%2664.706908	0	8.006544	0.00466086	
SDHA	%3590.276281	%3594.262657	0.24925	7.972752	0.004748669	
FAM131A	%1320.830029	%1324.804716	0	7.949374	0.004810401	
DRAP1	%964.813071	%968.738172	0.06648	7.850202	0.005081503	
ATAD2	%6458.451341	%6462.373043	0.20194	7.843404	0.005100647	
PDZD7	%2715.686624	%2719.587049	0.12946	7.80085	0.005222166	
OAS1	%2330.470847	%2334.365044	999	7.788394	0.005258292	
SDAD1	%3554.634365	%3558.509863	0	7.750996	0.005368293	
ALOX15	%3884.396096	%3888.23644	0	7.680688	0.005581488	
RPS23	%645.084014	%648.871071	0	7.574114	0.005921248	
ILKAP	%1841.0265	%1844.811713	0	7.570426	0.005933376	
TEKT5	%2695.321657	%2699.069956	0.18865	7.496598	0.006181565	
ELF4	%3310.801955	%3314.546601	0.28889	7.489292	0.006206695	0.008280255
KIAA0562	%4760.019309	%4763.763839	0.13201	7.48906	0.006207495	0.008359873
CWC22	%4318.727368	%4322.418053	0.0744	7.38137	0.006590295	0.00843949
ZNF570	%2394.062874	%2397.696541	0	7.267334	0.007021996	0.008519108
CES5A	%3265.100636	%3268.715127	0.24916	7.228982	0.007173587	0.008598726
SLC5A3	%3196.232165	%3199.809211	0	7.154092	0.007479315	0.008678344
LHX2	%1796.359802	%1799.935731	0	7.151858	0.007488637	0.008757962
ADNP2	%5612.000344	%5615.571742	0.13749	7.142796	0.007526572	0.00883758
NPY1R	%1730.160795	%1733.694986	0	7.068382	0.007845607	0.008917197
TTYH1	%2169.286887	%2172.763724	0.07737	6.953674	0.008364727	0.008996815
CYP4F11	%2992.706669	%2996.179235	0.13652	6.945132	0.008404764	0.009076433

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
SEC14L5	%3456.517287	%3459.988276	0.14716	6.941978	0.008419596	0.009156051
IRX6	%2443.246953	%2446.693137	0.09147	6.892368	0.008656452	0.009235669
SCN1B	%1018.789719	%1022.154478	0	6.729518	0.009483022	0.009315287
KCNG2	%1850.551418	%1853.904215	0.13187	6.705594	0.009611091	
ZNF528	%3225.886444	%3229.226157	0.12966	6.679426	0.009753203	
KANK3	%4442.239653	%4445.571707	0.2285	6.664108	0.009837388	
HIST1H2AL	%744.299314	%747.596064	0	6.5935	0.010235175	
TAGLN	%885.053458	%888.28878	0	6.470644	0.010967078	
MIER1	%1903.109517	%1906.313191	0	6.407348	0.011364903	
USP18	%2026.885071	%2030.067029	0.17399	6.363916	0.011646422	
HMGCR	%4420.607119	%4423.784223	0.08775	6.354208	0.011710321	0.009952229
UBLCP1	%1381.208979	%1384.275848	0	6.133738	0.013262618	
RAE1	%1759.519698	%1762.585294	0.0908	6.131192	0.013281729	
SLC6A4	%3062.271467	%3065.317755	0.09221	6.092576	0.013575103	
FBXL12	%1532.601451	%1535.64344	0	6.083978	0.013641326	
DGAT1	%2575.227281	%2578.264606	0	6.07465	0.013713547	
DNAJC30	%1246.362029	%1249.398239	0	6.07242	0.013730871	
PITPNM1	%6233.942098	%6236.977743	0.26387	6.07129	0.013739658	
TBR1	%2895.59107	%2898.623567	0	6.064994	0.013788722	
SLC16A8	%2346.438661	%2349.435326	0.1181	5.99333	0.014360069	
DLEC1	%9085.971384	%9088.95051	0.3661	5.958252	0.014648557	
TMCC3	%2203.91212	%2206.854465	0	5.88469	0.015273086	
CDC37	%1705.414401	%1708.351115	0.07249	5.873428	0.015371092	
ACCN1	%2710.987245	%2713.918394	0	5.862298	0.015468585	
MOAP1	%1705.376748	%1708.2966	0.09594	5.839704	0.015668462	
SPIB	%1095.413992	%1098.316937	0	5.80589	0.015972582	
EFS	%2801.769752	%2804.661105	0.11025	5.782706	0.016184606	0.011226115
NR2C2	%2829.382734	%2832.26393	0.09776	5.762392	0.016372768	
RNF208	%1198.572763	%1201.431467	0	5.717408	0.01679751	
SULF2	%4178.736636	%4181.567757	0.18504	5.662242	0.017333951	
PLB1	%7860.636076	%7863.450815	0.27603	5.629478	0.01766089	
MSL2	%2520.878614	%2523.684713	0	5.612198	0.017835877	
DMGDH	%4203.725843	%4206.518963	0.10168	5.58624	0.018102113	
SCT	%523.82309	%526.613045	0	5.57991	0.018167656	
TUBB	%2153.430281	%2156.216889	0	5.573216	0.018237235	
SLC4A4	%4931.962555	%4934.741293	0.08127	5.557476	0.018401927	
PAX9	%1574.17583	%1576.947012	0.08416	5.542364	0.018561493	
EPB41L1	%4096.280213	%4099.044119	0	5.527812	0.018716496	
SEMA6B	%4179.793776	%4182.551702	0.18602	5.515852	0.018844892	
HIST1H3G	%641.629555	%644.362337	0	5.465564	0.019394794	
SUSD3	%1285.438982	%1288.16157	0.08503	5.445176	0.019622438	
DCAF7	%1558.854566	%1561.575861	0	5.44259	0.019651509	
TTLL9	%2361.001633	%2363.702104	0.08778	5.400942	0.020125886	
DACT2	%4065.084051	%4067.783432	0.26524	5.398762	0.02015104	
OVOL2	%1300.916482	%1303.615374	0.15304	5.397784	0.020162336	
LHFPL2	%1092.797227	%1095.488162	0	5.38187	0.020347057	
WSB2	%1866.170804	%1868.856176	0	5.370744	0.020477241	
CHRDL2	%2444.775381	%2447.454838	0	5.358914	0.020616608	
COPS4	%1959.32907	%1961.995405	0	5.33267	0.020929299	
NLGN3	%3586.285918	%3588.88851	0	5.205184	0.022519631	
NDUFA6	%804.007192	%806.606779	0	5.199174	0.022597624	
DSCR3	%1519.424875	%1522.017013	0	5.184276	0.022792167	
LRRTM3	%2556.449157	%2559.038691	0	5.179068	0.022860583	
TNIP3	%2037.845013	%2040.434369	0	5.178712	0.022865267	
NR1D2	%2650.553425	%2653.118567	0.14829	5.130284	0.02351188	
CDCA2	%5452.561207	%5455.113559	0.27625	5.104704	0.02386105	
SMC2	%5402.48951	%5405.031323	0.19067	5.083626	0.024152808	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
CLK4	%2165.503149	%2168.022924	0	5.03955	0.024774925	
CA10	%1497.543413	%1500.057668	0	5.02851	0.02493334	
COL5A2	%6698.896246	%6701.402366	0.17421	5.01224	0.025168721	
ZNF235	%3661.0665	%3663.564346	0.27111	4.995692	0.025410491	
SEMA4B	%3998.057429	%4000.530168	0.21798	4.945478	0.026159004	
L3MBTL1	%3975.567806	%3978.00744	0.10016	4.879268	0.027181144	
ATG16L1	%2891.495013	%2893.934029	0	4.878032	0.027200615	
PDK3	%1819.462485	%1821.894922	0	4.864874	0.0274088	
SLC25A23	%2099.408135	%2101.82778	0.14894	4.83929	0.027818346	
PPM1K	%1667.459664	%1669.877879	0	4.83643	0.027864523	
CDK13	%6756.392108	%6758.794168	0.17953	4.80412	0.028391763	
GPR89A	%1485.416595	%1487.805101	0	4.777012	0.028842125	
RD3	%982.777392	%985.163455	0.07484	4.772126	0.028924087	
PLP1	%1161.913483	%1164.288295	0	4.749624	0.029304697	
SLC35C1	%1829.318253	%1831.687792	0.13076	4.739078	0.029484869	
NR1I3	%1718.890343	%1721.246709	0	4.712732	0.029940035	
GCGR	%2923.864361	%2926.215479	0.22253	4.702236	0.030123403	
RC3H1	%5132.010303	%5134.36001	0	4.699414	0.030172903	
KRTAP4%7	%1359.892864	%1362.233245	0	4.680762	0.030502215	
ADAT2	%895.888531	%898.223994	0	4.670926	0.030677383	
ZNF324B	%3117.101836	%3119.436148	0.30654	4.668624	0.03071853	
C11orf80	%3562.694331	%3565.027485	0.21019	4.666308	0.030759985	
SHPRH	%8159.357152	%8161.673452	0.16675	4.6326	0.031369991	
PM20D2	%2163.192521	%2165.506572	0	4.628102	0.031452339	
SOAT2	%2726.300426	%2728.609945	0.21247	4.619038	0.031618967	
CDC23	%2707.80438	%2710.08136	0	4.55396	0.032842704	
OAZ2	%820.45698	%822.72411	0	4.53426	0.033222818	
CMBL	%1195.370535	%1197.63695	0	4.53283	0.033250588	
C10orf11	%974.500173	%976.766504	0	4.532662	0.033253852	
PLEKHA5	%4834.983749	%4837.210457	0.10785	4.453416	0.034831506	
CD2AP	%3054.060286	%3056.285562	0	4.450552	0.034889967	
ME2	%2646.274922	%2648.439345	0.1124	4.328846	0.037471643	
C17orf51	%1208.581924	%1210.731381	0	4.298914	0.038136718	
GFRAL	%2055.682712	%2057.82627	0.11339	4.287116	0.038402254	
HELB	%5542.376748	%5544.488657	0.17904	4.223818	0.039860373	
SQSTM1	%2439.930274	%2441.967464	0	4.07438	0.043538241	
PIGA	%2361.139308	%2363.16778	0	4.056944	0.043990041	
PNLIPRP3	%2313.205203	%2315.19749	0.12216	3.984574	0.045918711	
RTN4RL2	%1987.699968	%1989.67444	0.3266	3.948944	0.046900791	0.016719745
MBD6	%4425.443575	%4427.358975	0	3.8308	0.05031891	
MAGEB17	%1974.604281	%1976.506901	0.28549	3.80524	0.051092453	
FKRP	%2435.302383	%2437.185742	0.23832	3.766718	0.052282123	
CAV1	%809.399235	%811.275855	0	3.75324	0.052705255	
STUB1	%1347.877786	%1349.750391	0	3.74521	0.052959072	
PLS3	%2740.774435	%2742.586055	0.20172	3.62324	0.056977808	
GFOD2	%1867.470596	%1869.269628	0.17625	3.598064	0.0578469	
ASCC3	%10024.04417	%10025.83117	0.34432	3.573998	0.058690847	
MAP4K5	%5019.577822	%5021.359656	0.17747	3.563668	0.059057104	
CNTN6	%5057.649041	%5059.420401	0.3022	3.54272	0.05980731	
UGT1A3	%2747.817767	%2749.564416	0.30136	3.493298	0.061617716	
DHRS7	%1625.947409	%1627.689025	0.14012	3.483232	0.061993549	
MAGEB3	%1940.245342	%1941.978623	999	3.466562	0.062621337	
S1PR3	%1732.166243	%1733.873005	0	3.413524	0.064664217	
ITGB8	%3617.53763	%3619.229383	0.21537	3.383506	0.065851834	
ACOT12	%2907.111011	%2908.792513	0.24626	3.363004	0.066676337	
OR6X1	%1672.441118	%1674.121184	0.21588	3.360132	0.066792714	
RBCK1	%2218.757092	%2220.425274	0.1128	3.336364	0.067764199	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
RABEP1	%3980.904211	%3982.57151	0.14548	3.334598	0.067836982	
GCDH	%2326.917696	%2328.559949	0.3677	3.284506	0.069936672	
C9orf9	%839.843682	%841.477411	0.27709	3.267458	0.070667045	
CHMP5	%937.877506	%939.50073	0	3.246448	0.071578417	
ERC1	%5074.634544	%5076.256844	0.27057	3.2446	0.07165918	
MPZL2	%1008.250319	%1009.863905	0.15029	3.227172	0.072425658	
DCAF12L2	%2617.882015	%2619.48013	0	3.19623	0.073808229	
NPFFR1	%2090.238488	%2091.831029	0.11886	3.185082	0.074313269	
PLAU	%2338.96651	%2340.558376	0.28628	3.183732	0.074374679	
PRMT6	%1671.966436	%1673.542522	0	3.152172	0.07582597	
FAM126B	%2587.393553	%2588.969325	0	3.151544	0.075855156	
DCAF5	%4504.114444	%4505.682983	0.20844	3.137078	0.076530802	
PCDHB5	%4602.169747	%4603.731915	0.41743	3.124336	0.077131289	
TBCB	%1153.057251	%1154.611921	0	3.10934	0.077844499	
MAP4K3	%4017.60561	%4019.127209	0.36402	3.043198	0.081076049	
HIST1H2AJ	%620.351488	%621.859651	0	3.016326	0.082430015	
MYL6B	%1176.76576	%1178.268981	0	3.006442	0.08293415	
SMR3B	%484.765595	%486.268522	999	3.005854	0.082964246	
MRGPRD	%1876.208948	%1877.705851	999	2.993806	0.083583506	
PRPF4B	%4588.450954	%4589.939856	0	2.977804	0.084413732	
RPL26	%712.40403	%713.89046	0	2.97286	0.084672039	
DUSP1	%1011.279256	%1012.764755	0	2.970998	0.084769544	
MRPL20	%882.064924	%883.524681	0	2.919514	0.087514219	
ZBTB38	%5739.335081	%5740.793079	0.3321	2.915996	0.087705247	
SUV39H1	%1814.111869	%1815.5657	0	2.907662	0.088159592	
RBM7	%1282.541853	%1283.98225	0	2.880794	0.08964181	
DCAF4L1	%1947.749267	%1949.189153	0.27089	2.879772	0.089698722	
LSM10	%586.274573	%587.706131	0	2.863116	0.090631776	
ICT1	%1154.279174	%1155.704755	0	2.851162	0.09130792	
CEP78	%3500.660777	%3502.061916	0.1679	2.802278	0.094130482	
FLT3	%4934.989766	%4936.388643	999	2.797754	0.094396455	
EPB49	%1818.331553	%1819.720992	0	2.778878	0.095515061	
MAT2A	%1792.585457	%1793.968673	0	2.766432	0.096260512	
LTK	%4352.418129	%4353.78934	0.28336	2.742422	0.097716561	
METAP1D	%1549.796404	%1551.165782	0	2.738756	0.097940985	
GPR176	%2453.565488	%2454.921725	0.3875	2.712474	0.09956647	
C9orf46	%559.518623	%560.86232	0	2.687394	0.101145113	
NXT1	%642.059909	%643.403121	0	2.686424	0.101206716	
LPAR3	%1796.685166	%1798.012188	0	2.654044	0.103286837	
CDC20	%2280.719468	%2282.04536	999	2.651784	0.103433758	
ZFYVE20	%3771.966027	%3773.289031	0.28577	2.646008	0.103810292	
ADH1A	%2350.97797	%2352.299248	999	2.642556	0.104036043	
C20orf160	%2426.570264	%2427.890539	0	2.64055	0.104167476	
FANCG	%3680.14711	%3681.467352	0.23911	2.640484	0.104171804	
CAPN7	%3743.344764	%3744.662126	0	2.634724	0.104550228	
GJA4	%1636.687926	%1637.994777	0.14531	2.613702	0.105944182	
FAM167A	%1034.837991	%1036.136569	0	2.597156	0.107055669	
SH3D21	%4133.166113	%4134.450322	999	2.568418	0.109016705	
LAPTM4B	%2137.212236	%2138.491766	0.23338	2.55906	0.109663771	
ASB1	%1625.015796	%1626.294323	0	2.557054	0.109803026	
MED7	%980.949476	%982.218078	0	2.537204	0.11119153	
ERCC3	%3773.691633	%3774.954053	0.31795	2.52484	0.112066147	
ALKBH3	%1305.978329	%1307.236922	0	2.517186	0.112611378	
EPSTI1	%2232.015731	%2233.273092	0.23665	2.514722	0.112787522	
POLR2F	%562.609247	%563.85482	0	2.491146	0.114488333	
TMEM43	%2109.760697	%2111.000467	0.2366	2.47954	0.115335981	
LRRC27	%2936.915956	%2938.14349	2.3798	2.455068	0.117146096	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
SNRPA1	%1117.342391	%1118.569697	0	2.454612	0.117180121	
DDHD2	%3298.420805	%3299.645014	0	2.448418	0.117643381	
SYNPO2L	%4887.140651	%4888.362478	0.27147	2.443654	0.118001066	
SLC31A1	%858.948111	%860.168721	0	2.44122	0.118184276	
DCTN6	%847.845301	%849.064627	0	2.438652	0.118377914	
SDC2	%947.343261	%948.556696	0	2.42687	0.119270836	
TMEM105	%685.902323	%687.114623	0	2.4246	0.119443727	
MLXIPL	%3536.875992	%3538.082234	0.22392	2.412484	0.120371228	
ANGEL2	%2366.273456	%2367.478913	0	2.410914	0.120491997	
ARHGEF25	%2845.460655	%2846.663825	0	2.40634	0.120844607	
TMEM18	%652.281507	%653.48371	0	2.404406	0.120994043	
ARL6IP1	%939.801719	%940.997656	0	2.391874	0.12196734	
SMC5	%5111.759103	%5112.942355	0.24664	2.366504	0.123964389	
PTPRCAP	%1095.290106	%1096.461346	0	2.34248	0.125888994	
GNG5P2	%852.059839	%853.226556	0	2.333434	0.126622271	
MBTPS2	%2423.698959	%2424.85788	0.17272	2.317842	0.127897352	
VPREB1	%805.379129	%806.531113	0.16529	2.303968	0.129043963	
C14orf180	%1003.647967	%1004.79358	0.27727	2.291226	0.130107116	
NUDCD1	%2710.013137	%2711.156038	0.16669	2.285802	0.130562637	
ZC3H12D	%2707.883773	%2709.013657	0.35785	2.259768	0.132773951	
GOLGA6C	%5057.058458	%5058.185646	1.79584	2.254376	0.133237153	
RCN2	%1491.565944	%1492.69231	0.20213	2.252732	0.13337874	
GIMAP2	%1823.522163	%1824.641155	0.25611	2.237984	0.134656442	
GNPAT	%3338.325109	%3339.440235	0.3177	2.230252	0.135331774	
CHM	%3029.338137	%3030.452154	0.1709	2.228034	0.135526198	
MBNL2	%1567.08714	%1568.195763	0	2.217246	0.136476316	
CHST4	%1995.958746	%1997.065752	0.17148	2.214012	0.136762591	
ENOPH1	%1178.058846	%1179.161421	0	2.20515	0.137550514	
IL10RA	%3126.64878	%3127.75036	0.33258	2.20316	0.137728144	
CD300C	%1371.916658	%1373.018052	0.33872	2.202788	0.137761377	
C8orf40	%467.375964	%468.476527	0	2.201126	0.137909967	
C21orf59	%1401.046884	%1402.136105	0.17071	2.178442	0.139956079	
SHMT2	%2376.28499	%2377.361865	0.26377	2.15375	0.142222146	
C19orf68	%3302.184144	%3303.256221	0.62644	2.144154	0.143113908	
TMC8	%3631.882935	%3632.945848	0.30686	2.125826	0.144834683	
USP26	%5056.314529	%5057.360221	1.86038	2.091384	0.148131821	
FAM111A	%3299.839487	%3300.866669	3.59806	2.054364	0.151770616	
BCCIP	%1570.407273	%1571.427748	999	2.04095	0.153113996	
PNKP	%2842.386311	%2843.396496	0.40001	2.02037	0.15520132	
PLK2	%3091.043497	%3092.032632	0.18948	1.97827	0.159572777	
BLNK	%2338.637419	%2339.614421	0.19175	1.954004	0.162156034	
MAGEA8	%1511.105043	%1512.079791	999	1.949496	0.162641172	
PPM1E	%3396.71719	%3397.679644	0.1938	1.924908	0.165316614	
HEYL	%1751.61698	%1752.569817	0.19302	1.905674	0.167444591	
LIPH	%2244.458548	%2245.398453	0.28841	1.87981	0.170355744	
TACR2	%1978.441673	%1979.378759	0.23609	1.874172	0.170998019	
KMO	%2495.438551	%2496.34673	0.4092	1.816358	0.177747406	
GUCY2F	%5372.063474	%5372.967954	0.37834	1.80896	0.178633038	
CPA5	%2348.57573	%2349.462511	0.34588	1.773562	0.182941867	
OR6M1	%1728.893736	%1729.763148	0.30245	1.738824	0.187287903	
OR1N2	%1645.26937	%1646.136432	0.2097	1.734124	0.18788508	
C1orf101	%5588.638607	%5589.495708	2.44149	1.714202	0.190441089	
MPV17L	%1181.397085	%1182.253375	0.16514	1.71258	0.190650971	
KIAA0947	%12218.13611	%12218.97495	0.63097	1.677672	0.195234076	
CCDC132	%4366.564279	%4367.397491	0.41607	1.666424	0.196738196	
STH	%711.759268	%712.571653	0.22154	1.62477	0.20242796	
PRRG1	%979.263392	%980.060319	0.22288	1.593854	0.206776368	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
ZNF575	%1658.463984	%1659.258644	999	1.58932	0.207423314	
CDCA3	%1244.692552	%1245.484444	999	1.583784	0.20821648	
HES5	%658.656322	%659.446001	0	1.579358	0.208853193	
WISP3	%1792.57428	%1793.362077	0.22734	1.575594	0.209396485	
HSD17B3	%1581.568556	%1582.353343	999	1.569574	0.21026889	
MRPL21	%1129.823542	%1130.604044	0.22886	1.561004	0.211518276	
TMEM42	%680.256287	%681.033644	0	1.554714	0.212440874	
ORC2	%2606.094274	%2606.867406	999	1.546264	0.213687824	
MS4A7	%1300.366416	%1301.127643	0.32495	1.522454	0.217248507	
GEMIN7	%641.812786	%642.573764	0.23244	1.521956	0.217323732	
COX5B	%678.314194	%679.066709	999	1.50503	0.219899033	
DENND4B	%7194.220321	%7194.96639	0.33826	1.492138	0.221885033	
RNF34	%1771.906493	%1772.649099	16.39712	1.485212	0.222960834	
MAP2	%8749.402593	%8750.137163	0.50226	1.46914	0.225481431	
AGPAT2	%1422.111986	%1422.839454	0.15003	1.454936	0.227737578	
DARC	%1863.699203	%1864.418495	0.24279	1.438584	0.230368618	
GP1BA	%4201.23681	%4201.946237	0.42561	1.418854	0.233592121	
GAL3ST4	%2423.922203	%2424.626119	999	1.407832	0.235416627	
RAD21L1	%2718.797845	%2719.501144	999	1.406598	0.235621967	
MDM4	%2142.482792	%2143.183624	0.20269	1.401664	0.236445161	
COL20A1	%6577.483213	%6578.171363	0.59872	1.3763	0.240732399	
PINX1	%1712.024884	%1712.711012	0.42657	1.372256	0.24142465	
GPR179	%14282.6845	%14283.33981	0.67831	1.310612	0.252283879	
TMEM61	%1209.667704	%1210.319015	0.38494	1.302622	0.25373484	
CAPS2	%2949.850631	%2950.500013	0.47753	1.298764	0.254439117	
PRKRIP1	%903.648592	%904.289106	999	1.281028	0.257707984	
GCK	%2425.528991	%2426.158374	0.18518	1.258766	0.261884799	
CYLC1	%3425.946309	%3426.561799	61.56125	1.23098	0.267216536	
KPTN	%2402.42006	%2403.03157	0.47562	1.22302	0.268768789	
TMEM38B	%1444.238602	%1444.849436	999	1.221668	0.269033555	
OR51F2	%1557.162986	%1557.769687	0.29138	1.213402	0.27065941	
DNAJC17	%1455.741677	%1456.346701	999	1.210048	0.271322616	
TTC29	%2306.74059	%2307.327468	0.40457	1.173756	0.278630826	
CCDC36	%3126.409805	%3126.99002	0.4071	1.16043	0.28137638	
GPT2	%2457.934015	%2458.513378	0.43692	1.158726	0.281729914	
MRPL43	%1379.24451	%1379.804497	0.40031	1.119974	0.289924052	
KRT36	%2449.728801	%2450.274618	0.37067	1.091634	0.296109451	
TSSK2	%1690.620288	%1691.155159	16.0685	1.069742	0.301003729	
C4orf33	%1021.56087	%1022.089621	0.34595	1.057502	0.303785613	
CPT1B	%3717.557641	%3718.085763	999	1.056244	0.304073407	
CCDC157	%3831.36541	%3831.890366	2.83119	1.049912	0.305527355	
SREK1	%2712.525609	%2713.046497	0.34506	1.041776	0.307408781	
LHFPL5	%927.588394	%928.099805	0.21741	1.022822	0.311850557	
LRPPRC	%7708.02387	%7708.533739	0.54466	1.019738	0.312581164	
OR1A2	%1539.552783	%1540.062586	2.66947	1.019606	0.312612485	
SLC24A4	%2703.41499	%2703.920354	0.35598	1.010728	0.314728496	
CXCR5	%1773.867239	%1774.372201	0.22237	1.009924	0.314921047	
SV2B	%3188.343746	%3188.845969	0.35683	1.004446	0.316237092	
TNFAIP8L3	%1464.884232	%1465.365996	0.36598	0.963528	0.326299599	
TMEM139	%1120.254694	%1120.727779	999	0.94617	0.330696111	
DEF8	%2620.427827	%2620.880764	0.58453	0.905874	0.341211543	
RNF216	%4385.585414	%4386.030756	0.37708	0.890684	0.345292018	
PPP1R12A	%4513.348	%4513.792253	2.02744	0.888506	0.345882489	
H2AFB3	%625.161437	%625.598759	999	0.874644	0.349672853	
CASP8	%2454.095063	%2454.529644	0.38531	0.869162	0.351187407	
WFDC11	%494.17414	%494.602758	0	0.857236	0.354513335	
AGGF1	%3402.872135	%3403.295989	0.48452	0.847708	0.357201543	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
AHSA1	%1499.35619	%1499.767039	999	0.821698	0.364684178	
LDB3	%3919.699744	%3920.083419	0.71836	0.76735	0.381038102	
ITGB3BP	%887.211283	%887.594956	0.2768	0.767346	0.381039343	
INTS6	%4110.202514	%4110.57012	0.52193	0.735212	0.391198976	
LAMA4	%8656.74366	%8657.107899	0.65699	0.728478	0.393376973	
ZNF275	%2173.358007	%2173.720464	0.28249	0.724914	0.394536743	
ARV1	%1317.472192	%1317.83365	0.41918	0.722916	0.395189071	
NSUN3	%1618.629731	%1618.986548	999	0.713634	0.398240045	
C11orf20	%1249.695201	%1250.043019	63.01992	0.695636	0.404253958	
YTHDC1	%3078.159057	%3078.505319	4.36211	0.692524	0.405307199	
PPIG	%3511.616691	%3511.960388	0.29844	0.687394	0.407052195	
LYG1	%1103.182048	%1103.524751	0.30281	0.685406	0.40773138	
KLRG2	%2205.224974	%2205.564952	0.29331	0.679956	0.409601876	
GPRASP2	%4102.211535	%4102.542896	999	0.662722	0.415600617	
DIRC2	%2214.062675	%2214.391647	6.57373	0.657944	0.417286728	
MOCS3	%2332.893407	%2333.222015	0.43906	0.657216	0.417544524	
COQ3	%1950.437685	%1950.764472	999	0.653574	0.418837772	
IFNA2	%1005.648608	%1005.975011	999	0.652806	0.419111244	
MED19	%1130.121957	%1130.445191	7.85595	0.646468	0.421378299	
SCG3	%2151.995667	%2152.318469	0.30963	0.645604	0.421688763	
ZNF652	%2780.462097	%2780.781748	0.31129	0.639302	0.423963666	
STX2	%1320.764606	%1321.082466	999	0.63572	0.42526491	
MLLT6	%4824.731172	%4825.041007	286.52238	0.61967	0.431169942	
MTG1	%1717.921573	%1718.229136	0.31174	0.615126	0.432864283	
MPHOSPH9	%4891.186772	%4891.49409	2.18326	0.614636	0.433047595	
GCOM1	%2848.563386	%2848.868039	999	0.609306	0.435049233	
CLEC4E	%1201.524502	%1201.828951	999	0.608898	0.435203035	
OR5AS1	%1662.673764	%1662.976477	2.19927	0.605426	0.436515218	
C1orf27	%2080.411494	%2080.709399	999	0.59581	0.440181181	
TGM1	%4089.769372	%4090.064439	0.32806	0.590134	0.442367306	
FXYD3	%495.310977	%495.601056	999	0.580158	0.446250397	
FTSJ2	%1310.625946	%1310.915776	6.7416	0.57966	0.446445621	
IL17RB	%2645.145134	%2645.426789	0.60821	0.56331	0.452929659	
METTL6	%1402.763801	%1403.04396	0.33705	0.560318	0.454132144	
VCX2	%904.059729	%904.336026	1.80532	0.552594	0.45725972	
TMEM232	%3272.028912	%3272.295993	0.57597	0.534162	0.464862305	
POFUT2	%2134.793465	%2135.057324	0.34709	0.527718	0.467567843	
PSMD9	%1064.360043	%1064.622263	999	0.52444	0.468953825	
BROX	%1818.122267	%1818.382916	0.34768	0.521298	0.470288517	
LAMC2	%5963.308866	%5963.568913	0.62255	0.520094	0.470801587	
MRPL55	%877.558579	%877.81592	999	0.514682	0.473119048	
ZBP1	%2566.876219	%2567.131445	2.06832	0.510452	0.474943254	
ZNF20	%2602.706914	%2602.961412	48.6143	0.508996	0.475573803	
OR2J3	%1698.405472	%1698.655594	0.48574	0.500244	0.47939293	
C1orf187	%1762.453739	%1762.701143	0.36161	0.494808	0.481790369	
G6PC	%1733.803045	%1734.045995	0.36118	0.4859	0.485761943	
FZR1	%2348.630685	%2348.870245	0.40031	0.47912	0.488821191	
TMED4	%1060.788186	%1061.025885	999	0.475398	0.490514262	
WDR5B	%1588.816676	%1589.053796	0.36974	0.47424	0.49104301	
JAM2	%1441.386946	%1441.613801	0.37811	0.45371	0.50057838	
MRGPRE	%1602.537368	%1602.760706	0.40202	0.446676	0.50391771	
B4GALT5	%1749.881887	%1750.103806	4.4978	0.443838	0.50527581	
LETM2	%2523.131764	%2523.353582	0.53396	0.443636	0.505372714	
CPB2	%2230.687358	%2230.908233	0.38346	0.44175	0.506279012	
C7orf60	%1789.518281	%1789.737089	4.43677	0.437616	0.508275361	
ASPH	%3782.66885	%3782.885966	0.68067	0.434232	0.509919643	
ZNF30	%3412.458451	%3412.67219	0.71913	0.427478	0.513229057	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
DEFB110	%340.308222	%340.521348	999	0.426252	0.513833789	
MARVELD3	%1940.808369	%1941.019849	0.361	0.42296	0.515463745	
IL19	%1203.448146	%1203.656621	0.59796	0.41695	0.518462872	
NDP	%593.25467	%593.461013	0.39567	0.412686	0.520609337	
C4orf7	%518.736383	%518.937169	999	0.401572	0.526278525	
APOBEC1	%1256.990414	%1257.190474	0.39106	0.40012	0.52702729	
PIP4K2C	%1757.317099	%1757.515995	0.40004	0.397792	0.528231769	
PPP2R2C	%2048.69176	%2048.885555	23.10117	0.38759	0.533568928	
MSRB2	%997.043196	%997.233795	0.70021	0.381198	0.536962783	
TBRG1	%1916.741914	%1916.930873	0.41275	0.377918	0.538719599	
RESP18	%1251.280919	%1251.469761	1.8818	0.377684	0.538845334	
FBXO22	%1930.62708	%1930.814359	0.41468	0.374558	0.54053019	
CCDC69	%1442.396463	%1442.581066	0.41667	0.369206	0.543437385	
NT5M	%972.574187	%972.758593	999	0.368812	0.543652543	
NUP88	%3816.827626	%3817.006073	0.56964	0.356894	0.550236309	
CYP3A5	%2731.021565	%2731.199007	0.42477	0.354884	0.551361352	
MFSD6L	%3312.106213	%3312.282408	0.68543	0.35239	0.552763317	
GPR39	%2381.148384	%2381.321894	0.46451	0.34702	0.555804903	
AGAP10	%4366.505943	%4366.676669	1.31184	0.341452	0.558992297	
FMO6P	%713.08688	%713.254722	0.47291	0.335684	0.562331157	
LSM7	%453.512197	%453.679955	0	0.335516	0.562428978	
CCL24	%713.117719	%713.285398	0.47309	0.335358	0.562521007	
TMEM179	%903.138616	%903.305864	455.03689	0.334496	0.563023597	
CISH	%1389.908606	%1390.075447	0.43632	0.333682	0.563498994	
CCRL1	%1662.589732	%1662.751864	0.4415	0.324264	0.569056335	
CAPN11	%3812.376195	%3812.534224	0.70719	0.316058	0.573986329	
OR10G3	%1724.387594	%1724.544344	0.44001	0.3135	0.575540345	
TMEM194A	%2096.545571	%2096.700637	0.44807	0.310132	0.577599196	
C9orf142	%1044.022715	%1044.174463	0.45351	0.303496	0.581698998	
PLEKHB2	%1115.847824	%1115.994549	0.45786	0.29345	0.588018124	
PRRC1	%2120.3207	%2120.457178	0.53258	0.272956	0.60135572	
ZNF540	%3154.033535	%3154.167204	0.5098	0.267338	0.60512308	
SYNJ2BP	%647.222438	%647.348064	0.48711	0.251252	0.616194882	
WFDC6	%441.659453	%441.783646	0.48772	0.248386	0.618213844	
SUMF1	%1881.652178	%1881.770273	0.61838	0.23619	0.626971543	
ZNF574	%4505.789434	%4505.90687	0.63593	0.234872	0.627934611	
OR13J1	%1778.923356	%1779.039532	0.65747	0.232352	0.629785314	
PER3	%6656.616104	%6656.728188	0.7828	0.224168	0.635882299	
CNPY1	%413.520712	%413.631326	0.5075	0.221228	0.638105833	
C11orf40	%1331.198014	%1331.294505	1.60398	0.192982	0.660446227	
RGS18	%1078.674418	%1078.770005	0.57262	0.191174	0.661941299	
PADI1	%3539.778597	%3539.874149	0.67733	0.191104	0.661999352	
OR14A2	%1605.933077	%1606.028169	0.71448	0.190184	0.66276352	
EBI3	%1154.287578	%1154.380269	0.57739	0.185382	0.666788258	
KDM5D	%8470.189689	%8470.279611	1.26854	0.179844	0.671507339	
KLHDC4	%2856.132783	%2856.221321	0.74056	0.177076	0.673898216	
DEFB103A	%335.180111	%335.259933	0.56403	0.159644	0.689484489	
CCDC73	%5510.595454	%5510.668703	0.71922	0.146498	0.701904714	
OR5H6	%1746.054459	%1746.126614	0.74825	0.14431	0.704033336	
ZNF561	%3224.323025	%3224.394214	1.50363	0.142378	0.70592831	
IFI44	%2283.319674	%2283.390275	0.7523	0.141202	0.707088974	
WDR63	%4324.711301	%4324.781562	0.72349	0.140522	0.707762624	
SECTM1	%1274.902479	%1274.964614	0.7297	0.12427	0.724448695	
ZNF302	%2361.605483	%2361.667549	1.4514	0.124132	0.724595505	
DNAJC5G	%1132.596273	%1132.656678	0.73407	0.12081	0.728157634	
ZMYND17	%2328.02562	%2328.079403	1.44738	0.107566	0.74293241	
PCDHA1	%5051.707612	%5051.759957	0.79144	0.10469	0.746272432	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
FCRL2	%3056.338951	%3056.390549	0.81053	0.103196	0.748027504	
EXPH5	%10700.81575	%10700.86236	0.87018	0.09323	0.760110351	
SEC13	%1770.297882	%1770.338062	0.6985	0.08036	0.776810142	
FGF2	%1338.428633	%1338.465685	1.35994	0.074104	0.785452481	
ATAD5	%9294.722015	%9294.754243	1.14855	0.064456	0.799586828	
ADAM9	%3865.575209	%3865.607166	0.7285	0.063914	0.800413353	
DBX1	%2070.955492	%2070.987331	0.7461	0.063678	0.800774407	
TSSK4	%1833.764541	%1833.795042	0.74746	0.061002	0.804919191	
ZFP57	%2766.755241	%2766.782494	0.74642	0.054506	0.815400189	
ROBO4	%5267.166419	%5267.193085	0.74994	0.053332	0.817363574	
FAM55B	%2830.180804	%2830.203968	1.25921	0.046328	0.829580673	
TFEC	%1628.676756	%1628.698926	0.76882	0.04434	0.833222314	
EXD1	%2906.310689	%2906.329936	1.25372	0.038494	0.844454506	
FAAH2	%2752.420331	%2752.439263	1.14011	0.037864	0.845716483	
PAFAH1B1	%1902.154168	%1902.171764	0.79176	0.035192	0.851193904	
TAC4	%627.935695	%627.952841	1.23552	0.034292	0.853087077	
PMFBP1	%5170.029396	%5170.045997	0.8683	0.033202	0.855414661	
LAIR1	%1743.812914	%1743.827799	1.17361	0.02977	0.863013135	
RBBP7	%2090.836119	%2090.847561	0.87899	0.022884	0.879759117	
OR1N1	%1423.184799	%1423.195984	0.83047	0.02237	0.881107004	
PTTG2	%1130.119653	%1130.129991	1.17915	0.020676	0.885665103	
ZNF192	%2773.049445	%2773.059578	0.838	0.020266	0.886796681	
WDR74	%1903.561594	%1903.569296	1.15279	0.015404	0.901225923	
TXNDC11	%4977.755075	%4977.760692	0.87643	0.011234	0.915589838	
C1orf43	%1159.297651	%1159.3029	0.88067	0.010498	0.918391761	
CA5A	%1403.985973	%1403.989406	1.0715	0.006866	0.933961802	
VSIG1	%2093.650429	%2093.65342	0.90899	0.005982	0.938350374	
CENPT	%3154.589831	%3154.591895	0.96016	0.004128	0.948771553	
ZFP37	%3100.921577	%3100.923549	0.91022	0.003944	0.949924751	
PRSS55	%2131.580547	%2131.582501	0.95142	0.003908	0.950153515	
CEBPZ	%5165.546572	%5165.547938	1.03201	0.002732	0.958314723	
C19orf47	%2052.382773	%2052.383608	1.04863	0.00167	0.967403015	
ZNF117	%3440.187324	%3440.188104	1.01278	0.00156	0.968494277	
SOCS4	%1990.215122	%1990.215729	0	0.001214	0.972205329	
TSPAN8	%1578.484378	%1578.484884	1.02842	0.001012	0.974622019	
C12orf5	%1454.503188	%1454.503482	0.97227	0.000588	0.980654224	
IDO2	%2229.349763	%2229.350053	0.98275	0.00058	0.980786253	
CCDC68	%1603.613563	%1603.613788	0	0.00045	0.983075582	
TRAIP	%2304.926898	%2304.927061	0	0.000326	0.985594602	
WDFY2	%1824.215545	%1824.215682	0	0.000274	0.986793264	
DLX6	%1107.77776	%1107.777834	0	0.000148	0.990293555	
NPY5R	%1990.417869	%1990.417926	0	0.000114	0.991481086	
DERL1	%1106.312857	%1106.312913	0	0.000112	0.991556141	
PIAS1	%2899.376991	%2899.377045	0	0.000108	0.99170829	
EIF2C4	%3719.55317	%3719.553222	0	0.000104	0.991863283	
RHOB	%856.699884	%856.699933	0	9.8E%05	0.992101475	
ABHD10	%1500.948102	%1500.948143	0	8.2E%05	0.992774947	
ASH2L	%2901.990514	%2901.990552	0	7.6E%05	0.993044292	
GMNN	%1035.10325	%1035.103288	0	7.6E%05	0.993044292	
GLYAT	%1578.33193	%1578.331965	0	7E%05	0.993324497	
RNF11	%655.292812	%655.292847	0	7E%05	0.993324497	
CD69	%1045.196338	%1045.196371	0	6.6E%05	0.993518026	
GSC	%1065.457466	%1065.457498	0	6.4E%05	0.993616992	
DNAJC24	%685.156699	%685.156729	0	6E%05	0.993819675	
LRRC2	%1794.284442	%1794.284467	0	5E%05	0.994358151	
HIST1H3F	%761.424527	%761.424551	0	4.8E%05	0.994472138	
PYGO2	%1791.658402	%1791.658426	0	4.8E%05	0.994472138	

Gene	Free&nL	Fixed&nL	branch_w	2ΔlnL	Pvalue	k
ARCN1	%2281.996002	%2281.996025	0	4.6E%05	0.994588525	
PNMA1	%1586.9628	%1586.962823	0	4.6E%05	0.994588525	
EPT1	%1772.758408	%1772.75843	0	4.4E%05	0.994707471	
FBL	%1605.955322	%1605.955344	0	4.4E%05	0.994707471	
MTIF3	%1539.553177	%1539.553195	0	3.6E%05	0.995212721	
FAM165B	%284.955579	%284.955594	0	3E%05	0.995629828	
DDB2	%2011.728837	%2011.728847	0	2E%05	0.996431764	
ZC4H2	%923.282204	%923.282214	0	2E%05	0.996431764	
ZNRD1	%572.059204	%572.059214	0	2E%05	0.996431764	
C14orf181	%762.339246	%762.339255	0	1.8E%05	0.996614873	
THY1	%745.9053	%745.905309	0	1.8E%05	0.996614873	
RAB17	%1171.41937	%1171.419379	0	1.8E%05	0.996614873	
GPHA2	%627.57699	%627.576998	0	1.6E%05	0.99680847	
PFDN6	%550.824183	%550.82419	0	1.4E%05	0.997014596	
FAM103A1	%520.816492	%520.816499	0	1.4E%05	0.997014596	
TMEM106B	%1217.607899	%1217.607906	0	1.4E%05	0.997014596	
BET1	%508.096101	%508.096107	0	1.2E%05	0.997236052	
RPL23A	%869.3576	%869.357606	0	1.2E%05	0.997236052	
IFI27L1	%554.400599	%554.400603	0	8E%06	0.997743245	
NPFF	%606.916154	%606.916158	0	8E%06	0.997743245	
RBP7	%647.188539	%647.188543	0	8E%06	0.997743245	
TMEM92	%872.351116	%872.35112	1.00321	8E%06	0.997743245	
VPS52	%3325.904609	%3325.904613	0	8E%06	0.997743245	
GNAT2	%1603.340311	%1603.340313	0	4E%06	0.998404232	
HNRNPD	%1491.679042	%1491.679044	0	4E%06	0.998404232	
FOSB	%1438.019208	%1438.019209	0	2E%06	0.998871621	
CCDC115	%881.708097	%881.708098	0	2E%06	0.998871621	
AMBN	%2392.873056	%2392.87281	0	%0.000492	#NUM!	
ANKRD52	%5051.05294	%5051.052793	0.96985	%0.000294	#NUM!	
ATP5H	%762.138943	%762.138314	0	%0.001258	#NUM!	
C1QTNF7	%1371.255474	%1371.255473	0	%2E%06	#NUM!	
C22orf41	%394.970541	%394.970535	0	%1.2E%05	#NUM!	
C8orf39	%460.66294	%460.662939	0	%2E%06	#NUM!	
CCNB1	%1927.041312	%1927.041307	0	%1E%05	#NUM!	
DDTL	%774.799537	%774.799509	0	%5.6E%05	#NUM!	
FAM64A	%1289.124842	%1282.343497	0.88731	%13.56269	#NUM!	
GADD45A	%733.845815	%733.845796	0	%3.8E%05	#NUM!	
GNAO1	%2133.570861	%2115.472946	0	%36.19583	#NUM!	
GUCA1B	%890.17185	%890.17184	0	%2E%05	#NUM!	
HAUS2	%1109.529271	%1109.529261	0	%2E%05	#NUM!	
HLF	%1269.765226	%1269.765222	0	%8E%06	#NUM!	
HM13	%1874.075885	%1874.07584	0	%9E%05	#NUM!	
ISYNA1	%2712.086992	%2712.08661	0	%0.000764	#NUM!	
MBLAC2	%1292.951432	%1292.951426	0	%1.2E%05	#NUM!	
OLA1	%1684.85874	%1684.858735	0	%1E%05	#NUM!	
POU2F2	%2166.079542	%2166.0795	0	%8.4E%05	#NUM!	
RGS8	%947.962657	%885.363479	0	%125.198356	#NUM!	
RPS12	%691.385485	%640.385936	0	%101.999098	#NUM!	
S100A4	%429.462573	%429.462545	0	%5.6E%05	#NUM!	
SIX6	%1100.566686	%1100.56668	0	%1.2E%05	#NUM!	
SLC45A2	%2723.250236	%2718.582092	278.55217	%9.336288	#NUM!	
TIAF1	%617.587777	%617.587691	0	%0.000172	#NUM!	
TMEM208	%764.313333	%764.313328	0	%1E%05	#NUM!	
TRIM39	%2367.106658	%2367.106645	0	%2.6E%05	#NUM!	
TSPAN15	%1377.409714	%1377.409474	0	%0.00048	#NUM!	
ZCCHC17	%1050.546679	%1050.546678	0	%2E%06	#NUM!	
ZNF157	%2665.960444	%2379.258442	0.00422	%573.404004	#NUM!	
ZNF569	%3122.819885	%3122.819839	0	%9.2E%05	#NUM!	

Gorilla

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
HIST1H3F	(761.424527	(843.734663	164.620272	0.0001	1.10729E(37	
HIST1H2AL	(743.532442	(798.418825	109.772766	0.0001	1.09893E(25	
MYL6B	(1181.611213	(1205.516773	47.81112	0.10877	4.69323E(12	
APC2	(11995.6663	(12017.99552	44.658448	0.12501	2.34583E(11	
NCOR2	(12226.47529	(12248.05795	43.165326	0.10483	5.03043E(11	
BCL9L	(7012.51155	(7030.470968	35.918836	0.05104	2.0571E(09	
SPTB	(11267.9448	(11285.65552	35.421448	0.09909	2.65547E(09	
ANO1	(4808.924374	(4822.577975	27.307202	0.02141	1.73564E(07	
FKRP	(2437.252384	(2450.632494	26.76022	0.02321	2.3033E(07	
USP7	(4826.350612	(4839.69613	26.691036	0	2.38726E(07	
CHL1	(6211.000814	(6224.273182	26.544736	0.0819	2.57505E(07	
PPP2R2C	(2050.782139	(2064.027733	26.491188	0.04041	2.64743E(07	
JAG2	(6296.120202	(6309.222495	26.204586	0.02813	3.07092E(07	
STAT5B	(3675.641875	(3688.569981	25.856212	0	3.67819E(07	
ZNF592	(5978.381866	(5991.05794	25.352148	0.05629	4.7762E(07	
MEGF10	(5513.956013	(5526.202559	24.493092	0	7.45767E(07	
GRIK3	(4315.41378	(4327.325712	23.823864	0.02435	1.05566E(06	
EPB41L1	(4094.969219	(4106.190476	22.442514	0	2.16528E(06	
ROR2	(4589.553436	(4600.722029	22.337186	0.02669	2.28734E(06	
CNTN6	(5056.099903	(5066.771519	21.343232	0.059	3.83974E(06	
C4orf31	(2781.789364	(2791.910696	20.242664	0	6.82145E(06	
EPHB3	(4498.898852	(4508.087597	18.37749	0	1.81186E(05	
NCKAP1L	(5397.035892	(5406.178128	18.284472	0.11229	1.90252E(05	
RTN4RL2	(1988.494077	(1997.627672	18.26719	0	1.91986E(05	
SLC4A4	(4930.247111	(4939.103816	17.71341	0	2.5681E(05	
TBC1D9	(5834.048489	(5842.793221	17.489464	0	2.88904E(05	
EIF2C2	(4034.06698	(4042.801104	17.468248	0	2.92146E(05	
SLC24A4	(2704.457615	(2712.922299	16.929368	0.04082	3.87967E(05	
STUB1	(1347.877786	(1356.066503	16.377434	0	5.18995E(05	
RALGDS	(4387.331359	(4395.42189	16.181062	0.08308	5.75668E(05	
SEMA4B	(3997.356685	(4005.403623	16.093876	0.03801	6.02786E(05	
SMC5	(5108.575767	(5116.389993	15.628452	0	7.70859E(05	
DIRC2	(2214.279329	(2222.046577	15.534496	0	8.10133E(05	
KIDINS220	(8391.734798	(8399.423536	15.377476	0.12646	8.80314E(05	
PDZD7	(2714.47848	(2722.088333	15.219706	0.02483	9.56996E(05	
SLC7A14	(3657.796778	(3665.282922	14.972288	0.04726	0.000109102	
PLCH2	(7498.087894	(7505.540027	14.904266	0.17425	0.000113107	
ADRA1B	(2498.376592	(2505.752456	14.751728	0.079	0.000122635	
ISYNA1	(2712.071134	(2719.424927	14.707586	0.05721	0.00012554	
SIPA1	(4987.425677	(4994.686357	14.52136	0.13585	0.000138579	
CHST2	(2515.522503	(2522.748271	14.451536	0	0.000143813	
SOCS4	(1988.938561	(1996.095095	14.313068	0	0.000154787	
POFUT2	(2133.981167	(2141.038201	14.114068	0	0.000172052	
C1orf101	(5585.206135	(5592.262617	14.112964	0.16511	0.000172153	
PCDH7	(5420.621687	(5427.596019	13.948664	0	0.000187871	
ME2	(2645.732597	(2652.601767	13.73834	0	0.000210121	
SLIT1	(7417.342626	(7424.14987	13.614488	0.18928	0.000224447	
C11orf20	(1247.721466	(1254.528545	13.614158	0.0625	0.000224486	
ARHGAP4	(5882.835642	(5889.639315	13.607346	0.06856	0.000225302	
ZFP64	(3247.67512	(3254.467413	13.584586	0	0.00022805	
CXCR5	(1772.785919	(1779.572303	13.572768	0	0.000229491	
PITPNM1	(6236.025224	(6242.803674	13.5569	0.14018	0.000231439	
ZBTB38	(5739.345785	(5746.07591	13.46025	0.08357	0.000243671	
LHX2	(1795.850632	(1802.571186	13.441108	0.0645	0.00024617	
ERCC3	(3775.906232	(3782.522136	13.231808	0	0.000275238	
POU2F2	(2166.06691	(2172.647216	13.160612	0.17236	0.000285895	
KDM5D	(8474.862749	(8481.439615	13.153732	0.24631	0.000286947	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
LAMA4	(8660.595244	(8667.094809	12.99913	0.16881	0.000311636	
GSC	(1064.696228	(1071.176583	12.96071	0	0.000318097	
CDT1	(2995.054598	(3001.518717	12.928238	0.10238	0.000323662	
STX2	(1320.419958	(1326.8406	12.841284	0	0.000339055	
GJA4	(1636.947663	(1643.292836	12.690346	0.04708	0.000367548	
ECEL1	(3728.100522	(3734.414362	12.62768	0.06885	0.000380077	
CDC37	(1706.975069	(1713.267647	12.585156	0	0.000388823	
COL5A2	(6698.180741	(6704.445199	12.528916	0	0.000400702	
PCDHA3	(4895.918398	(4902.165424	12.494052	0.05478	0.00040825	
MARK2	(3519.997843	(3526.066481	12.137276	0.05091	0.000494239	
KCNJ9	(1729.307429	(1735.368524	12.12219	0	0.000498254	
PRPF4B	(4587.799105	(4593.752897	11.907584	0	0.000559059	
KCNB1	(3940.724515	(3946.634482	11.819934	0.05307	0.000585999	
RD3	(981.247466	(987.140933	11.786934	0	0.000596479	
IL17REL	(1707.593833	(1713.427113	11.66656	0.04482	0.000636336	
GFOD2	(1869.086569	(1874.907221	11.641304	0	0.000645034	
DEF8	(2631.755845	(2637.567067	11.622444	0.03928	0.000651607	
AGPAT2	(1421.672926	(1427.456552	11.567252	0.12794	0.000671235	
PNPLA7	(6802.616823	(6808.377237	11.520828	0.22015	0.000688207	
RAP1GAP2	(3635.795433	(3641.536626	11.482386	0.04742	0.000702589	
HSPBP1	(1503.098667	(1508.746868	11.296402	0	0.000776574	
GPR176	(2455.925892	(2461.478355	11.104926	0	0.000860987	
TBC1D17	(3152.150905	(3157.700062	11.098314	0.11233	0.000864062	
CLCN4	(3597.200471	(3602.575026	10.74911	0	0.001043295	
DNAJC17	(1457.24509	(1462.585549	10.680918	0	0.001082463	
TJP2	(6016.446879	(6021.763229	10.6327	0.10477	0.001111054	
TOP3A	(5199.66187	(5204.927656	10.531572	0.18229	0.001173524	
TGM1	(4090.214718	(4095.467482	10.505528	0.09616	0.001190179	
ASCC3	(10025.87695	(10031.12307	10.492234	0.15613	0.001198773	
HEYL	(1749.247664	(1754.405429	10.31553	0	0.001319154	
LRRTM3	(2556.204485	(2561.360955	10.31294	0	0.001321007	
TNS3	(7655.725917	(7660.858424	10.265014	0.18349	0.001355767	
MRGPRE	(1603.334581	(1608.423827	10.178492	0.07742	0.001420883	
DCAF12L2	(2616.935995	(2622.00588	10.13977	0	0.001451043	
FBXL12	(1531.180665	(1536.240241	10.119152	0.09295	0.001467365	
ASB1	(1624.849998	(1629.892464	10.084932	0	0.001494867	
NR2C2	(2829.571755	(2834.604014	10.064518	0	0.001511521	
IRF8	(2086.773238	(2091.792187	10.037898	0.05934	0.001533521	
MRPL20	(881.316562	(886.318581	10.004038	0.33678	0.001561974	
SULF2	(4179.555461	(4184.534536	9.95815	0.11263	0.001601389	
PLB1	(7860.671109	(7865.628423	9.914628	0.31161	0.001639703	
SLC35C1	(1829.504877	(1834.421595	9.833436	0.0791	0.001713679	
SQSTM1	(2440.093737	(2444.994264	9.801054	0.05675	0.001744119	
TMCC3	(2203.6243	(2208.520404	9.792208	0	0.001752529	
PRKCD	(3135.964677	(3140.849759	9.770164	0	0.001773666	
TMC8	(3632.068189	(3636.875444	9.61451	0.11782	0.00193046	
GPT2	(2463.751775	(2468.551195	9.59884	0	0.001947003	
CDK9	(1677.519059	(1682.302613	9.567108	0	0.001980946	
MAP4K3	(4021.388625	(4026.120917	9.464584	0.06195	0.002094769	
NPY1R	(1730.053118	(1734.763486	9.420736	0	0.002145454	
CARD11	(5872.557472	(5877.234666	9.354388	0.44421	0.002224522	
NPFFR1	(2089.956076	(2094.625692	9.339232	0.05298	0.002242995	
KLHDC4	(2858.064918	(2862.718873	9.30791	0.13343	0.002281666	
ZNF574	(4508.442769	(4513.071283	9.257028	0.14621	0.002345934	
YLPM1	(9690.61012	(9695.224806	9.229372	0.14904	0.002381633	
ARHGAP19	(2377.683211	(2382.282639	9.198856	0	0.002421664	
UBLCP1	(1381.099834	(1385.696465	9.193262	0	0.002429076	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
MED19	(1132.634976	(1137.221677	9.173402	0	0.002455577	
TBR1	(2895.560751	(2900.092117	9.062732	0	0.002608719	
COL20A1	(6580.495507	(6584.90078	8.810546	0.27574	0.002994944	
PLAU	(2338.228948	(2342.426626	8.395356	0.17358	0.003761808	
TUBB	(2153.009605	(2157.191076	8.362942	0	0.003829501	
KIAA0947	(12219.10907	(12223.27717	8.336196	0.37442	0.003886288	
TRIM39	(2366.23745	(2370.377089	8.279278	0	0.004010007	
MAT2A	(1792.260947	(1796.399357	8.27682	0	0.004015439	
WDR74	(1903.650893	(1907.76873	8.235674	0.07402	0.004107492	
B4GALT5	(1751.327912	(1755.413759	8.171694	0	0.004254915	
MAP3K7	(2660.70385	(2664.700343	7.992986	0	0.004695891	
SV2B	(3190.859187	(3194.775615	7.832856	0.07318	0.005130497	
PNLIPRP3	(2311.410004	(2315.310821	7.801634	0	0.005219901	
MBTPS2	(2423.475621	(2427.371539	7.791836	0.13263	0.005248284	
C22orf41	(394.337054	(398.173488	7.672868	0	0.005605729	
TBCB	(1153.181428	(1157.0062	7.649544	0.06891	0.005678667	
GUCY2F	(5371.885922	(5375.705099	7.638354	0.12654	0.005714004	
PLS3	(2742.700496	(2746.514649	7.628306	0.08037	0.005745925	
ASH2L	(2901.488346	(2905.239687	7.502682	0	0.006160718	
DDHD2	(3297.961872	(3301.697409	7.471074	0.0833	0.006269814	
ZNF335	(6610.619453	(6614.35386	7.468814	0.16683	0.006277689	
DCTN6	(847.70342	(851.40887	7.4109	0	0.006482988	
TEKT5	(2695.332628	(2699.015528	7.3658	0.18686	0.006647602	
SLC5A3	(3196.239485	(3199.822475	7.16598	0	0.007429909	
ABHD4	(1660.461762	(1664.041623	7.159722	0	0.007455875	
ITGB8	(3617.479822	(3621.049994	7.140344	0.07808	0.00753687	
PAX9	(1574.130519	(1577.66087	7.060702	0	0.007879312	
LGALS7	(625.773803	(629.298264	7.048922	0	0.007931297	
ADH1A	(2353.262073	(2356.772405	7.020664	0.49386	0.008057435	
KMO	(2494.089052	(2497.544326	6.910548	0.13764	0.008568872	
INTS6	(4109.963097	(4113.378568	6.830942	0.08023	0.0089592	
MTIF3	(1536.421943	(1539.77432	6.704754	0	0.00961562	
OVOL2	(1302.298598	(1305.61277	6.628344	0.06521	0.010036853	
SMC2	(5401.352277	(5404.603759	6.502964	0.24517	0.010769481	
SDSL	(1769.676099	(1772.911211	6.470224	0.08433	0.010969671	
FAM167A	(1034.356455	(1037.555308	6.397706	0	0.011426792	
FANCG	(3678.566641	(3681.753021	6.37276	0.09282	0.011588522	
CASP8	(2452.585187	(2455.746273	6.322172	0	0.011923749	0.013595707
MSL2	(2520.834166	(2523.973716	6.2791	0	0.012217013	0.013685152
CCDC132	(4369.938068	(4373.000042	6.123948	0	0.013336263	0.013774597
PRSS55	(2131.982908	(2135.037405	6.108994	0.28965	0.013449566	0.013864043
TMED4	(1062.020182	(1065.065261	6.090158	0	0.013593693	0.013953488
JAM2	(1441.212044	(1444.240931	6.057774	0.09191	0.013845209	0.014042934
WDR63	(4324.404731	(4327.425402	6.041342	0.19163	0.013974657	0.014132379
DUSP1	(1011.279256	(1014.290918	6.023324	0	0.014118032	0.014221825
HIST1H2AJ	(620.351488	(623.345356	5.987736	0	0.01440568	0.01431127
TSPAN15	(1376.99915	(1379.983025	5.96775	0	0.01456986	0.014400716
ZNF561	(3224.094933	(3227.075939	5.962012	0.5245	0.014617351	
MAP2	(8749.774914	(8752.753036	5.956244	0.34304	0.014665251	
SHPRH	(8156.749057	(8159.704175	5.910236	0.37041	0.015053155	
WDR33	(6004.582666	(6007.534322	5.903312	0.20479	0.015112441	
NR1D2	(2650.815437	(2653.746376	5.861878	0	0.015472277	
ABHD10	(1500.80646	(1503.736954	5.860988	0.14936	0.015480102	
RBBP6	(8239.111407	(8242.02625	5.829686	0.30897	0.015757936	
CYP4F11	(2992.973786	(2995.864588	5.781604	0.22422	0.016194756	
PPP1R12A	(4526.749569	(4529.635051	5.770964	0	0.016293095	
SCG3	(2151.478346	(2154.344959	5.733226	0	0.016646875	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
ANKRD52	(5053.120706	(5055.986333	5.731254	0.09849	0.016665578	
TBXA2R	(1666.703065	(1669.568153	5.730176	0.25207	0.016675811	
PNKP	(2843.813111	(2846.666427	5.706632	0.2207	0.016900935	
ZNF652	(2779.405217	(2782.252013	5.693592	0	0.017026968	
CYP3A5	(2730.461045	(2733.299662	5.677234	0.3621	0.017186441	
HM13	(1873.951343	(1876.754527	5.606368	0	0.017895318	
HNRPLL	(2492.428968	(2495.218517	5.579098	0	0.018176082	
MLLT6	(4826.090526	(4828.876593	5.572134	0	0.018248508	
EPB49	(1818.279838	(1821.052698	5.54572	0	0.018525934	
PCDHB5	(4600.184978	(4602.956831	5.543706	0.48754	0.018547265	
CLK4	(2166.088266	(2168.84239	5.508248	0.15691	0.018926997	
FAM111A	(3297.167613	(3299.915194	5.495162	0	0.019069161	
DNAI2	(3181.088793	(3183.824476	5.471366	0.23235	0.019330511	
DCAF7	(1558.854378	(1561.579968	5.45118	0	0.019555114	
IL17RB	(2644.485648	(2647.190955	5.410614	0.16081	0.020014675	
ZC3H13	(7600.863047	(7603.561483	5.396872	0.29278	0.020172875	
DMGDH	(4203.915354	(4206.607648	5.384588	0.16239	0.020315385	
TNFSF9	(1174.477091	(1177.16769	5.381198	0	0.020354896	
C9orf46	(559.344906	(562.03529	5.380768	0	0.020359913	
SOAT2	(2725.340836	(2728.020422	5.359172	0	0.020613559	
NXT1	(642.059909	(644.73777	5.355722	0	0.020654381	
TMEM38B	(1445.371047	(1448.027619	5.313144	0	0.021165128	
CYTH1	(1780.511712	(1783.133652	5.24388	0.0888	0.022024101	
SLC6A4	(3061.951942	(3064.554309	5.204734	0	0.022525461	
ELF4	(3309.978757	(3312.580324	5.203134	0	0.022546203	
PLK2	(3090.77955	(3093.354154	5.149208	0	0.023256978	
LAMC2	(5963.246751	(5965.81986	5.146218	0.33703	0.023297062	
ZNF275	(2173.134575	(2175.706595	5.14404	0.17917	0.023326304	
GCK	(2420.347118	(2422.902968	5.1117	0.36895	0.023765023	
HLF	(1269.628897	(1272.141958	5.026122	0	0.024967744	
CDC20	(2289.951047	(2292.459737	5.01738	0	0.025094111	
PAFAH1B1	(1902.11542	(1904.612743	4.994646	0	0.025425854	
DACT2	(4065.065821	(4067.56277	4.993898	0.29967	0.025436846	
PIP4K2C	(1756.942501	(1759.417994	4.950986	0	0.026075793	
PSMD4	(1696.814302	(1699.264207	4.89981	0	0.026859651	
KANK3	(4442.259281	(4444.70505	4.891538	0.30138	0.026988634	
KPTN	(2402.535854	(2404.973921	4.876134	0.15588	0.027230543	
FZR1	(2351.351945	(2353.771537	4.839184	0.07167	0.027820056	
LETM2	(2519.179461	(2521.571067	4.783212	999	0.028738469	
WFDC11	(492.479691	(494.843362	4.727342	0	0.029686729	
ZFP57	(2766.500541	(2768.843762	4.686442	0.24717	0.030401537	
ZNF324B	(3117.522629	(3119.846087	4.646916	0.18442	0.031109391	
LPAR3	(1796.943301	(1799.250023	4.613444	0.21129	0.031722263	
FBL	(1605.454294	(1607.740891	4.573194	0	0.032475961	
OR5AS1	(1663.047799	(1665.333931	4.572264	0	0.032493595	
C11orf84	(2730.748917	(2732.998415	4.498996	0.18325	0.033914761	
OAZ2	(820.46084	(822.709366	4.497052	0	0.033953341	
DBX1	(2071.063212	(2073.289362	4.4523	0.33136	0.034854274	
DLEC1	(9085.547746	(9087.765445	4.435398	0.45224	0.035201012	
ABCB11	(6822.539013	(6824.753553	4.42908	0.31498	0.035331547	
ENOPH1	(1177.854593	(1180.067185	4.425184	0	0.035412295	
VPREB1	(804.739764	(806.9461	4.412672	0.10942	0.035672923	
RHOB	(856.632362	(858.82624	4.387756	0	0.036197926	
SDAD1	(3556.415381	(3558.607849	4.384936	0.22025	0.036257853	
AHSA1	(1500.470198	(1502.640032	4.339668	0	0.037234183	
ZFYVE20	(3772.053707	(3774.133943	4.160472	0.22832	0.041377872	
UPF2	(5621.923137	(5623.968175	4.090076	0.25426	0.043135702	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
WDR5B	(1588.890968	(1590.911582	4.041228	0.18471	0.044401501	
ADAM9	(3866.374807	(3868.394608	4.039602	0.12078	0.044444302	
RAE1	(1759.335257	(1761.343251	4.015988	0.12127	0.045070809	
RFX7	(6743.321614	(6745.329283	4.015338	0.32237	0.045088185	
SCN1B	(1017.551704	(1019.548675	3.993942	0.16907	0.045664113	
ZC3H12D	(2708.391789	(2710.373337	3.963096	0.15933	0.04650809	
NLGN3	(3585.610038	(3587.552502	3.884928	0.12571	0.048721351	
LHFPL5	(930.163819	(932.09246	3.857282	0	0.049530505	
CD2AP	(3055.009393	(3056.929012	3.839238	0.17449	0.05006627	
MOAP1	(1705.584942	(1707.48242	3.794956	0.12853	0.051407224	
DGAT1	(2571.130408	(2573.000918	3.74102	0.53429	0.053092026	
LDB3	(3932.055376	(3933.901052	3.691352	0.27923	0.054695264	
CA10	(1495.465715	(1497.311249	3.691068	0.1314	0.054704578	
ROBO4	(5267.393476	(5269.221344	3.655736	0.27248	0.055876462	
FLT3	(4939.070544	(4940.888518	3.635948	0.31685	0.056544393	
EFS	(2802.294782	(2804.103155	3.616746	0.2729	0.05720065	
SHMT2	(2376.521194	(2378.316747	3.591106	0.1334	0.05808957	
CORO1C	(2135.909044	(2137.674674	3.53126	0.13806	0.060222007	
CAPN11	(3813.303153	(3815.065721	3.525136	0.40006	0.060444866	
CDK13	(6755.816095	(6757.569355	3.50652	0.26062	0.061127728	
CACNG6	(1274.565959	(1276.31498	3.498042	0.32786	0.061441431	
RABGGTA	(2637.829187	(2639.548997	3.43962	0.21165	0.063650331	
HES5	(658.424295	(660.139416	3.430242	0	0.064012721	
DHTKD1	(4800.694107	(4802.401558	3.414902	0.3724	0.06461025	
SH3D21	(4134.933789	(4136.639216	3.410854	0.32199	0.064768919	
OR2J3	(1693.277136	(1694.959311	3.36435	4.80784	0.06662187	
FAM126B	(2576.851132	(2578.499741	3.297218	0.51948	0.069397324	
TMEM121	(1355.171932	(1356.820505	3.297146	0	0.069400366	
MRGPRD	(1879.361664	(1880.991881	3.260434	0.26488	0.070970341	
DCAF5	(4503.854695	(4505.482096	3.254802	0.25111	0.071214538	
CHMP5	(937.877506	(939.500521	3.24603	0	0.071596676	
TAGLN	(885.111653	(886.727751	3.232196	0	0.072203807	
GPRASP2	(4102.909782	(4104.52488	3.230196	0.33238	0.072292036	
C1orf187	(1762.500356	(1764.108472	3.216232	0.25018	0.072911285	
WISP3	(1792.449465	(1794.042778	3.186626	0.15216	0.0742431	
DDTL	(773.533633	(775.125494	3.183722	0	0.074375135	
ZNF575	(1655.870566	(1657.459737	3.178342	999	0.074620411	
VPS52	(3325.78759	(3327.374567	3.173954	0.14076	0.074821105	
MPV17L	(1181.257778	(1182.814332	3.113108	0.22957	0.077664628	
L3MBTL1	(3975.993612	(3977.510787	3.03435	0.20216	0.081519193	
KIAA0562	(4759.980287	(4761.496718	3.032862	0.41143	0.081593975	
SPIB	(1095.633665	(1097.146413	3.025496	0	0.081965255	
ALOX15	(3880.67271	(3882.183775	3.02213	0.60401	0.082135523	
GPHA2	(626.864689	(628.374089	3.0188	0	0.082304346	
LTK	(4352.356277	(4353.86067	3.008786	0.31675	0.082814293	
FAM103A1	(520.70642	(522.204301	2.995762	0	0.08348263	
CNTFR	(1738.27813	(1739.764069	2.971878	0	0.084723447	
RNF208	(1198.646706	(1200.120961	2.94851	0	0.085956775	
CAV1	(809.506379	(810.977565	2.942372	0	0.086283941	
BLNK	(2337.606628	(2339.067696	2.922136	0.44657	0.087372136	
TMEM232	(3271.990752	(3273.445962	2.91042	0.26798	0.088008953	
MIER1	(1902.732236	(1904.183479	2.902486	0.13006	0.088443056	
TAC4	(626.510353	(627.956114	2.891522	0.22251	0.089046767	
RGS8	(885.094951	(886.537256	2.88461	0	0.089429658	
FTSJ2	(1311.51054	(1312.95101	2.88094	0.27556	0.089633683	
BET1	(507.301974	(508.741577	2.879206	0	0.089730257	
SEC13	(1771.169895	(1772.578796	2.817802	0	0.093223983	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
GADD45A	(733.78536	(735.18308	2.79544	0	0.094532814	
LRPPRC	(7707.290938	(7708.678044	2.774212	0.27245	0.095793791	
TMEM43	(2108.304428	(2109.690793	2.77273	0.3374	0.095882505	
RNF11	(655.292812	(656.678539	2.771454	0	0.09595896	
CWC22	(4319.260101	(4320.641594	2.762986	0.30018	0.096468028	
PIGA	(2362.059001	(2363.42747	2.736938	0.23268	0.098052487	
NPY5R	(1990.231065	(1991.599146	2.736162	0	0.098100123	
C7orf60	(1791.645387	(1793.008475	2.726176	0	0.098715388	
CCDC115	(881.215409	(882.567922	2.705026	0	0.100032451	
RGS18	(1078.365562	(1079.717449	2.703774	0.14116	0.100111016	
TTLL9	(2357.918914	(2359.260461	2.683094	0.48674	0.10141851	
CPB2	(2230.382117	(2231.720972	2.67771	0.2843	0.101761968	
ZNRD1	(571.586734	(572.905975	2.638482	0	0.104303162	
IFI44	(2282.228878	(2283.542674	2.627592	0.22755	0.10502088	
TXNDC11	(4978.104128	(4979.412845	2.617434	0.36725	0.105695236	
DSCR3	(1519.618164	(1520.913438	2.590548	0	0.107503135	
FOLR2	(1278.367457	(1279.659422	2.58393	0.14826	0.107953337	
CPT1B	(3719.248337	(3720.538274	2.579874	0.30639	0.108230277	
LHFPL2	(1093.121841	(1094.402984	2.562286	0	0.109440231	
FOSB	(1437.961447	(1439.226322	2.52975	0	0.111717915	
DDB2	(2011.481913	(2012.734962	2.506098	0	0.113406419	
SNRPA1	(1117.342391	(1118.584164	2.483546	0	0.115042621	
C9orf9	(840.158513	(841.399177	2.481328	0	0.115204943	
ZCCHC17	(1050.493317	(1051.724671	2.462708	0	0.116577643	
CHST4	(1995.470742	(1996.698235	2.454986	0	0.117152213	
OAS1	(2332.965148	(2334.183377	2.436458	0.29421	0.118543629	
SDC2	(947.343242	(948.556721	2.426958	0	0.119264139	
PPM1K	(1667.73948	(1668.94919	2.41942	0	0.119839294	
CCRL1	(1661.943231	(1663.12512	2.363778	0	0.124181121	
STH	(711.430581	(712.604197	2.347232	0	0.125505684	
PLEKHB2	(1115.801001	(1116.974328	2.346654	0	0.125552238	
CMBL	(1195.919549	(1197.052546	2.265994	0	0.132241339	
PLCB1	(5509.388164	(5510.518806	2.261284	0.31548	0.132644042	
CNPY1	(412.651147	(413.73385	2.165406	0	0.141147339	
CAPS2	(2950.036711	(2951.109525	2.145628	0.32368	0.14297652	
CPA5	(2348.102873	(2349.170137	2.134528	0.37886	0.144014784	
FAAH2	(2754.130006	(2755.183913	2.107814	0.425	0.14654853	
ARV1	(1314.771299	(1315.820564	2.09853	999	0.14744083	
MARVELD3	(1940.732151	(1941.774591	2.08488	0.47164	0.148763912	
PYGO2	(1791.417129	(1792.459566	2.084874	0	0.148764497	
ZNF157	(2379.2782	(2380.312854	2.069308	0.18243	0.1502897	
IRX6	(2444.253689	(2445.263914	2.02045	0.33601	0.155193144	
SMR3B	(486.018015	(487.023811	2.011592	0	0.156101436	
C9orf142	(1044.015462	(1045.009311	1.987698	0.27806	0.158581782	
FAM64A	(1281.922825	(1282.914107	1.982564	0.18933	0.159120555	
GPR39	(2381.34005	(2382.322214	1.964328	0.2289	0.161051202	
ILKAP	(1841.123743	(1842.090513	1.93354	0.19116	0.164371671	
ACOT12	(2907.073916	(2908.036022	1.924212	0.31707	0.165393075	
GNAT2	(1602.800818	(1603.752744	1.903852	0.19441	0.167647791	
MOCS3	(2332.974123	(2333.896394	1.844542	0.29238	0.174419529	
RABEP1	(3980.293585	(3981.207689	1.828208	0.29185	0.176339354	
ALKBH3	(1306.123682	(1307.023289	1.799214	0.20433	0.179807547	
PIAS1	(2896.528738	(2897.421728	1.78598	0.20642	0.181416728	
ATG16L1	(2891.765578	(2892.655092	1.779028	0.20689	0.182268728	
ASPH	(3783.589674	(3784.474427	1.769506	0.42381	0.183443227	
CCDC69	(1442.22481	(1443.103977	1.758334	0.20806	0.184832453	
METTL6	(1400.839456	(1401.713735	1.748558	999	0.186058115	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
WDFY2	(1823.990434	(1824.828	1.675132	0.21685	0.195572553	
PADI1	(3540.636793	(3541.473645	1.673704	0.33654	0.195763148	
MRPL43	(1378.379459	(1379.213674	1.66843	0.55458	0.196468955	
FCRL2	(3056.002079	(3056.835239	1.66632	0.41516	0.196752166	
CES5A	(3260.521167	(3261.335628	1.628922	1.81357	0.201852216	
CDCA3	(1246.328837	(1247.142248	1.626822	0.31414	0.202143175	
FGF2	(1339.754937	(1340.5657	1.621526	0.22273	0.20287914	
MFSD6L	(3312.334214	(3313.114185	1.559942	0.5002	0.211673713	
C10orf11	(974.09427	(974.866697	1.544854	999	0.213896741	
RPL26	(709.881779	(710.642549	1.52154	999	0.217386594	
GNG5P2	(351.980663	(352.727545	1.493764	999	0.221633371	
CHRDL2	(2445.389171	(2446.132031	1.48572	0.28603	0.222881715	
ZNF117	(3441.997219	(3442.733185	1.471932	0.61651	0.225041115	
ADAM29	(4769.650301	(4770.381292	1.461982	0.52582	0.226615027	
SUMF1	(1881.767501	(1882.498253	1.461504	0.44258	0.22669097	
OR1A2	(1539.242861	(1539.969527	1.453332	3.10319	0.227994057	
RAD21L1	(2719.577933	(2720.273293	1.39072	0.39096	0.238283547	
G6PC	(1729.141253	(1729.823648	1.36479	999	0.242709055	
SLC25A23	(2100.70417	(2101.374074	1.339808	0.16113	0.247067831	
OR1N2	(1643.679612	(1644.343627	1.32803	2.97839	0.249155985	
OR13J1	(1777.651989	(1778.31531	1.326642	104.60121	0.249403489	
FAM120A	(5421.532526	(5422.193068	1.321084	0.49986	0.250397599	
TMEM61	(1209.668629	(1210.323675	1.310092	0.38246	0.252377999	
ABCD3	(3235.474862	(3236.129059	1.308394	0.5777	0.252685636	
GIMAP2	(1823.893685	(1824.543709	1.300048	0.38536	0.254204456	
NUP88	(3817.013941	(3817.653703	1.279524	0.38907	0.257987558	
MAGEB3	(1941.351053	(1941.983887	1.265668	2.89822	0.260580936	
VSIG1	(2093.627118	(2094.234747	1.215258	0.45266	0.270293283	
OR51F2	(1557.163386	(1557.769586	1.2124	0.29139	0.270857328	
DNAJC5G	(1131.956485	(1132.55941	1.20585	42.80764	0.272155579	
TMEM92	(872.330936	(872.926912	1.191952	0.32415	0.274936168	
TSSK4	(1833.556375	(1834.144768	1.176786	0.21055	0.278011275	
SREK1	(2710.447209	(2711.034763	1.175108	999	0.278354164	
GNPAT	(3337.480258	(3338.064661	1.168806	0.5103	0.279646711	
HRH3	(2194.138173	(2194.719956	1.163566	0.18928	0.280727209	
TTYH1	(2169.088433	(2169.663097	1.149328	0.21385	0.283689867	
SEC14L5	(3455.381652	(3455.935379	1.107454	0.36284	0.292636063	
GFRAL	(2057.012423	(2057.560888	1.09693	0.34138	0.294940829	
PRRC1	(2120.516689	(2121.062351	1.091324	0.34556	0.296178039	
S1PR3	(1732.208906	(1732.739588	1.061364	0.20487	0.302904294	
CAPN7	(3742.84186	(3743.369653	1.055586	0.34755	0.304224079	
MRPL55	(877.053694	(877.560895	1.014402	999	0.313850561	
GCGR	(2919.420306	(2919.921813	1.003014	2.65016	0.316582306	
MBD6	(4426.237947	(4426.730003	0.984112	0.31009	0.321185724	
DRAP1	(962.436952	(962.926375	0.978846	896.83559	0.322483876	
ZNF569	(3120.194548	(3120.682157	0.975218	0.52248	0.323382263	
TNFAIP8L3	(1464.887536	(1465.372414	0.969756	0.3644	0.324741039	
TMEM139	(1120.247915	(1120.729181	0.962532	999	0.326549766	
SUSD3	(1285.822942	(1286.293801	0.941718	0.39247	0.331836407	
DEFB110	(339.725869	(340.189541	0.927344	0.2369	0.335554037	
MS4A7	(1299.57116	(1300.031551	0.920782	999	0.337269728	
PRKRIP1	(905.917886	(906.377777	0.919782	0.37241	0.337532218	
MAGEB17	(1974.991373	(1975.443213	0.90368	0.58722	0.341796881	
C19orf47	(2052.897309	(2053.345115	0.895612	0.47086	0.343961026	
HMGCR	(4409.761577	(4410.206597	0.89004	0.7386	0.345466469	
LAPTM4B	(2137.479346	(2137.916943	0.875194	0.53595	0.349521392	
CCDC36	(3126.580436	(3127.015283	0.869694	0.56998	0.351040036	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
C8orf39	(460.662939	(461.079672	0.833466	999	0.36127221	
MDM4	(2142.402773	(2142.814907	0.824268	0.26988	0.363935251	
HSD17B3	(1583.404861	(1583.814718	0.819714	0.47122	0.365263799	
RESP18	(1251.067707	(1251.472481	0.809548	999	0.368253918	
DLX6	(1106.357156	(1106.761631	0.80895	999	0.368430866	
ADNP2	(5610.927744	(5611.32551	0.795532	0.49469	0.372432594	
TNIP3	(2039.696452	(2040.092044	0.791184	0.58942	0.37374235	
PDK3	(1818.663331	(1819.057455	0.788248	0.26925	0.374630418	
RNF34	(1774.727464	(1775.104611	0.754294	0.29094	0.385120121	
TBRG1	(1916.727512	(1917.102169	0.749314	0.4136	0.386693509	
EXPH5	(10701.24439	(10701.61312	0.737454	0.66114	0.390477675	
C1QTNF7	(1369.761043	(1370.128496	0.734906	19.66291	0.39129757	
ORC2	(2608.756742	(2609.121785	0.730086	0.44123	0.392855314	
YTHDC1	(3080.336798	(3080.698375	0.723154	0.28736	0.395111285	
NPFF	(606.634563	(606.984905	0.700684	999	0.402553956	
ZNF235	(3660.370243	(3660.717012	0.693538	0.61286	0.404963577	
LSM10	(586.358196	(586.685147	0.653902	0.30451	0.418721058	
CISH	(1389.879935	(1390.206079	0.652288	0.43907	0.419295846	
IFNA2	(1005.649134	(1005.975099	0.65193	999	0.419423498	
TMEM208	(762.163315	(762.477712	0.628794	49.83904	0.427798028	
C12orf5	(1454.592391	(1454.901789	0.618796	0.31806	0.431495052	
ANGEL2	(2365.262561	(2365.557671	0.59022	7.24194	0.442334059	
C4orf33	(1021.06654	(1021.350045	0.56701	999	0.451449515	
TMEM42	(678.588336	(678.86964	0.562608	999	0.453211344	
WSB2	(1865.128615	(1865.407874	0.558518	999	0.45485798	
METAP1D	(1550.471267	(1550.748597	0.55466	0.33946	0.456419847	
PNPT1	(3658.60064	(3658.868778	0.536276	69.45473	0.463980184	
ZMYND17	(2328.693407	(2328.957635	0.528456	0.47864	0.467256713	
OR10G3	(1722.457365	(1722.717625	0.52052	1.72345	0.470619949	
LIPH	(2244.407935	(2244.654149	0.492428	0.57729	0.482846224	
MSRB2	(999.338938	(999.581859	0.485842	0.36486	0.485787979	
C1orf27	(2081.001575	(2081.241064	0.478978	0.52061	0.488885606	
LSM7	(453.441074	(453.680098	0.478048	0	0.489307825	
OR5H6	(1746.133777	(1746.363761	0.459968	0.63203	0.497638929	
CCDC82	(2745.979457	(2746.202651	0.446388	0.54589	0.504055245	
MAGEA8	(1513.619967	(1513.841105	0.442276	0.38297	0.506025968	
GMNN	(1034.361342	(1034.570417	0.41815	999	0.517861605	
GALNT12	(3041.637179	(3041.843628	0.412898	0.76677	0.520502248	
C19orf68	(3319.186195	(3319.38595	0.39951	999	0.527342422	
TTC29	(2306.815323	(2307.010165	0.389684	0.40688	0.532465552	
ZNF570	(2394.111091	(2394.299732	0.377282	0.41089	0.539061465	
OLA1	(1684.382817	(1684.570191	0.374748	0.41417	0.540427508	
FBXO22	(1930.626692	(1930.813433	0.373482	0.41519	0.541112371	
ZNF192	(2773.178509	(2773.360064	0.36311	0.42036	0.546784074	
RCN2	(1490.705959	(1490.887029	0.36214	47.96213	0.54732013	
TACR2	(1978.206898	(1978.384945	0.356094	0.45768	0.550683571	
HAUS2	(1109.316599	(1109.493189	0.35318	0.57078	0.552318506	
NDUFA6	(804.654663	(804.82918	0.349034	0.57344	0.554660469	
NSUN3	(1619.468634	(1619.640215	0.343162	0.42915	0.558009717	
RPL23A	(857.299318	(857.470186	0.341736	0.79859	0.55882888	
PTPRCAP	(1095.611065	(1095.777939	0.333748	0.42432	0.56346042	
PMFBP1	(5170.165417	(5170.331441	0.332048	0.68746	0.564455633	
CCDC73	(5509.552047	(5509.717974	0.331854	1.28855	0.56456942	
SYNPO2L	(4886.876423	(4887.04216	0.331474	0.67614	0.56479243	
LYG1	(1103.376537	(1103.540263	0.327452	0.64954	0.567163309	
COQ3	(1950.400636	(1950.559875	0.318478	2.05061	0.57252375	
ATAD5	(9295.98297	(9296.133874	0.301808	0.68655	0.582751181	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
TMEM18	(652.316876	(652.467393	0.301034	0.45432	0.583234921	
NR1I3	(1717.244131	(1717.394598	0.300934	1.79096	0.583297478	
SFRP1	(1507.625306	(1507.774104	0.297596	999	0.585393453	
ZNF30	(3412.361932	(3412.508842	0.29382	0.7581	0.58778292	
EPT1	(1772.464648	(1772.607365	0.285434	0.46479	0.593161499	
GEMIN7	(641.792259	(641.933403	0.282288	0.46646	0.595205487	
LRRC2	(1794.280477	(1794.417145	0.273336	0.47119	0.601102683	
GP1BA	(4200.921436	(4201.054656	0.26644	1.39273	0.60572991	
EPSTI1	(2232.465857	(2232.589543	0.247372	0.71711	0.618931642	
AMBN	(2392.845368	(2392.968499	0.246262	1.62909	0.619719504	
C11orf80	(3563.238738	(3563.359555	0.241634	1.61991	0.623028437	
DNAJC30	(1248.061317	(1248.162662	0.20269	0.5636	0.652558261	
LRRC27	(2939.374879	(2939.466487	0.183216	0.79821	0.668623905	
ATP10D	(7192.2646	(7192.350253	0.171306	0.67725	0.678953723	
DEFB103A	(335.207248	(335.292808	0.17112	0.54951	0.679118341	
EXD1	(2906.555611	(2906.631279	0.151336	0.69706	0.697261884	
GOLGA5	(3484.053966	(3484.128891	0.14985	0.68611	0.698678745	
OR14A2	(1605.686962	(1605.755133	0.136342	1.33873	0.711944986	
CEBPZ	(5166.975646	(5167.038725	0.126158	0.72825	0.722449297	
ZNF625	(1427.46004	(1427.521549	0.123018	0.62636	0.725784	
GLYAT	(1577.795155	(1577.852758	0.115206	1.44485	0.734293284	
C14orf180	(1003.793946	(1003.84731	0.106728	1.41336	0.743900461	
RAB17	(1170.766452	(1170.816045	0.099186	0.75971	0.752808661	
PPIG	(3499.892204	(3499.941566	0.098724	1.12667	0.753366291	
FXYD3	(495.77236	(495.821352	0.097984	0.66787	0.754262458	
DARC	(1863.169943	(1863.214076	0.088266	1.19303	0.766393261	
ZBP1	(2567.172046	(2567.212289	0.080486	1.25722	0.776639876	
SECTM1	(1274.86766	(1274.907013	0.078706	0.77684	0.779058718	
CLEC4E	(1201.994126	(1202.032909	0.077566	0.70481	0.780623398	
OR6M1	(1728.617892	(1728.65635	0.076916	1.3679	0.781521091	
CEP78	(3500.604667	(3500.643065	0.076796	0.73344	0.781687265	
CEACAM6	(2794.710878	(2794.749018	0.07628	0.93987	0.782403411	
SCT	(525.148965	(525.186441	0.074952	0.20958	0.784258591	
TRAIP	(2304.785978	(2304.821674	0.071392	0.71539	0.789320708	
HELB	(5542.491988	(5542.521839	0.059702	0.84218	0.806967563	
POGK	(2867.845717	(2867.874432	0.05743	0.74126	0.810605033	
ALDH1A3	(2495.589591	(2495.613898	0.048614	0.7557	0.825492809	
TSPAN8	(1578.28687	(1578.311104	0.048468	0.83052	0.825750838	
USP26	(5057.897031	(5057.92082	0.047578	1.15887	0.82733264	
IL19	(1203.292862	(1203.316637	0.04755	1.28137	0.827382655	
TMEM105	(687.209112	(687.229807	0.04139	1.24632	0.838786977	
CD300C	(1372.505338	(1372.52524	0.039804	0.84598	0.841864292	
PLXDC2	(2632.964933	(2632.984482	0.039098	1.25256	0.84325464	
C11orf40	(1331.179021	(1331.196763	0.035484	1.23903	0.850585069	
KRT36	(2448.255289	(2448.27227	0.033962	0.85011	0.85378767	
CCDC68	(1603.437046	(1603.45321	0.032328	1.22847	0.857309671	
POLR2F	(559.091109	(559.105851	0.029484	0.80642	0.863666266	
TTF1	(5078.235203	(5078.24991	0.029414	0.91163	0.863826619	
MAP4K5	(4983.205555	(4983.217912	0.024714	0.97384	0.875081814	
ITGB3BP	(887.403661	(887.415163	0.023004	0.83598	0.879446671	
GCDH	(2322.7214	(2322.731345	0.01989	0.91403	0.887844733	
TMEM178	(1340.470866	(1340.480514	0.019296	0.90613	0.889521235	
GPR179	(14282.1511	(14282.16024	0.01829	0.9486	0.892421706	
LEPREL4	(1972.739044	(1972.744634	0.01118	0.87225	0.915792198	
OR6X1	(1672.594051	(1672.599532	0.010962	1.09136	0.916614203	
TFEC	(1628.31667	(1628.321137	0.008934	1.11474	0.924696224	
ICT1	(1152.265008	(1152.267336	0.004656	0.96413	0.945598655	

Gene	Free&lnL	Fixed&lnL	2ΔlnL	branch_w	pvalue	k
OR1N1	(1423.050897	(1423.052856	0.003918	1.05414	0.950089864	
MRPL21	(1129.330562	(1129.33236	0.003596	0.92877	0.95218219	
AGGF1	(3402.36757	(3402.368947	0.002754	1.0623	0.958147373	
BCCIP	(1571.667002	(1571.667211	0.000418	1.01758	0.983688348	
ADAT2	(896.743749	(896.743922	0.000346	0	0.985159345	
NUDCD1	(2709.077156	(2709.077311	0.00031	1.02068	0.985952518	
CENPT	(3154.57581	(3154.575958	0.000296	1.01226	0.986273352	
GNAO1	(2115.472856	(2115.472968	0.000224	0	0.988058803	
PPM1E	(3396.768164	(3396.768249	0.00017	0	0.989597153	
TMEM179	(904.10158	(904.101639	0.000118	0	0.991332926	
SUV39H1	(1814.111869	(1814.111927	0.000116	0	0.991406686	
CHM	(3028.790727	(3028.790784	0.000114	0.9875	0.991481086	
DERL1	(1106.312857	(1106.312913	0.000112	0	0.991556141	
MED7	(980.949476	(980.949521	9E(05	0	0.992430716	
ACSM1	(3134.37204	(3134.372079	7.8E(05	1.00752	0.992953366	
GUCA1B	(890.171812	(890.17184	5.6E(05	0	0.994029234	
HNRNPD	(1491.679042	(1491.679068	5.2E(05	0	0.994246422	
PNMA1	(1586.9628	(1586.962823	4.6E(05	0	0.994588525	
PFDN6	(550.824179	(550.82419	2.2E(05	0	0.996257603	
C8orf40	(467.375964	(467.375973	1.8E(05	0	0.996614873	
THY1	(745.9053	(745.905309	1.8E(05	0	0.996614873	
NDP	(595.335341	(595.335349	1.6E(05	0	0.99680847	
TMEM106B	(1217.607899	(1217.607907	1.6E(05	0	0.99680847	
SYNJ2BP	(647.257622	(647.257628	1.2E(05	0	0.997236052	
COX5B	(679.311421	(679.311426	1E(05	0	0.997476872	
DNAJC24	(685.156712	(685.156714	4E(06	0	0.998404232	
MBNL2	(1567.260765	(1567.260767	4E(06	0	0.998404232	
ARCN1	(2281.996054	(2281.996039	(3E(05	0	#NUM!	
ARL6IP1	(1030.772326	(938.721128	(184.102396	0	#NUM!	
ATP5H	(762.138315	(762.138314	(2E(06	0	#NUM!	
C1orf43	(1161.44219	(1161.44218	(2E(05	0	#NUM!	
DENND4B	(8387.476587	(7199.934518	(2375.084138	0	#NUM!	
DHRS7	(1872.684652	(1626.310725	(492.747854	0	#NUM!	
MAP4K4	(6245.909299	(6066.429821	(358.958956	0	#NUM!	
PLP1	(1162.283126	(1162.283102	(4.8E(05	0	#NUM!	
PRRG1	(979.429873	(979.429869	(8E(06	0	#NUM!	
RC3H1	(5141.675221	(5133.260675	(16.829092	108.77545	#NUM!	
RPS23	(645.084014	(645.084007	(1.4E(05	0	#NUM!	
S100A4	(429.462564	(429.462545	(3.8E(05	0	#NUM!	
SLC22A17	(2376.654847	(2376.654803	(8.8E(05	0	#NUM!	
SLC31A1	(859.479825	(859.479754	(0.000142	0	#NUM!	
SLC45A2	(2725.960605	(2717.569874	(16.781462	187.40324	#NUM!	
TSSK2	(1695.775038	(1693.559721	(4.430634	14.47292	#NUM!	
ZC4H2	(923.282245	(923.282226	(3.8E(05	0	#NUM!	
ZFP37	(3104.646693	(3100.867257	(7.558872	198.359	#NUM!	
ZNF302	(2362.136781	(2362.108247	(0.057068	0.88147	#NUM!	

Orangutan

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
NCOR2	-12224.72095	-12282.23493	115.027966	0.10418	7.75954E-27	
GNAO1	-2115.120663	-2164.983057	99.724788	0.08301	1.75116E-23	
SPTB	-11263.78738	-11313.61181	99.648858	0.03022	1.8196E-23	
VPS13D	-20748.17741	-20787.73159	79.108356	0.11256	5.87951E-19	
APC2	-11988.52023	-12023.41785	69.795244	0.1753	6.57913E-17	
PLCH2	-7498.132689	-7532.543468	68.821558	0.09105	1.07788E-16	
CARD11	-5916.766581	-5950.674357	67.815552	0.02568	1.79528E-16	
JAG2	-6294.934236	-6328.067757	66.267042	0.11183	3.93788E-16	
CLCN4	-3594.403933	-3620.166603	51.52534	0	7.06789E-13	
COL5A2	-6696.831576	-6721.716197	49.769242	0.01825	1.72934E-12	
TBC1D9	-5834.213318	-5857.576158	46.72568	0.01794	8.1652E-12	
TEKT5	-2691.552042	-2714.914565	46.725046	0.03665	8.16784E-12	
SLIT1	-7420.410514	-7443.415543	46.010058	0.07581	1.17647E-11	
SLC35C1	-1827.303193	-1849.445447	44.284508	0.01821	2.83954E-11	
SDHA	-583.730542	-604.413284	41.365484	0.01966	1.26267E-10	
GRIK3	-4314.832952	-4335.470515	41.275126	0.03823	1.32241E-10	
GCK	-2420.991103	-2441.235048	40.48789	0.01363	1.97838E-10	
ZNF574	-4507.21289	-4526.844236	39.262692	0	3.70452E-10	
TGM1	-4089.723532	-4109.208241	38.969418	0.04558	4.30497E-10	
DCAF12L2	-2599.324095	-2618.400912	38.153634	0.2594	6.53878E-10	
PRKCD	-3136.196543	-3154.870079	37.347072	0.01658	9.88692E-10	
PRPF4B	-4588.402633	-4606.578644	36.352022	0.04497	1.64708E-09	
ZNF335	-6610.461771	-6628.446355	35.969168	0.10437	2.00465E-09	
PITPNM1	-6236.502446	-6254.07866	35.152428	0.07736	3.04881E-09	
TBC1D17	-3152.023603	-3169.256459	34.465712	0.01861	4.33827E-09	
C19orf68	-3317.726108	-3334.766848	34.08148	0.05659	5.28519E-09	
RALGDS	-4386.951378	-4403.970313	34.03787	0.06375	5.40498E-09	
TSSK2	-1689.367262	-1706.381809	34.029094	0	5.42941E-09	
KCNB1	-3940.990548	-3957.781364	33.581632	0.02135	6.8335E-09	
RAP1GAP2	-3634.325425	-3651.077043	33.503236	0.01853	7.11455E-09	
DCAF5	-4503.221118	-4519.487797	32.533358	0.0604	1.17164E-08	
ASB1	-1624.267115	-1640.448731	32.363232	0	1.27883E-08	
TNS3	-7653.960484	-7670.105411	32.289854	0.24465	1.32805E-08	
CPT1B	-3717.795969	-3733.869479	32.14702	0.03797	1.42936E-08	
SEMA6B	-4181.15983	-4197.213704	32.107748	0.07774	1.45854E-08	
KDM5D	-3474.720971	-3490.354372	31.266802	0.23435	2.24893E-08	
ERCC3	-3776.139325	-3791.761678	31.244706	0.02352	2.27467E-08	
FBXL12	-1532.75414	-1547.817015	30.12575	0.02208	4.04919E-08	
PLCB1	-5508.184868	-5523.039773	29.70981	0	5.01802E-08	
SLC16A8	-2344.691336	-2359.286277	29.189882	0.01926	6.5621E-08	
ALOX15	-3881.879469	-3896.315083	28.871228	0.06079	7.73535E-08	
RBBP6	-3240.539351	-3254.294644	27.510586	0.15794	1.56237E-07	
MEGF10	-5514.975163	-5528.513179	27.076032	0.1211	1.95608E-07	
RBCK1	-2217.260761	-2230.640948	26.760374	0	2.30312E-07	
MRGPRE	-1602.507272	-1615.755417	26.49629	0.03938	2.64045E-07	
ECEL1	-3727.644446	-3740.81672	26.344548	0.07306	2.85624E-07	
COL20A1	-6580.485623	-6593.449314	25.927382	0.25381	3.54505E-07	
ANO1	-4808.394415	-4821.322452	25.856074	0.11385	3.67845E-07	
ERC1	-5075.815613	-5088.727853	25.82448	0	3.73916E-07	
RNF208	-1197.879486	-1210.620831	25.48269	0	4.4637E-07	
STAT5B	-3675.25442	-3687.807273	25.105706	0.08797	5.4272E-07	
PIAS1	-2899.102415	-2911.552399	24.899968	0	6.03834E-07	
GPR39	-2379.771122	-2392.10469	24.667136	0.11206	6.81362E-07	
CHRDL2	-2443.084624	-2455.249707	24.330166	0.02844	8.11581E-07	
WDFY2	-1821.753055	-1833.688644	23.871178	0	1.03002E-06	
FKRP	-2437.171616	-2449.097465	23.851698	0.08408	1.0405E-06	
KCNJ9	-1728.65136	-1740.521465	23.74021	0	1.10255E-06	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
CNTFR	-1736.220266	-1748.065379	23.690226	0	1.13156E-06	
SUV39H1	-1814.111869	-1825.726424	23.22911	0	1.43804E-06	
TBXA2R	-1669.241643	-1680.613556	22.743826	0	1.85098E-06	
DENND4B	-7194.466671	-7205.836808	22.740274	0.1859	1.8544E-06	
ZNF324B	-3116.228448	-3127.512294	22.567692	0.08766	2.02868E-06	
RHOB	-854.376374	-865.642869	22.53299	0.03096	2.06565E-06	
SEMA4B	-3998.104196	-4009.197377	22.186362	0.09566	2.47425E-06	
ZC3H13	-7601.99534	-7613.074751	22.158822	0.15519	2.51E-06	
MBTPS2	-2422.880657	-2433.90052	22.039726	0	2.67065E-06	
FZR1	-2348.049281	-2359.068979	22.039396	0.07852	2.67111E-06	
STUB1	-1347.877786	-1358.857669	21.959766	0	2.78426E-06	
POGK	-2868.185674	-2879.164981	21.958614	0	2.78594E-06	
BCL9L	-7012.845976	-7023.823667	21.955382	0.1525	2.79063E-06	
DEF8	-2631.608966	-2642.533302	21.848672	0.04436	2.95021E-06	
ASCC3	-10025.99014	-10036.91207	21.843844	0.12167	2.95764E-06	
SEC14L5	-3456.755274	-3467.662238	21.813928	0.04958	3.00411E-06	
KRT36	-2448.842641	-2459.676333	21.667384	0.11683	3.24258E-06	
ADAMTS8	-4013.865119	-4024.531124	21.33201	0.13945	3.86228E-06	
SLC6A4	-3062.276541	-3072.816682	21.080282	0.07998	4.40437E-06	
SLC7A14	-3657.803213	-3668.25719	20.907954	0.05859	4.81889E-06	
PPP1R12A	-4526.256971	-4536.69806	20.882178	0.03216	4.88418E-06	
UPF2	-5623.374183	-5633.777238	20.80611	0.03417	5.08206E-06	
SLC25A23	-2100.367265	-2110.684265	20.634	0	5.55999E-06	
SV2B	-3191.160963	-3201.35487	20.387814	0.0322	6.32312E-06	
TMC8	-3632.199303	-3642.343982	20.289358	0.16026	6.65698E-06	
GCDH	-2327.864803	-2337.898435	20.067264	0.11576	7.47655E-06	
ZNF275	-2173.321018	-2183.266673	19.89131	0.03539	8.19721E-06	
CDT1	-2995.114739	-3005.01523	19.800982	0.19175	8.59385E-06	
CHST2	-2515.359401	-2525.056575	19.394348	0.14365	1.06321E-05	
NR2C2	-2829.250364	-2838.766774	19.03282	0	1.28489E-05	
ROR2	-4589.446072	-4598.93154	18.970936	0.08208	1.32725E-05	
C7orf60	-1790.725634	-1800.205806	18.960344	0	1.33464E-05	
ILKAP	-1840.198836	-1849.60305	18.808428	0	1.44527E-05	
LIPH	-2238.80828	-2248.194664	18.772768	0	1.47255E-05	
SHPRH	-8159.353252	-8168.445433	18.184362	0.15616	2.00519E-05	
PPP2R2C	-2050.851904	-2059.926889	18.14997	0	2.04173E-05	
GJA4	-1636.963044	-1645.928769	17.93145	0.05865	2.29005E-05	
UNC13C	-10553.16769	-10562.07658	17.817792	0.26787	2.43099E-05	
ANKRD52	-5050.696535	-5059.593872	17.794674	0	2.46071E-05	
RAE1	-1759.286738	-1768.134795	17.696114	0	2.59155E-05	
CNTN6	-5057.475257	-5066.304505	17.658496	0.12677	2.64332E-05	
NR1I3	-1717.303073	-1726.100838	17.59553	0.0432	2.7323E-05	
PLB1	-7860.520717	-7869.286306	17.531178	0.27205	2.82635E-05	
TMEM61	-1205.994018	-1214.753224	17.518412	0.05951	2.84539E-05	
MAT2A	-1791.575115	-1800.320721	17.491212	0	2.88639E-05	
CDC37	-1706.256626	-1714.971074	17.428896	0.02645	2.98257E-05	
VPS52	-8325.836967	-8334.53519	17.396446	0.09784	3.03393E-05	
MLLT6	-4826.501052	-4835.195157	17.38821	0.06895	3.0471E-05	
USP1	-8477.83453	-8486.45954	17.25002	0	3.27694E-05	
CDK13	-6756.595106	-6765.11748	17.044748	0.10062	3.65092E-05	
HIST1H3G	-641.629555	-650.069771	16.880432	0	3.98099E-05	
PNKP	-2844.076696	-2852.447703	16.742014	0.11783	4.28221E-05	
TMEM179	-902.522535	-910.755648	16.466226	0.16565	4.95245E-05	
CAPN7	-8742.532922	-8750.748081	16.430318	0	5.04715E-05	
GPR176	-2456.507938	-2464.700223	16.38457	0.04102	5.17044E-05	
GALNT12	-8050.331305	-8058.484655	16.3067	0.16495	5.38731E-05	
SCN1B	-1018.103701	-1026.216747	16.226092	0	5.62145E-05	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
C19orf47	&2052.504784	&2060.612071	16.214574	0	5.65573E&05	
TBCB	&1153.18488	&1161.273573	16.177386	0.03749	5.76786E&05	
SMC2	&5402.87198	&5410.918057	16.092154	0.08462	6.03335E&05	
CXCR5	&1773.987703	&1781.99502	16.014634	0.05653	6.28548E&05	
RC3H1	&5132.462802	&5140.438916	15.952228	0.10673	6.49613E&05	
S1PR3	&1732.102819	&1740.027846	15.850054	0.03298	6.85646E&05	
PCDH7	&5420.068291	&5427.989853	15.843124	0.10143	6.88161E&05	
PNPLA7	&6802.221495	&6810.126282	15.809574	0.30271	7.00472E&05	
KIDINS220	&8390.794067	&8398.674707	15.76128	0.17072	7.18582E&05	
CPA5	&2346.890972	&2354.767075	15.752206	0	7.22037E&05	
SLC24A4	&2704.432232	&2712.29961	15.734756	0.03922	7.28728E&05	
SMPD3	&8076.755316	&8084.584189	15.657746	0.09059	7.59011E&05	
PMFBP1	&5166.75642	&5174.584543	15.656246	0.19576	7.59613E&05	
EBI3	&1152.434091	&1160.210206	15.55223	0.05112	8.02569E&05	
DCAF7	&1558.703625	&1566.459652	15.512054	0	8.19808E&05	
ARHGAP4	&5884.332215	&5892.071723	15.479016	0.22197	8.34263E&05	
JAM2	&1438.700864	&1446.42641	15.451092	0	8.4668E&05	
WDR33	&6005.777629	&6013.44734	15.339422	0.08397	8.98224E&05	
TMEM43	&2110.039209	&2117.705671	15.332924	0.07479	9.01319E&05	
MAP2	&8749.775908	&8757.404649	15.257482	0.28795	9.38044E&05	
GNAT2	&1603.318763	&1610.941501	15.245476	0.04378	9.44026E&05	
SULF2	&4177.742622	&4185.328954	15.172664	0.16603	9.81135E&05	
TBR1	&2895.49145	&2903.065588	15.148276	0	9.9389E&05	
KIAA0562	&4760.232119	&4767.798626	15.133014	0.20603	0.000100196	
TJP2	&6015.835841	&6023.362437	15.053192	0.28387	0.000104523	
ME2	&2646.356849	&2653.86163	15.009562	0.07505	0.000106968	
EIF2C4	&3719.553171	&3726.966365	14.826388	0	0.000117875	
YTHDC1	&3080.590357	&3087.9905	14.800286	0	0.000119517	
ADAM9	&3865.362482	&3872.760681	14.796398	0.046	0.000119764	
LHX2	&1796.065402	&1803.448535	14.766266	0	0.000121693	
SPIB	&1095.841673	&1103.220367	14.757388	0.07097	0.000122268	
TMEM42	&679.861998	&687.102925	14.481854	0.0441	0.000141516	
ELF4	&3309.763877	&3316.958456	14.389158	0.08166	0.000148656	
CWC22	&4318.735732	&4325.819118	14.166772	0.12439	0.000167299	
ISYNA1	&2711.433153	&2718.488616	14.110926	0.09853	0.00017234	
ZFYVE20	&3771.954683	&3778.949825	13.990284	0.16709	0.000183758	
FAM126B	&2585.3828	&2592.337166	13.908732	0	0.000191905	
GADD45A	&733.490562	&740.439757	13.89839	0	0.000192964	
GFOD2	&1868.990857	&1875.924558	13.867402	0	0.000196172	
DSCR3	&1518.772218	&1525.702456	13.860476	0.15156	0.000196896	
POFUT2	&2134.715364	&2141.613048	13.795368	0.143	0.000203838	
RCN2	&1489.542707	&1496.419531	13.753648	0	0.000208416	
PADI1	&3540.768042	&3547.59823	13.660376	0.23169	0.000219028	
MFSD6L	&3310.719425	&3317.53797	13.63709	0.24214	0.000221761	
PCDHA1	&5052.558802	&5059.220252	13.3229	0.34891	0.000262184	
MPHOSPH9	&4892.54955	&4899.208893	13.318686	0.2308	0.000262774	
ADNP2	&5612.003787	&5618.660395	13.313216	0.18167	0.000263542	
AGPAT2	&1421.739633	&1428.395902	13.312538	0.0292	0.000263637	
CCDC132	&4368.889974	&4375.484583	13.189218	0.16755	0.000281564	
SOAT2	&2726.288955	&2732.880888	13.183866	0.20216	0.00028237	
MRPL21	&1128.536405	&1135.110278	13.147746	0.12231	0.000287865	
TMED4	&1062.378903	&1068.946132	13.134458	0.04456	0.000289914	
CYP4F11	&2992.556795	&2999.088311	13.063032	0.14873	0.000301181	
DLEC1	&9086.021981	&9092.494281	12.9446	0.32328	0.000320846	
ARCN1	&2281.991945	&2288.4413	12.89871	0.05155	0.000328809	
TXNDC11	&4977.912415	&4984.304943	12.785056	0.24464	0.000349399	
NLGN3	&3586.178292	&3592.55291	12.749236	0.0533	0.000356155	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
DHTKD1	-4801.286714	-4807.64763	12.721832	0.20378	0.000361412	
KLHDC4	-2858.247669	-2864.581984	12.66863	0.19669	0.000371842	
FOLR2	-1278.2188	-1284.533698	12.629796	0.07863	0.000379647	
PYGO2	-1791.038259	-1797.341947	12.607376	0.05981	0.000384228	
TTLL9	-2360.803318	-2367.102803	12.59897	0.11709	0.000385959	
GPT2	-2464.231022	-2470.518949	12.575854	0.04278	0.000390763	
LTK	-4352.383779	-4358.648431	12.529304	0.21556	0.000400619	
DCAF4L1	-1947.471944	-1953.701035	12.458182	0.08893	0.000416165	
WDR74	-1901.85243	-1908.028766	12.352672	0	0.000440356	
PLS3	-2742.576537	-2748.738242	12.32341	0	0.000447313	
WDR5B	-1588.102542	-1594.194099	12.183114	0.09089	0.000482241	
PSMD9	-1065.25962	-1071.316566	12.113892	0.08098	0.000500476	
ABCB11	-6822.51396	-6828.537319	12.046718	0.25684	0.000518836	
KANK3	-4441.53436	-4447.553967	12.039214	0.36199	0.000520929	
CYTH1	-1782.851822	-1788.762617	11.82159	0	0.000585478	
MAP4K4	-6065.285623	-6071.039157	11.507068	0.09194	0.000693321	
ZNF569	-3122.166389	-3127.900087	11.467396	0.05099	0.000708279	
KPTN	-2402.403923	-2408.107282	11.406718	0.18924	0.00073179	
OVOL2	-1302.351825	-1308.042647	11.381644	0.0413	0.000741734	
USP7	-4826.526834	-4832.186227	11.318786	0	0.000767269	
ATAD2	-6458.439942	-6463.993772	11.10766	0.20288	0.000859719	
SIPA1	-4986.498881	-4992.045356	11.09295	0.17577	0.000866565	
MAP4K5	-5016.97273	-5022.501555	11.05765	0.0505	0.00088322	
ADRA1B	-2498.055654	-2503.50468	10.898052	0.04107	0.000962654	
EPB49	-1818.171425	-1823.438611	10.534372	0	0.001171747	
C1QTNF7	-1369.859252	-1375.112739	10.506974	0	0.001189248	
RPS12	-638.858808	-644.074916	10.432216	0	0.001238361	
ADH1A	-2352.829787	-2358.036566	10.413558	0.2361	0.001250935	
LAPTM4B	-2137.460625	-2142.65077	10.38029	0.43557	0.001273677	
RNF216	-4385.639925	-4390.785221	10.290592	0.09488	0.001337102	
PRKRIP1	-905.078713	-910.203713	10.25	0	0.001366846	
PM20D2	-2164.059194	-2169.181089	10.24379	0.22805	0.001371455	
SLC45A2	-2716.979324	-2722.076046	10.193444	0.05798	0.001409408	
PLEKHA5	-4835.067555	-4840.154808	10.174506	0.16723	0.001423958	
TTYH1	-2169.190413	-2174.261771	10.142716	0.0561	0.001448726	
GUCY2F	-5372.197962	-5377.262692	10.12946	0.20603	0.001459182	
GCGR	-2923.620378	-2928.655037	10.069318	0.30517	0.001507588	
ACCN1	-2711.374933	-2716.407434	10.065002	0.09381	0.001511124	
PLXDC2	-2635.207004	-2640.237809	10.06161	0.17812	0.001513909	
CA10	-1497.469228	-1502.486004	10.033552	0	0.001537143	
FAM131A	-1320.592739	-1325.604038	10.022598	0	0.001546312	
KIAA0947	-12219.03625	-12224.0436	10.0147	0.44061	0.001552957	
ZC3H12D	-2708.412116	-2713.417358	10.010484	0.18896	0.001556516	
TMEM121	-1355.064928	-1360.067227	10.004598	0.03038	0.001561499	
HIST1H2AL	-744.283727	-749.275139	9.982824	0	0.001580072	
TSPAN15	-1377.399415	-1382.36704	9.93525	0.05539	0.001621434	
CAPN11	-3812.838833	-3817.727705	9.777744	0.17783	0.001766369	
ORC2	-2609.062815	-2613.930425	9.73522	0.05892	0.001807704	
HAUS2	-1106.839586	-1111.701059	9.722946	0	0.001819816	
C11orf84	-2729.849748	-2734.683258	9.66702	0.13701	0.001876054	
PAX9	-1574.04293	-1578.851021	9.616182	0	0.001928703	
KLRG2	-2204.296335	-2209.073028	9.553386	0.14736	0.001995809	
DNAI2	-3181.255885	-3186.009841	9.507912	0.10961	0.002045878	
SH3D21	-4133.9734	-4138.710673	9.474546	0.30302	0.002083424	
YLPM1	-9690.526324	-9695.218086	9.383524	0.1745	0.002189443	
DMGDH	-4203.909798	-4208.533837	9.248078	0.17204	0.002357427	
CHL1	-6212.566901	-6217.158687	9.183572	0.22722	0.00244197	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
S100A4	&429.462564	&434.049556	9.173984	0	0.002454796	
MTG1	&1716.674786	&1721.261661	9.17375	0.08229	0.00245511	
TACR2	&1978.331614	&1982.845081	9.026934	0.14436	0.002660303	
ZNF575	&1660.172701	&1664.660846	8.97629	0.12908	0.002735054	
IRF8	&2085.995	&2090.39562	8.80124	0.18111	0.003010259	
WSB2	&1866.613703	&1870.941378	8.65535	0.06941	0.003261024	
HM13	&1873.878532	&1878.201556	8.646048	0	0.003277715	
UGT1A3	&2747.538268	&2751.858725	8.640914	0.28669	0.003286965	
IL17REL	&1708.376656	&1712.683287	8.613262	0.08604	0.003337241	
FAM103A1	&520.442892	&524.725341	8.564898	0	0.003427062	
HSD17B3	&1582.523833	&1586.760884	8.474102	0.06433	0.003602382	
SEC13	&1771.491639	&1775.6805	8.377722	0.11431	0.003798482	
ATP10D	&7192.558899	&7196.710613	8.303428	0.35506	0.003957032	
ATAD5	&9295.954884	&9300.093988	8.278208	0.44398	0.004012371	
BLNK	&2338.293183	&2342.417076	8.247786	0.14223	0.004080174	
DDB2	&2011.713915	&2015.828177	8.228524	0.09357	0.004123705	
ZFP64	&3245.370368	&3249.46311	8.185484	0.19389	0.004222691	
SLC22A17	&2376.153805	&2380.236948	8.166286	0.07056	0.00426762	
RNF34	&1774.678275	&1778.758487	8.160424	0.09617	0.004281436	
FGGY	&2753.6891	&2757.767831	8.157462	0.19343	0.004288434	
NPFFR1	&2090.190221	&2094.224795	8.069148	0.0871	0.004502528	
ATG16L1	&2891.335032	&2895.358926	8.047788	0.18647	0.004555925	
DBX1	&2071.839757	&2075.858761	8.038008	0.21634	0.004580588	
NXT1	&642.059909	&646.075593	8.031368	0	0.00459741	
DIRC2	&2215.752139	&2219.759343	8.014408	0.08313	0.004640664	
CCDC157	&3833.710623	&3837.685939	7.950632	0.25875	0.004807059	
HIST1H2AJ	&620.351488	&624.323197	7.943418	0	0.004826259	
LPAR3	&1796.979732	&1800.940134	7.920804	0.11513	0.004886955	
NCKAP1L	&5396.910214	&5400.852587	7.884746	0.21531	0.004985348	
RTN4RL2	&1990.778148	&1994.622946	7.689596	0.15194	0.005554006	
FOSB	&1437.831877	&1441.648612	7.63347	0	0.005729497	
STX2	&1322.135534	&1325.948687	7.626306	0.12457	0.0057523	
ANGEL2	&2366.486475	&2370.236082	7.499214	0.19017	0.006172593	
SNRPA1	&1117.342391	&1121.009802	7.334822	0	0.006763138	
TMCC3	&2202.72641	&2206.391459	7.330098	0.18484	0.006780936	
LETM2	&2521.449996	&2525.049222	7.198452	0.21814	0.007296649	
GOLGA5	&3484.319745	&3487.869253	7.099016	0.17281	0.007712628	
NPY1R	&1730.158883	&1733.705349	7.092932	0	0.007738854	
ARHGAP19	&2378.878395	&2382.382844	7.008898	0.21025	0.008110559	
LHFPL2	&1093.315366	&1096.797652	6.964572	0.07836	0.008313932	
PRMT6	&1670.581826	&1674.030672	6.897692	0.11221	0.00863071	
MED19	&1132.724408	&1136.171483	6.89415	0	0.008647827	
COX5B	&675.994784	&679.41538	6.841192	0.09104	0.008907938	
OAZ2	&820.286105	&823.68548	6.79875	0	0.009122172	
TAGLN	&885.042131	&888.42525	6.766238	0	0.009289846	
C4orf31	&2783.938787	&2787.291596	6.705618	0.17839	0.009610961	
ICT1	&1154.007658	&1157.285749	6.556182	0.1276	0.010452039	
ZNF528	&3226.607414	&3229.866784	6.51874	0.28794	0.01067436	
LDB3	&3931.722856	&3934.943471	6.44123	0.27807	0.011150142	
CD2AP	&3055.07971	&3058.299093	6.438766	0.22552	0.011165618	
ABCD3	&3242.342726	&3245.534474	6.383496	0.22658	0.011518632	
C21orf59	&1401.41076	&1404.593862	6.366204	0.07257	0.011631415	
CCDC115	&881.516502	&884.679449	6.325894	0.13758	0.011898749	
MAP3K7	&2660.198288	&2663.333495	6.270414	0.08844	0.012277045	
BROX	&1818.404964	&1821.531637	6.253346	0.08622	0.012395894	
ZNRD1	&571.489218	&574.608581	6.238726	0.08723	0.012498635	
CDC20	&2289.850554	&2292.966744	6.23238	0	0.012543504	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
PCDHB5	-4602.486904	-4605.589754	6.2057	0.32415	0.012733958	
THY1	-745.742747	-748.833874	6.182254	0.07076	0.01290378	
RABEP1	-3980.166098	-3983.241756	6.151316	0.21272	0.013131435	
CDCA2	-5453.00286	-5456.062835	6.11995	0.452	0.013366458	
ABHD4	-1660.946236	-1664.004267	6.116062	0.09209	0.01339589	
FBL	-1605.808984	-1608.863317	6.108666	0.06409	0.013452062	
RFX7	-6743.967907	-6747.015932	6.09605	0.2357	0.013548439	
EXD1	-2905.427105	-2908.472438	6.090666	0.25644	0.013589785	
ZNF235	-3661.118268	-3664.137704	6.038872	0.34746	0.013994223	
FGF2	-1339.122706	-1342.140978	6.036544	0.09559	0.014012689	
EPB41L1	-4094.960583	-4097.971067	6.020968	0.21496	0.014136891	
C9orf142	-1043.159558	-1046.156535	5.993954	0.0999	0.01435499	
TNFAIP8L3	-1465.087631	-1468.06391	5.952558	0.14318	0.014695946	
SDSL	-1769.80392	-1772.740209	5.872578	0.27309	0.015378515	
CEBPZ	-5167.275234	-5170.2072	5.863932	0.3638	0.015454233	
ACSM1	-3134.184159	-3137.092796	5.817274	0.3764	0.015869522	
CA5A	-1403.295384	-1406.196149	5.80153	0	0.016012235	
TRAIP	-2304.885997	-2307.769569	5.767144	0.34967	0.01632855	
FLT3	-4939.077295	-4941.94727	5.73995	0.30437	0.016583265	
RGS8	-884.78502	-887.649131	5.728222	0	0.016694377	
MDM4	-2142.351697	-2145.195395	5.687396	0.19293	0.017087192	
C20orf160	-2426.6018	-2429.429413	5.655226	0.11892	0.017403432	
GPRASP2	-4102.554575	-4105.380899	5.652648	0.22297	0.017429034	
UBLCP1	-1378.521826	-1381.291356	5.53906	0.13505	0.018596569	
CDC23	-2708.187673	-2710.940423	5.5055	0.10351	0.01895676	
C10orf11	-974.172297	-976.911966	5.479338	0	0.019242545	
TBRG1	-1916.011095	-1918.703829	5.385468	0.10384	0.020305141	0.025448613
LAMC2	-5963.311345	-5966.002087	5.381484	0.36272	0.02035156	0.025530179
HIST1H3F	-761.424527	-764.101795	5.354536	0	0.020668433	0.025611746
ARL6IP1	-940.039252	-942.685789	5.293074	0.10603	0.021410395	0.025693312
COPS4	-1959.334919	-1961.980318	5.290798	0	0.021438394	0.025774878
FXYD3	-493.792135	-496.41495	5.24563	0	0.02200196	0.025856444
RPL23A	-868.007199	-870.616322	5.218246	0	0.022351084	0.02593801
PDK3	-1819.432513	-1822.039671	5.214316	0	0.022401658	0.026019576
FAM167A	-1034.932114	-1037.538742	5.213256	0.1934	0.022415318	0.026101142
NUP88	-3816.992313	-3819.58524	5.185854	0.36062	0.022771479	0.026182708
DGAT1	-2576.68645	-2579.268624	5.164348	0.25334	0.02305511	0.026264274
GCOM1	-2842.63495	-2845.214816	5.159732	0.52484	0.023116464	0.02634584
TMEM208	-763.954524	-766.527212	5.145376	0	0.023308362	0.026427406
OR10G3	-1723.667007	-1726.235177	5.13634	0.21155	0.023429994	0.026508972
RNF11	-655.292812	-657.850682	5.11574	0	0.023709752	0.026590538
CLK4	-2166.075582	-2168.631618	5.112072	0.10219	0.023759928	0.026672104
MBD6	-4426.228373	-4428.769409	5.082072	0.27497	0.024174464	0.02675367
MAP4K3	-4021.30132	-4023.840806	5.078972	0.15076	0.024217725	0.026835237
TSSK4	-1829.089508	-1831.623137	5.067258	999	0.024381922	0.026916803
PLEKHB2	-1116.047787	-1118.578187	5.0608	0.11184	0.024472939	0.026998369
OR2J3	-1698.380601	-1700.909792	5.058382	0.42158	0.024507108	0.027079935
MED7	-980.949476	-983.446103	4.993254	0	0.025446314	0.027161501
ZNF117	-3441.034751	-3443.529349	4.989196	0.29383	0.025506057	0.027243067
TMEM194A	-2095.832651	-2098.301101	4.9369	0.11534	0.026289146	0.027324633
DACT2	-4064.31424	-4066.761082	4.893684	0.41427	0.02695511	0.027406199
GNPAT	-3338.405295	-3340.851934	4.893278	0.24414	0.026961449	0.027487765
CDK9	-1673.262575	-1675.703298	4.881446	0.12644	0.027146868	0.027569331
HNRNPD	-1490.945854	-1493.383216	4.874724	0	0.027252799	0.027650897
PER3	-6656.95674	-6659.390115	4.86675	0.47242	0.027379017	0.027732463
PRRG1	-978.900211	-981.306149	4.811876	0	0.02826426	0.027814029
NDUFA6	-804.91421	-807.315965	4.80351	0.16116	0.028401817	0.027895595

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
C22orf41	&394.587071	&396.979723	4.785304	0	0.028703581	0.027977162
SFRP1	&1505.469732	&1507.841739	4.744014	0.21585	0.029400397	0.028058728
ZNF592	&5977.94987	&5980.307845	4.71595	0.30576	0.029884049	0.028140294
TMEM106B	&1217.605246	&1219.961184	4.711876	0.10094	0.029954946	0.02822186
AGGF1	&3403.040406	&3405.381398	4.681984	0.32242	0.030480526	0.028303426
LGALS7	&625.811706	&628.133412	4.643412	0.13392	0.031172966	0.028384992
GEMIN7	&640.74993	&643.055905	4.61195	0	0.03174991	0.028466558
TMEM92	&871.064397	&873.361568	4.594342	0.10581	0.032077654	0.028548124
POLR2F	&562.419792	&564.67285	4.506116	0	0.03377385	
ZBTB38	&5737.593329	&5739.846057	4.505456	0.39858	0.033786886	
FAAH2	&2754.040716	&2756.267188	4.452944	0.28364	0.034841133	
HNRPLL	&2492.218171	&2494.443022	4.449702	0.10882	0.034907338	
ENOPH1	&1177.856103	&1180.062951	4.413696	0	0.035651518	
POU2F2	&2165.687574	&2167.888404	4.40166	0.24206	0.035903966	
PLAU	&2338.940329	&2341.139539	4.39842	0.2843	0.035972243	
LRRC2	&1793.977934	&1796.161873	4.367878	0.26983	0.036622571	
EPSTI1	&2231.641737	&2233.825294	4.367114	0.25449	0.036638996	
LRRTM3	&2552.324422	&2554.449986	4.251128	0.22327	0.039224269	
RAB17	&1171.067732	&1173.190719	4.245974	0.15764	0.039343496	
HEYL	&1751.474129	&1753.592856	4.237454	0.17591	0.039541422	
DNAJC30	&1247.750916	&1249.826388	4.150944	0.20472	0.04161132	
SDAD1	&3556.448872	&3558.46129	4.024836	0.22715	0.044834979	
DNAJC17	&1457.380352	&1459.383525	4.006346	0.28646	0.04532929	
MYL6B	&1176.587735	&1178.58984	4.00421	0	0.045386762	
GUCA1B	&890.171812	&892.173649	4.003674	0	0.045401196	
ADAM29	&4769.704924	&4771.691045	3.972242	0.43094	0.046256145	
OR5H6	&1746.168419	&1748.131633	3.926428	0.53043	0.047532805	
TMEM18	&652.018838	&653.974915	3.912154	0	0.047938118	
DHRS7	&1626.162328	&1628.102625	3.880594	0.23486	0.048847272	
CENPT	&3153.565908	&3155.4964	3.860984	0.46696	0.049421336	
RD3	&981.964481	&983.886342	3.843722	0.22911	0.049932561	
TOP3A	&5197.366752	&5199.272122	3.81074	0.50864	0.050924947	
MS4A7	&1300.033315	&1301.929582	3.792534	0.28187	0.051481654	
PAFAH1B1	&1902.930965	&1904.820895	3.77986	0.19614	0.051873001	
TFEC	&1628.28516	&1630.172015	3.77371	0.12925	0.052064033	
ZMYND17	&2324.951474	&2326.822685	3.742422	999	0.053047499	
MBLAC2	&1292.732562	&1294.570087	3.67505	0.13258	0.055232597	
C14orf180	&1003.278922	&1005.112009	3.666174	0.27388	0.055527511	
LSM7	&451.917613	&453.739965	3.644704	0.08836	0.056247801	
GPR179	&14282.69178	&14284.4926	3.601634	0.65789	0.05772281	
DRAP1	&963.602556	&965.390079	3.575046	0.28107	0.058653824	
PSMD4	&1695.977219	&1697.75422	3.554002	0.13682	0.059402019	
IL17RB	&2645.259642	&2647.033475	3.547666	0.37025	0.05962927	
PDZD7	&2712.562043	&2714.318249	3.512412	0.3818	0.060910717	
ITGB8	&3616.901967	&3618.658084	3.512234	0.29655	0.060917261	
HELB	&5542.943567	&5544.692721	3.498308	0.48559	0.061431562	
OR1N2	&1644.91684	&1646.656856	3.480032	0.25964	0.062113539	
PPM1K	&1668.000713	&1669.733292	3.465158	0.14068	0.06267452	
ARV1	&1317.386263	&1319.115762	3.458998	0.2089	0.062908426	
CHMP5	&937.877506	&939.569618	3.384224	0	0.065823157	
WDR63	&4325.007806	&4326.698356	3.3811	0.38631	0.065948027	
DLX6	&1106.911078	&1108.577303	3.33245	0	0.067925622	
CMBL	&1195.675508	&1197.291652	3.232288	0	0.072199751	
CEP78	&3500.490189	&3502.093461	3.206544	0.47231	0.073344251	
FBXO22	&1930.667591	&1932.2582	3.181218	0.28151	0.074489185	
EPT1	&1772.395755	&1773.975666	3.159822	0.27728	0.075471412	
PNLIPRP3	&2313.918771	&2315.49631	3.155078	0.37384	0.075691074	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
ROBO4	&5267.011397	&5268.584761	3.146728	0.46315	0.076079376	
NR1D2	&2650.249207	&2651.811668	3.124922	0.19739	0.077103562	
TRIM39	&2365.647741	&2367.199982	3.104482	0.3016	0.078077065	
FAM55B	&2830.68659	&2832.204208	3.035236	0.35532	0.081474701	
CASP8	&2453.969631	&2455.463092	2.986922	0.30787	0.08393958	
OR1N1	&1421.831417	&1423.322039	2.981244	0.41041	0.084234507	
MRGPRD	&1879.41949	&1880.901584	2.964188	0.28616	0.085127188	
MBNL2	&1567.066368	&1568.535851	2.938966	0.16398	0.086466067	
DNAJC24	&684.691623	&686.147521	2.911796	0	0.087933901	
LSM10	&586.27303	&587.705526	2.864992	0	0.09052616	
FMO6P	&713.082293	&714.514232	2.863878	0.29902	0.09058886	
CCL24	&713.113762	&714.544898	2.862272	0.29914	0.090679336	
PCDHA3	&4893.399697	&4894.824496	2.849598	0.473	0.091396788	
BET1	&507.31565	&508.737645	2.84399	0	0.091716211	
DUSP1	&1011.279256	&1012.697127	2.835742	0	0.09218821	
OR6M1	&1728.964362	&1730.38055	2.832376	0.408	0.092381591	
SQSTM1	&2431.82588	&2433.226164	2.800568	0.50862	0.094230919	
GP1BA	&4201.263284	&4202.628105	2.729642	0.57897	0.098501363	
GPHA2	&627.386322	&628.739297	2.70595	0.14141	0.099974512	
PINX1	&1712.018895	&1713.371825	2.70586	0.39565	0.099980154	
PNMA1	&1586.626798	&1587.975945	2.698294	0	0.100455686	
CAV1	&808.868343	&810.212848	2.68901	0.14046	0.101042575	
ZNF570	&2392.444634	&2393.778502	2.667736	0.32443	0.102401598	
MOCS3	&2332.972906	&2334.306077	2.666342	0.28545	0.102491345	
KRTAP4&7	&1355.559924	&1356.887593	2.655338	999	0.103202818	
KMO	&2495.228335	&2496.552373	2.648076	0.27429	0.103675308	
NDP	&595.239879	&596.554812	2.629866	0	0.104870564	
DARC	&1863.480235	&1864.755051	2.549632	0.26216	0.110319948	
RBBP7	&2093.740678	&2095.010255	2.539154	0.23289	0.111054276	
FTSJ2	&1311.504407	&1312.766921	2.525028	0.29504	0.112052792	
BCCIP	&1570.77242	&1572.034571	2.524302	0.23402	0.112104376	
TNIP3	&2039.58646	&2040.843979	2.515038	0.45357	0.112764915	
RBM7	&1282.36825	&1283.615972	2.495444	0.30427	0.114176172	
CCRL1	&1662.503077	&1663.750073	2.493992	0.29194	0.114281525	
CLEC4E	&1201.454278	&1202.663653	2.41875	0.22502	0.119890563	
ZNF302	&2361.155752	&2362.359532	2.40756	0.63597	0.120750446	
GMNN	&1035.065142	&1036.262431	2.394578	0.26775	0.121756602	
PLP1	&1162.116392	&1163.304191	2.375598	0	0.123244396	
GPR89A	&1485.507777	&1486.694073	2.372592	0	0.123481873	
C1orf43	&1161.238325	&1162.417314	2.357978	0	0.124643655	
CES5A	&3265.966238	&3267.119965	2.307454	0.5495	0.128754791	
MSL2	&2519.012952	&2520.159222	2.29254	0.25167	0.129997029	
ASH2L	&2901.035212	&2902.180467	2.29051	0.25108	0.130167146	
NUDCD1	&2709.861648	&2711.006238	2.28918	0.3534	0.130278735	
NPY5R	&1990.150747	&1991.271468	2.241442	0.16973	0.134355633	
B4GALT5	&1751.475123	&1752.58557	2.220894	0.16993	0.136154198	
PIP4K2C	&1756.08403	&1757.192358	2.216656	0.37925	0.136528493	
C8orf40	&467.375964	&468.473317	2.194706	0	0.13848563	
MAGEA8	&1513.58665	&1514.677477	2.181654	0.37508	0.139664295	
CISH	&1389.933179	&1391.017981	2.169604	0.3227	0.140762477	
ASPH	&3783.648765	&3784.725808	2.154086	0.38667	0.142191035	
SUMF1	&1881.960343	&1883.022441	2.124196	0.35117	0.144988844	
DDHD2	&298.91407	&299.971311	2.114482	0.3905	0.145911417	
CPB2	&2230.656598	&2231.705401	2.097606	0.43271	0.147529972	
MSRB2	&999.31295	&1000.360198	2.094496	0.17943	0.147830454	
DEFB103A	&835.978796	&837.001656	2.04572	0	0.152634755	
OLA1	&1684.190199	&1685.20652	2.032642	0.2733	0.153952778	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
HRH3	-2191.869354	-2192.873626	2.008544	0.33499	0.156415371	
ALDH1A3	-2495.040908	-2496.04169	2.001564	0.37975	0.157136995	
PPIG	-3511.591926	-3512.584389	1.984926	0.37254	0.158872423	
C1orf101	-5590.268594	-5591.258705	1.980222	0.62511	0.159367021	
TMEM232	-3272.074788	-3273.061724	1.973872	0.48689	0.16003747	
FAM64A	-1282.183072	-1283.164839	1.963534	0.41589	0.161135867	
PRSS55	-2132.15633	-2133.123767	1.934874	0.50284	0.16422619	
CEACAM6	-2794.752415	-2795.712975	1.92112	0.51223	0.165733245	
HLF	-1267.932471	-1268.87492	1.884898	0.1963	0.169778501	
VCX2	-905.01904	-905.949171	1.860262	0.48	0.172594565	
AMBN	-2391.016037	-2391.939762	1.84745	0.44962	0.174080266	
ZNF192	-2773.176187	-2774.090136	1.827898	0.48151	0.176376025	
CORO1C	-2135.661561	-2136.551346	1.77957	0.20638	0.182202137	
MAGEB17	-1975.035171	-1975.879737	1.689132	0.46634	0.19371543	
INTS6	-4108.243372	-4109.079181	1.671618	999	0.196041957	
PIGA	-362.58321	-2363.418315	1.67021	0.47004	0.196230409	
CYP3A5	-2730.724446	-2731.557922	1.666952	0.21147	0.196667287	
ACOT12	-2906.272807	-2907.099087	1.65256	0.48795	0.198610859	
ZNF561	-3217.90419	-3218.727049	1.645718	1.40678	0.199542738	
RESP18	-1250.437038	-1251.249499	1.624922	0.38327	0.202406848	
CCNB1	-1924.143147	-1924.923843	1.561392	5.08738	0.211461521	
FAM120A	-5403.205645	-5403.986111	1.560932	0.71197	0.21152881	
PTPRCAP	-1093.827442	-1094.589836	1.524788	0.51862	0.216896362	
ZFP37	-3100.294374	-3101.05546	1.522172	0.40811	0.217291101	
TIAF1	-616.082005	-616.835063	1.506116	0.23428	0.219732708	
CCDC73	-5508.719109	-5509.471284	1.50435	2.02116	0.220003255	
EFS	-2802.120981	-2802.85561	1.469258	0.44267	0.225462801	
AHSA1	-1500.759392	-1501.476472	1.43416	0.33775	0.231086722	
HMGCR	-4420.757787	-4421.467568	1.419562	0.43844	0.233475509	
METAP1D	-1548.655341	-1549.358657	1.406632	999	0.235616306	
LYG1	-1101.909567	-1102.610109	1.401084	2.44518	0.236542158	
RAD21L1	-2718.089407	-2718.785148	1.391482	2.83811	0.238154985	
C1orf187	-1760.830539	-1761.524571	1.388064	0.5237	0.238732316	
OR51F2	-1557.152016	-1557.836992	1.369952	0.54587	0.241820131	
PNPT1	-3658.046457	-3658.71551	1.338106	0.49912	0.247368255	
RABGGTA	-2636.662591	-2637.32835	1.331518	0.45894	0.248535343	
GLYAT	-1578.305413	-1578.96215	1.313474	0.4502	0.251766631	
TUBB	-2134.816899	-2135.468966	1.304134	0.64962	0.253459479	
SCG3	-2151.791388	-2152.434085	1.285394	0.30732	0.256898516	
GOLGA6C	-5060.790182	-5061.416069	1.251774	0.74996	0.263213923	
WFDC11	-494.113193	-494.737385	1.248384	0.25351	0.263861349	
GFRAL	-2057.086425	-2057.707896	1.242942	0.49138	0.264904811	
TMEM178	-1347.039863	-1347.638464	1.197202	0.20755	0.273881626	
OR1A2	-1539.506479	-1540.081896	1.150834	0.6809	0.283374632	
MARK2	-3512.115824	-3512.652043	1.072438	0.54781	0.300395408	
SUSD3	-1284.296241	-1284.824786	1.05709	999	0.303879828	
ZFP57	-2766.742388	-2767.269191	1.053606	0.54762	0.304678052	
ZNF20	-2603.184056	-2603.6959	1.023688	0.51406	0.3116458	
ZBP1	-2567.15208	-2567.64662	0.98908	0.63409	0.319967335	
MRPL55	-878.040282	-878.521731	0.962898	0.37988	0.326457807	
OR6X1	-1670.878703	-1671.359386	0.961366	2.11879	0.326842955	
TMEM38B	-1444.995504	-1445.457464	0.92392	0.52382	0.336447809	
SLC4A4	-4929.571762	-4930.030823	0.918122	0.50932	0.337968557	
FAM165B	-284.949495	-285.403835	0.90868	0.31684	0.340464896	
MAGEB3	-1942.382682	-1942.832134	0.898904	0.5718	0.343075759	
WISP3	-1792.324144	-1792.770688	0.893088	0.45625	0.344641859	
IRX6	-2443.809124	-2444.253637	0.889026	0.57438	0.345741389	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
RPL26	-711.744146	-712.186812	0.885332	0.47879	0.346745434	
WFDC6	-441.336459	-441.777176	0.881434	2.59874	0.347809219	
NT5M	-972.981002	-973.4004	0.838796	0	0.359741343	
C14orf181	-761.652798	-762.065887	0.826178	2.46311	0.363380034	
SMC5	-5108.021426	-5108.400406	0.75796	0.67903	0.38396769	
PPM1E	-3396.422004	-3396.79892	0.753832	0.50477	0.385265702	
GNG5P2	-352.560768	-352.934881	0.748226	999	0.387038472	
MOAP1	-1704.868932	-1705.227257	0.71665	0.51304	0.397244973	
C1orf27	-2079.506174	-2079.859449	0.70655	999	0.400591513	
USP18	-2026.940767	-2027.291821	0.702108	0.65966	0.402076281	
FAM111A	-3300.472399	-3300.821874	0.69895	1.42261	0.403136735	
SHMT2	-2374.32627	-2374.674118	0.695696	0.54027	0.404233691	
CCDC68	-1603.557967	-1603.903698	0.691462	0.51323	0.405667545	
MIER1	-1903.273829	-1903.610691	0.673724	0	0.411756256	
ZNF625	-1427.501477	-1427.832643	0.662332	0.44104	0.415737865	
SLC31A1	-859.475077	-859.796985	0.643816	0.31403	0.422332337	
SDC2	-946.867961	-947.182229	0.628536	0.48683	0.427892828	
ITGB3BP	-887.269066	-887.578577	0.619022	0.31713	0.431410949	
MPZL2	-1007.594511	-1007.893099	0.597176	0.45538	0.439657543	
ZNF157	-2379.212483	-2379.508604	0.592242	0.552	0.441553458	
COQ3	-1949.929888	-1950.221204	0.582632	2.15899	0.445282506	
METTL6	-1402.761818	-1403.050987	0.578338	0.33023	0.44696451	
MTIF3	-1539.427516	-1539.713441	0.57185	0.65666	0.449524711	
PGAM1	-1120.590217	-1120.866677	0.55292	999	0.457127032	
NPFF	-606.301065	-606.576537	0.550944	0.47014	0.457932233	
DERL1	-1105.391763	-1105.662502	0.541478	0.34311	0.46182084	
SYNPO2L	-4880.202414	-4880.469287	0.533746	1.32646	0.465036207	
APOBEC1	-1256.731159	-1256.992233	0.522148	0.57448	0.469926842	
CHST4	-1993.840865	-1994.096126	0.510522	0.68861	0.474912974	
DEFB110	-339.937923	-340.184863	0.49388	0.27011	0.482201612	
GSC	-1061.855257	-1062.082346	0.454178	25.39823	0.500357537	
C17orf51	-1209.790626	-1210.01714	0.453028	1.44787	0.500900502	
CD69	-1045.174658	-1045.400505	0.451694	0.52956	0.501531597	
IFNA2	-1005.585925	-1005.798986	0.426122	1.95634	0.513897985	
IFI27L1	-554.304655	-554.516539	0.423768	0.42174	0.515062849	
NSUN3	-1619.100126	-1619.293799	0.387346	0.60321	0.533697766	
C4orf33	-1021.496481	-1021.690107	0.387252	0.62854	0.533747416	
TTC29	-2305.720551	-2305.90688	0.372658	1.59732	0.541558983	
CD300C	-1372.519172	-1372.701602	0.36486	0.66721	0.545819427	
TTF1	-5078.240751	-5078.422161	0.36282	0.79367	0.546944236	
DCTN6	-845.466994	-845.645776	0.357564	0.4227	0.54986225	
MPV17L	-1181.660015	-1181.828571	0.337112	0.65518	0.561500993	
AGAP10	-4366.914788	-4367.083031	0.336486	0.82854	0.561864626	
ABHD10	-1500.323267	-1500.488663	0.330792	0.5758	0.565193102	
ZNF540	-3153.75444	-3153.910094	0.311308	0.6866	0.576878651	
CCDC69	-1442.237275	-1442.391608	0.308666	0.62382	0.578499937	
IL10RA	-3125.976119	-3126.112783	0.273328	0.76963	0.601108008	
CDCA3	-1246.124755	-1246.260897	0.272284	0.65214	0.601803745	
ZNF652	-2772.886785	-2773.021585	0.2696	0.76973	0.603600222	
USP26	-5057.691983	-5057.821049	0.258132	1.29293	0.61140641	
TAC4	-627.759082	-627.878198	0.238232	1.72898	0.625485984	
STH	-712.441928	-712.559154	0.234452	1.69081	0.628242208	
GIMAP2	-1824.150252	-1824.260255	0.220006	0.73143	0.639035347	
C11orf20	-1250.488051	-1250.593107	0.210112	0.57162	0.646679634	
ZNF30	-3411.171969	-3411.275832	0.207726	1.32942	0.64855561	
GAL3ST4	-2423.473765	-2423.577101	0.206672	1.40235	0.649388456	
PFDN6	-548.950851	-549.053315	0.204928	0.51534	0.650772169	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	Pvalue	k
C4orf7	-518.327969	-518.428707	0.201476	0.5944	0.65353209	
DNAJC5G	-1132.567675	-1132.662121	0.188892	0.67101	0.663840401	
OAS1	-2334.358664	-2334.451661	0.185994	1.29634	0.666271903	
OR14A2	-1605.722585	-1605.809157	0.173144	1.55868	0.677332618	
LRPPRC	-7708.027181	-7708.110661	0.16696	0.88925	0.682827806	
RBP7	-647.185617	-647.266595	0.161956	0.59817	0.687362023	
ATP5H	-760.853279	-760.92347	0.140382	1.50847	0.707901548	
HSPB2	-809.778519	-809.844871	0.132704	1.48495	0.71564475	
IDO2	-2229.951165	-2230.014864	0.127398	0.79553	0.721145285	
IFI44	-2281.936299	-2281.987749	0.1029	1.10262	0.74837689	
L3MBTL1	-3975.76727	-3975.817854	0.101168	76.86343	0.750432465	
LRRC27	-2939.332875	-2939.382776	0.099802	0.87401	0.752067371	
PTTG2	-1130.175755	-1130.224838	0.098166	0.79667	0.754041706	
PRRC1	-2120.167757	-2120.210893	0.086272	0.69085	0.76897114	
C12orf5	-1453.530304	-1453.570562	0.080516	0.87863	0.776599358	
EXPH5	-10699.53023	-10699.56477	0.069074	0.927	0.792689836	
FCRL2	-3056.253752	-3056.283302	0.0591	0.88604	0.807924123	
FANCG	-3680.66821	-3680.695421	0.054422	1.16976	0.815539925	
DDTL	-774.594983	-774.618372	0.046778	1.3295	0.828767765	
TMEM139	-1120.610583	-1120.630421	0.039676	1.18592	0.84211541	
SMR3B	-486.806771	-486.826107	0.038672	0.85477	0.844099893	
LAIR1	-1743.823452	-1743.836984	0.027064	0.92686	0.869328575	
RGS18	-1078.393113	-1078.401173	0.01612	0.86117	0.898968447	
VSIG1	-2093.587192	-2093.594662	0.01494	0.89861	0.902717428	
CCDC36	-3126.612989	-3126.616358	0.006738	0.95372	0.934578866	
CYLC1	-3426.597334	-3426.599229	0.00379	0.97237	0.950910862	
ADAT2	-896.393812	-896.39568	0.003736	9.55827	0.95126139	
CCDC82	-2745.824761	-2745.826237	0.002952	0.95666	0.956670407	
TSPAN8	-1578.173712	-1578.174781	0.002138	0.97263	0.963120147	
IL19	-1203.301211	-1203.301836	0.00125	1.0284	0.971796397	
MLXIPL	-3536.733038	-3536.733474	0.000872	659.02618	0.976442175	
H2AFB3	-626.31617	-626.316293	0.000246	0	0.987486183	
MRPL43	-1378.232281	-1378.23236	0.000158	0.98991	0.989971011	
PLK2	-3091.218566	-3091.21862	0.000108	0	0.99170829	
OR13J1	-1779.142835	-1779.142871	7.2E-05	0	0.993229806	
VPREB1	-805.561659	-805.561678	3.8E-05	1.00734	0.99508154	
ZC4H2	-923.282204	-923.282214	2E-05	0	0.996431764	
CNPY1	-413.535206	-413.535212	1.2E-05	0	0.997236052	
RPS23	-645.083991	-645.083997	1.2E-05	0	0.997236052	
C8orf39	-460.662939	-460.662939	0	0	1	
C9orf9	-878.927042	-841.109223	-75.635638	0	#NUM!	
EIF2C2	-4476.569068	-4036.790303	-879.55753	0	#NUM!	
KCNG2	-1852.660891	-1852.660887	-8E-06	1.04743	#NUM!	

Gibbon

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
GNAO1	&2115.471065	&2173.12704	115.31195	0.07053	6.72424E&27	
NCOR2	&12227.13468	&12275.86669	97.464022	0.07817	5.48438E&23	
JAG2	&6294.322233	&6336.71451	84.784554	0.02916	3.32713E&20	
APC2	&11996.17469	&12036.29516	80.240938	0.10158	3.31429E&19	
SULF2	&4177.867509	&4211.050843	66.366668	0.02269	3.7438E&16	
CARD11	&5918.567778	&5950.066647	62.997738	0.05085	2.06944E&15	
PNPLA7	&6799.850995	&6830.409672	61.117354	0.15089	5.37721E&15	
PLCH2	&7498.549398	&7528.072543	59.04629	0.11614	1.54006E&14	
FZR1	&2349.820912	&2378.354784	57.067744	0	4.21055E&14	
GRIK3	&4315.212039	&4342.499488	54.574898	0.01103	1.49635E&13	
VPS13D	&20745.53353	&20771.86717	52.667282	0.2036	3.95119E&13	
SPTB	&11259.48771	&11285.68967	52.403922	0.20052	4.51821E&13	
SEMA6B	&4181.648172	&4207.831401	52.366458	0.04248	4.60523E&13	
EPHB3	&4499.344225	&4525.448741	52.209032	0.02129	4.98961E&13	
EIF2C2	&4032.921109	&4059.022804	52.20339	0	5.00397E&13	
KIDINS220	&8391.464681	&8417.501949	52.074536	0.05256	5.34334E&13	
UNC13C	&10555.40238	&10578.79746	46.79017	0.14643	7.90087E&12	
SEC14L5	&3456.310436	&3478.744967	44.869062	0.04431	2.1066E&11	
SLC7A14	&3655.169686	&3676.822808	43.306244	0	4.68087E&11	
MAP4K4	&6064.165208	&6085.637079	42.943742	0.0331	5.63368E&11	
WDR33	&6004.669905	&6025.719422	42.099034	0.02091	8.6766E&11	
SIPA1	&4987.98284	&5008.921085	41.87649	0.03215	9.72246E&11	
SLIT1	&7419.932554	&7440.39929	40.933472	0.0936	1.575E&10	
PITPNM1	&6236.487923	&6256.907641	40.839436	0.08961	1.65264E&10	
LAMA4	&8659.749199	&8679.885833	40.273268	0.12634	2.2081E&10	
ANO1	&4809.585365	&4828.828075	38.48542	0.05749	5.51643E&10	
COL20A1	&6580.595763	&6599.061085	36.930644	0.2151	1.22407E&09	
KCNB1	&3940.805872	&3959.261029	36.910314	0.03519	1.2369E&09	
TNS3	&7655.20922	&7673.650673	36.882906	0.20711	1.25441E&09	
SMPD3	&3077.897825	&3096.226976	36.658302	0.03329	1.40758E&09	
ZNF335	&6610.262205	&6628.394271	36.264132	0.09255	1.72306E&09	
TGM1	&4090.243734	&4108.23063	35.973792	0.08068	1.99989E&09	
YLPM1	&9690.016281	&9707.734126	35.43569	0.08466	2.63612E&09	
DEF8	&2631.742658	&2649.420092	35.354868	0.0586	2.74781E&09	
PNKP	&2844.06936	&2861.635625	35.13253	0.12444	3.08012E&09	
TBC1D9	&5831.190222	&5848.697841	35.015238	0.05621	3.27135E&09	
SV2B	&3191.079563	&3208.476777	34.794428	0.02066	3.66421E&09	
PAX9	&1572.816392	&1589.959355	34.285926	0	4.7581E&09	
SHPRH	&8158.977608	&8176.050814	34.146412	0.11931	5.11174E&09	
GPT2	&2464.190928	&2480.860387	33.338918	0.03381	7.74177E&09	
FAM120A	&5417.104747	&5433.608734	33.007974	0.0235	9.17817E&09	
SLC6A4	&3062.301596	&3078.617967	32.632742	0.0703	1.11324E&08	
PCDHA3	&4895.707618	&4911.685531	31.955826	0.09663	1.57719E&08	
ARHGAP4	&5865.130751	&5880.997534	31.733566	0.42579	1.76839E&08	
TMC8	&3632.068334	&3647.80145	31.466232	0.14452	2.02939E&08	
ASCC3	&10025.91726	&10041.60444	31.374352	0.10022	2.12773E&08	
EIF2C4	&3719.55317	&3735.122753	31.139166	0	2.40176E&08	
ROR2	&4588.12692	&4603.319464	30.385088	0.10197	3.54241E&08	
CA10	&1497.079837	&1512.153473	30.147272	0	4.0045E&08	
USP7	&4826.295083	&4841.320265	30.050364	0	4.2097E&08	
SEMA4B	&3998.318349	&4013.168829	29.70096	0.12265	5.04099E&08	
ISYNA1	&2712.023556	&2726.502241	28.95737	0.03911	7.39888E&08	
PRPF4B	&4588.662094	&4603.094981	28.865774	0.06804	7.75716E&08	
PCDH7	&5421.033179	&5435.41881	28.771262	0.04374	8.14508E&08	
PLK2	&3091.104452	&3105.468892	28.72888	0.10569	8.32529E&08	
TBXA2R	&1670.767958	&1685.07626	28.616604	0.03197	8.82224E&08	
CCDC132	&4369.346981	&4383.649282	28.604602	0.02339	8.8771E&08	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
CDT1	&2995.289807	&3009.432858	28.286102	0.15463	1.04645E&07	
MAP4K3	&4018.586135	&4032.7256	28.27893	0	1.05033E&07	
SMC2	&5402.652956	&5416.61327	27.920628	0.06555	1.26395E&07	
BCL9L	&7013.00579	&7026.829824	27.648068	0.13902	1.45517E&07	
PRKCD	&3136.267296	&3150.070449	27.606306	0.01641	1.48693E&07	
TMEM43	&2107.132529	&2120.895399	27.52574	0	1.55018E&07	
CPT1B	&3719.156815	&3732.866444	27.419258	0.0722	1.63792E&07	
CDK9	&1677.167214	&1690.750712	27.166996	0	1.86617E&07	
ME2	&2644.867753	&2658.425876	27.116246	0	1.91581E&07	
SLC16A8	&2346.438205	&2359.809436	26.742462	0.07661	2.32457E&07	
PPP1R12A	&4526.787342	&4540.154753	26.734822	0.06353	2.33378E&07	
GPR176	&2455.645953	&2468.947824	26.603742	0.02746	2.4976E&07	
ABCD3	&3240.878664	&3254.148522	26.539716	0.02705	2.58175E&07	
NR1D2	&2649.367513	&2662.514114	26.293202	0	2.93319E&07	
TTLL9	&2361.089288	&2374.138847	26.099118	0.17579	3.24332E&07	
ZC3H13	&7602.031044	&7615.005915	25.949742	0.11923	3.50422E&07	
TMEM121	&1354.424836	&1367.323767	25.797862	0	3.79108E&07	
ECEL1	&3728.237282	&3741.042738	25.610912	0.04939	4.17671E&07	
CDK13	&6755.428689	&6768.12476	25.392142	0.03055	4.6782E&07	
HIST1H2AJ	&620.351497	&632.659169	24.615344	0	6.99922E&07	
CLCN4	&3597.3791	&3609.627919	24.497638	0.02407	7.4401E&07	
MLLT6	&4826.345506	&4838.561856	24.4327	0.05232	7.69514E&07	
FBXL12	&1532.062192	&1543.978411	23.832438	0	1.05096E&06	
CDC37	&1706.798077	&1718.676336	23.756518	0	1.09325E&06	
SREK1	&2710.858447	&2722.576259	23.435624	0	1.29164E&06	
ZBTB38	&5739.803463	&5751.180982	22.755038	0.14959	1.84021E&06	
FLT3	&4937.344748	&4948.69459	22.699684	0.13727	1.89399E&06	
EPB41L1	&4094.814551	&4106.144421	22.65974	0.14752	1.93377E&06	
PRMT6	&1672.065466	&1683.378141	22.62535	0.02784	1.9687E&06	
ZNF324B	&3117.125031	&3128.357697	22.465332	0.23986	2.13971E&06	
ZNF592	&5978.560667	&5989.764504	22.407674	0.06067	2.20491E&06	
C19orf68	&3319.584714	&3330.723141	22.276854	0.10437	2.36035E&06	
HMGCR	&4418.343289	&4429.473544	22.26051	0.057	2.38052E&06	
SLC22A17	&2376.070543	&2387.095276	22.049466	0	2.65714E&06	
MSL2	&2521.092093	&2532.103979	22.023772	0.03375	2.69294E&06	
RABEP1	&3980.918449	&3991.809921	21.782944	0.08467	3.05302E&06	
RAP1GAP2	&3633.043114	&3643.928021	21.769814	0.17052	3.07399E&06	
CEBPZ	&5164.616114	&5175.221333	21.210438	0.16674	4.11517E&06	
SFRP1	&1508.622172	&1519.182175	21.120006	0.01894	4.31401E&06	
DDB2	&2011.402031	&2021.896001	20.98794	0.06773	4.62184E&06	
SYNPO2L	&4885.787713	&4896.2561	20.936774	0.25011	4.74694E&06	
C19orf47	&2053.284893	&2063.568115	20.566444	0.03272	5.75969E&06	
SUV39H1	&1814.111869	&1824.243138	20.262538	0	6.75096E&06	
ILKAP	&1840.121545	&1850.219515	20.19594	0	6.99011E&06	
CHL1	&6212.322146	&6222.404187	20.164082	0.14413	7.10751E&06	
RNF216	&4385.924033	&4395.985097	20.122128	0.16989	7.26513E&06	
SLC35C1	&1829.431951	&1839.480717	20.097532	0.05918	7.35916E&06	
AGPAT2	&1421.109128	&1431.109676	20.001096	0.02022	7.73978E&06	
DCAF5	&4504.040243	&4513.954717	19.828948	0.0867	8.46903E&06	
LEPREL4	&1975.589718	&1985.499771	19.820106	0.02215	8.5083E&06	
CORO1C	&2135.277854	&2145.183983	19.812258	0	8.5433E&06	
IRF8	&2086.863624	&2096.751318	19.775388	0.09638	8.7097E&06	
GFOD2	&1869.048459	&1878.835753	19.574588	0.05157	9.67475E&06	
PLCB1	&5510.498636	&5520.245951	19.49463	0.0741	1.00883E&05	
UPF2	&5623.545226	&5633.140337	19.190222	0.10167	1.18318E&05	
TOP3A	&5199.647551	&5209.236442	19.177782	0.20565	1.19091E&05	
L3MBTL1	&8976.04886	&8985.586596	19.075472	0.26923	1.25649E&05	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
GCK	&2423.708914	&2433.223608	19.029388	0.02308	1.28721E&05	
RFX7	&6743.965089	&6753.422444	18.91471	0.1992	1.36695E&05	
RALGDS	&4383.354471	&4392.750312	18.791682	0.22957	1.45802E&05	
MRGPRE	&1603.331413	&1612.718362	18.773898	0.08103	1.47168E&05	
RBBP6	&8240.509184	&8249.858763	18.699158	0.16671	1.5305E&05	
ZFP64	&3247.544414	&3256.803601	18.518374	0.10646	1.68274E&05	
GMNN	&1031.012631	&1040.224421	18.42358	0	1.76856E&05	
GCGR	&2922.43163	&2931.611247	18.359234	0.10579	1.8293E&05	
FKRP	&2437.533092	&2446.592826	18.119468	0.07035	2.07469E&05	
C21orf59	&1400.172942	&1409.229876	18.113868	0	2.0808E&05	
NLGN3	&8585.908873	&8594.908382	17.999018	0	2.21019E&05	
DCAF12L2	&2615.661084	&2624.660198	17.998228	0	2.21111E&05	
ADAM9	&3866.288718	&3875.235284	17.893132	0.1299	2.33663E&05	
YTHDC1	&3080.430981	&3089.313476	17.76499	0	2.4994E&05	
ERC1	&5074.006266	&5082.864507	17.716482	0.1525	2.56395E&05	
KLHDC4	&2858.093348	&2866.796363	17.40603	0.15774	3.01867E&05	
ALKBH3	&1306.071976	&1314.747584	17.351216	0.13348	3.10699E&05	
POGK	&2869.753469	&2878.394203	17.281468	0.07452	3.22315E&05	
PDZD7	&2715.584392	&2724.216203	17.263622	0.10481	3.25357E&05	
PLS3	&2742.372769	&2750.980382	17.215226	0	3.33751E&05	
PLXDC2	&2634.527813	&2643.095661	17.135696	0.04727	3.4802E&05	
ASH2L	&2901.82797	&2910.33622	17.0165	0.04195	3.70564E&05	
LHX2	&1796.16207	&1804.659968	16.995796	0.04947	3.74627E&05	
HNRPLL	&2492.633661	&2500.953672	16.640022	0.04006	4.51874E&05	
TMEM179	&901.134542	&909.437689	16.606294	0	4.59981E&05	
RTN4RL2	&1990.917659	&1999.177597	16.519876	0.12019	4.81428E&05	
ATG16L1	&2891.834451	&2900.072935	16.476968	0.07406	4.92447E&05	
ADRA1B	&2498.285279	&2506.508572	16.446586	0.12365	5.00402E&05	
SOAT2	&2726.275021	&2734.492946	16.43585	0.19828	5.03244E&05	
SLC4A4	&4931.702234	&4939.91824	16.432012	0.0599	5.04264E&05	
ALOX15	&3885.912266	&3894.02697	16.229408	0.22245	5.61162E&05	
TMCC3	&2203.133253	&2211.132784	15.999062	0	6.33739E&05	
PIAS1	&2899.211409	&2907.114664	15.80651	0	7.01607E&05	
CXCR5	&1773.930236	&1781.781407	15.702342	0.05165	7.41323E&05	
MAP3K7	&2660.679251	&2668.486055	15.613608	0.04378	7.76934E&05	
GNPAT	&3337.353814	&3345.11302	15.518412	0.10391	8.17055E&05	
KIAA0947	&12219.1207	&12226.82029	15.399176	0.38822	8.70262E&05	
SQSTM1	&2440.577176	&2448.263197	15.372042	0.1542	8.8285E&05	
ZC3H12D	&2708.068469	&2715.636546	15.136154	0.12584	0.000100029	
NPY5R	&1990.410673	&1997.971224	15.121102	0.07449	0.00010083	
MBLAC2	&1291.947507	&1299.472847	15.05068	0	0.000104663	
POFUT2	&2135.223977	&2142.681861	14.915768	0.07146	0.000112419	
TJP2	&6016.340273	&6023.787054	14.893562	0.25743	0.000113751	
CYTH1	&1782.827404	&1790.240436	14.826064	0	0.000117895	
TBR1	&2895.500083	&2902.862671	14.725176	0	0.000124374	
ROBO4	&5267.35271	&5274.68425	14.66308	0.28873	0.00012854	
DHTKD1	&4801.247024	&4808.566895	14.639742	0.23721	0.000130141	
MARK2	&3518.778138	&3526.025667	14.495058	0	0.000140528	
ABHD4	&1660.906688	&1668.072912	14.332448	0.04474	0.000153201	
CAV1	&809.602323	&816.699472	14.194298	0.03722	0.000164869	
CHST2	&2516.548077	&2523.643184	14.190214	0.10151	0.000165228	
GADD45A	&733.47672	&740.55979	14.16614	0	0.000167355	
NPFFR1	&2090.232837	&2097.265623	14.065572	0.11942	0.000176546	
ORC2	&2607.37338	&2614.387448	14.028136	0	0.000180096	
PADI1	&3540.802788	&3547.799835	13.994094	0.21841	0.000183386	
PCDHB5	&4602.532169	&4609.506859	13.94938	0.2622	0.0001878	
DCAF7	&1558.731619	&1565.678738	13.894238	0	0.00019339	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
DENND4B	&7193.665103	&7200.581746	13.833286	0.26632	0.000199766	
ZNF117	&8440.298677	&8447.209216	13.821078	0.45403	0.000201068	
ATP10D	&7192.592858	&7199.412995	13.640274	0.28261	0.000221385	
CPA5	&2349.096025	&2355.909481	13.626912	0.17271	0.000222966	
HIST1H2AL	&744.227674	&751.015439	13.57553	0	0.000229153	
NCKAP1L	&5395.100508	&5401.831552	13.462088	0.27306	0.000243433	
PIP4K2C	&1755.757957	&1762.394739	13.273564	0	0.000269175	
C20orf160	&2424.592503	&2431.159267	13.133528	0.04421	0.000290058	
CYP4F11	&2992.882801	&2999.407363	13.049124	0.19942	0.000303426	
COL5A2	&6696.760428	&6703.281864	13.042872	0.22234	0.000304441	
LDB3	&3932.071574	&3938.57455	13.005952	0.09096	0.000310502	
TBC1D17	&3152.391453	&3158.888812	12.994718	0.09329	0.000312371	
LRRTM3	&2556.07049	&2562.51244	12.8839	0	0.000331421	
TMEM232	&3270.174801	&3276.556815	12.764028	0.15695	0.000353349	
NUDCD1	&2709.542345	&2715.842316	12.599942	0.15172	0.000385759	
DUSP1	&1011.279256	&1017.55436	12.550208	0	0.000396162	
CAPN7	&3743.473375	&3749.72407	12.50139	0.13577	0.000406649	
DNAI2	&3179.929086	&3186.128209	12.398246	0.25758	0.000429737	
TMED4	&1061.521	&1067.658917	12.275834	0	0.000458862	
SNRPA1	&1117.342391	&1123.442262	12.199742	0	0.000477961	
ZCCHC17	&1050.227413	&1056.295882	12.136938	0	0.000494329	
LTK	&4352.41079	&4358.369524	11.917468	0.26517	0.0005561	
ZNF275	&2173.335776	&2179.271351	11.87115	0.13339	0.000570102	
DSCR3	&1519.558215	&1525.452299	11.788168	0.11997	0.000596084	
PGAM1	&1123.089752	&1128.976721	11.773938	0.05197	0.000600658	
ERCC3	&3771.681273	&3777.502614	11.642682	0.20859	0.000644556	
MPZL2	&1006.496888	&1012.314406	11.635036	0	0.000647211	
TUBB	&2152.497843	&2158.233209	11.470732	0	0.000707008	
MED19	&1132.54594	&1138.243673	11.395466	0	0.000736236	
ZNF625	&1427.8139	&1433.488224	11.348648	0.15375	0.000755029	
PSMD4	&1696.614421	&1702.268641	11.30844	0	0.000771556	
OVOL2	&1301.615192	&1307.241796	11.253208	0	0.000794855	
MAP4K5	&5017.246748	&5022.792158	11.09082	0.08391	0.000867561	
METTL6	&1400.111537	&1405.650226	11.077378	0.09091	0.000873873	
ABCB11	&6822.544939	&6828.073032	11.056186	0.27108	0.000883918	
STAT5B	&675.970698	&681.4804	11.019404	0.09592	0.000901631	
CAPS2	&2948.999302	&2954.500094	11.001584	0.16891	0.000910341	
SLC24A4	&2703.939903	&2709.411287	10.942768	0.14235	0.000939697	
SIX6	&1100.564314	&1105.985289	10.84195	0.04827	0.000992262	
SCN1B	&1018.51697	&1023.914955	10.79597	0	0.001017213	
FBXO22	&1929.708822	&1935.080129	10.742614	0.06817	0.001046963	
C9orf46	&558.9259	&564.277861	10.703922	0	0.001069087	
MBTPS2	&2423.546064	&2428.840554	10.58898	0	0.001137637	
USP1	&480.547832	&485.784728	10.473792	0.16778	0.001210799	
GUCA1B	&890.171812	&895.389164	10.434704	0	0.001236694	
HIST1H3F	&761.424527	&766.591192	10.33333	0	0.001306493	
MOCS3	&2332.166264	&2337.315795	10.299062	0.13991	0.001330978	
PNPT1	&3659.548888	&3664.68267	10.267564	0.19735	0.001353894	
GJA4	&1636.944145	&1642.066211	10.244132	0.04577	0.001371201	
STUB1	&1347.877786	&1352.973399	10.191226	0	0.001411105	
ARCN1	&2281.992359	&2287.074236	10.163754	0.06105	0.001432287	
FOSB	&1437.763914	&1442.813019	10.09821	0	0.001484134	
TAGLN	&884.977231	&889.995746	10.03703	0	0.001534244	
ATAD2	&6458.475194	&6463.449711	9.949034	0.24202	0.001609338	
GCDH	&2328.233257	&2333.157558	9.848602	0.16031	0.001699609	
EFS	&2801.691091	&2806.577972	9.773762	0.15582	0.001770199	
KANK3	&4442.174917	&4447.060612	9.77139	0.31355	0.001772484	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
MYL6B	&1176.854321	&1181.706793	9.704944	0.05651	0.001837729	
SMC5	&5111.586527	&5116.42177	9.670486	0.30102	0.001872518	
LSM10	&586.291941	&591.085688	9.587494	0.05973	0.001959071	
ASPH	&783.535223	&788.324727	9.579008	0.25112	0.001968147	
EPB49	&1818.080148	&1822.806935	9.453574	0.04647	0.002107381	
FBL	&1605.159171	&1609.845062	9.371782	0.22057	0.002203512	
NR1I3	&1717.934209	&1722.60959	9.350762	0	0.002228928	
ZFP57	&2765.809146	&2770.405156	9.19202	0.21288	0.002430725	
ZNF302	&2360.230307	&2364.825379	9.190144	0.16983	0.002433217	
GALNT12	&3050.326791	&3054.91824	9.182898	0.15232	0.002442869	
FAM126B	&2587.206836	&2591.763207	9.112742	0.06545	0.002538351	
NDUFA6	&803.101006	&807.542677	8.883342	0	0.002877843	
DMGDH	&4203.058303	&4207.463294	8.809982	0.31683	0.00299587	
TBCB	&1152.152082	&1156.55136	8.798556	0.12475	0.003014691	
MIER1	&1903.212927	&1907.5983	8.770746	0.05649	0.003061002	
ZNF652	&2778.766636	&2783.147768	8.762264	0	0.003075271	
G6PC	&1733.622273	&1738.003266	8.761986	0.16871	0.003075739	
C11orf84	&2716.026733	&2720.395128	8.73679	0.60132	0.00311853	
C1orf27	&2080.033937	&2084.382967	8.69806	0.14031	0.003185489	
CDC23	&2708.133841	&2712.435136	8.60259	0.12283	0.003356853	
KMO	&2494.015178	&2498.308178	8.586	0.186	0.003387573	
TSPAN15	&1377.291218	&1381.553947	8.525458	0.09343	0.003502126	
SUMF1	&1881.996014	&1886.247781	8.503534	0.2927	0.003544574	
GPR39	&2381.334747	&2385.54178	8.414066	0.23434	0.00372329	
HSPB2	&813.384553	&817.510298	8.25149	0.07306	0.004071856	
DERL1	&1105.790094	&1109.843831	8.107474	0	0.004408311	
ACCN1	&2699.520979	&2703.564265	8.086572	0.47824	0.004459443	
RD3	&982.519327	&986.551931	8.065208	0.04733	0.00451233	
PLEKHA5	&4835.066794	&4839.086818	8.040048	0.25052	0.004575432	
ABHD10	&1500.57812	&1504.557656	7.959072	0.12093	0.004784694	
TRIM39	&2367.092457	&2371.023319	7.861724	0.12307	0.005049223	
RBBP7	&2092.607591	&2096.535238	7.855294	0	0.005067211	
MS4A7	&1298.632822	&1302.552742	7.83984	0.13622	0.005110713	
TMEM38B	&1445.920539	&1449.833065	7.825052	0.10001	0.005152696	
PPIG	&510.912068	&514.751087	7.678038	0.14755	0.005589691	
MED7	&980.949476	&984.75877	7.618588	0	0.00577697	
ASB1	&1624.889226	&1628.687973	7.597494	0	0.005844949	
HLF	&1269.550468	&1273.331767	7.562598	0	0.005959202	
LHFPL2	&1093.406534	&1097.155583	7.498098	0.11938	0.006176419	
FOLR2	&1278.228133	&1281.976753	7.49724	0.0668	0.006179362	
ALDH1A3	&2496.872363	&2500.571723	7.39872	0.11886	0.00652703	
CCNB1	&1926.780328	&1930.471936	7.383216	0.16762	0.006583534	
SDC2	&946.502068	&950.169864	7.335592	0	0.006760241	
MARVELD3	&1940.57838	&1944.243054	7.329348	0.32552	0.006783766	
RPL23A	&867.477013	&871.125971	7.297916	0	0.006903464	
RABGGTA	&2637.763981	&2641.411464	7.294966	0.13415	0.006914808	
GPR89A	&1485.312096	&1488.926761	7.22933	0	0.007172197	
ARL6IP1	&939.257374	&942.871602	7.228456	0	0.00717569	
PLAU	&2338.546405	&2342.108067	7.123324	0.20975	0.007608751	
HM13	&1873.378261	&1876.90371	7.050898	0.07447	0.007922552	
RC3H1	&5132.269928	&5135.791897	7.043938	0.20688	0.007953397	
POU2F2	&2165.621033	&2169.142818	7.04357	0.2209	0.007955031	
CACNG6	&1274.377003	&1277.89526	7.036514	0.26695	0.007986433	
MPHOSPH9	&4893.300865	&4896.775203	6.948676	0.36126	0.008388129	
FAM167A	&1035.086901	&1038.560803	6.947804	0.16385	0.008392219	
ANGEL2	&2366.462378	&2369.923192	6.921628	0.09436	0.008515941	
PLEKHB2	&1116.094658	&1119.516751	6.844186	0.13986	0.008893021	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
PCDHA1	&5051.976003	&5055.378476	6.804946	0.42504	0.00909057	
ENOPH1	&1177.640132	&1180.954686	6.629108	0	0.010032549	
MAP2	&8749.153076	&8752.391423	6.476694	0.43229	0.010929809	
PYGO2	&1791.484022	&1794.714326	6.460608	0.19884	0.01102919	
CNTFR	&1737.614551	&1740.828321	6.42754	0.20041	0.01123641	
PFDN6	&550.439976	&553.623906	6.36786	0	0.011620565	
HELB	&5542.759932	&5545.940316	6.360768	0.34291	0.011667103	
TMEM18	&652.582911	&655.755843	6.345864	0.17978	0.011765529	
APOBEC1	&1256.250388	&1259.415184	6.329592	0.15506	0.011873963	
C9orf9	&840.041679	&843.200799	6.31824	0.05998	0.011950218	
DNAJC17	&1458.476047	&1461.594768	6.237442	0.08841	0.0125077	
ICT1	&1153.248133	&1156.360828	6.22539	0	0.012593117	
LRRC2	&1793.459231	&1796.568738	6.219014	0.19368	0.012638548	
COPS4	&1959.833068	&1962.91791	6.169684	0.08815	0.012995782	
TNFAIP8L3	&1464.879143	&1467.955894	6.153502	0.08857	0.013115215	
UBLCP1	&1381.208509	&1384.263313	6.109608	0	0.013444895	
ZFYVE20	&3771.952638	&3774.998448	6.09162	0.26015	0.01358245	
GUCY2F	&5372.136388	&5375.158443	6.04411	0.30609	0.013952765	
MAGEA8	&1513.575975	&1516.597611	6.043272	0.28095	0.013959389	
TRAIP	&2304.255029	&2307.248525	5.986992	0.18194	0.014411758	
FAM103A1	&520.580443	&523.533875	5.906864	0	0.015081998	
NR2C2	&2826.190801	&2829.131237	5.880872	0.18675	0.015306239	
S1PR3	&1731.898526	&1734.836044	5.875036	0.14452	0.015357059	
ATAD5	&9296.086341	&9299.004231	5.83578	0.48628	0.015703446	
CHST4	&1996.011136	&1998.926648	5.831024	0.24499	0.015745955	
IL17REL	&1709.017047	&1711.892244	5.750394	0.18965	0.016484959	
GOLGA6C	&5060.393725	&5063.233598	5.679746	0.5113	0.017161852	
SHMT2	&2376.439887	&2379.254571	5.629368	0.09317	0.017661998	
HIST1H3G	&641.629555	&644.439634	5.620158	0	0.017755048	
C1orf187	&1762.461401	&1765.244126	5.56545	0.18266	0.018318302	
CNTN6	&5056.944304	&5059.722588	5.556568	0.3485	0.018411474	
TTYH1	&2168.885212	&2171.609149	5.447874	0.16873	0.019592155	
C7orf60	&1791.506771	&1794.221611	5.42968	0	0.019797307	
IDO2	&2229.302248	&2232.015741	5.426986	0.26808	0.019827872	
ZC4H2	&923.282245	&925.967655	5.37082	0	0.020476349	
GPR179	&14282.64699	&14285.31819	5.342406	0.60288	0.020812728	
WDFY2	&1824.208535	&1826.837874	5.258678	0.10792	0.0218376	
OR5AS1	&1664.012458	&1666.618302	5.211688	0.26447	0.022435542	
LETM2	&522.085024	&524.690296	5.210544	0.2569	0.022450309	0.027090301
B4GALT5	&1751.754017	&1754.337421	5.166808	0.09398	0.023022482	0.027173913
TMEM208	&763.952368	&766.533719	5.162702	0	0.023076969	0.027257525
FAM55B	&2830.476722	&2833.050075	5.146706	0.31045	0.023290515	0.027341137
CHM	&3029.442443	&3032.014686	5.144486	0.29783	0.023320313	0.027424749
CLK4	&2165.912981	&2168.480879	5.135796	0.2003	0.023437337	0.027508361
TSPAN8	&1577.571863	&1580.129702	5.115678	4.12104	0.0237106	
VPS52	&3325.509507	&3328.046955	5.074896	0.16675	0.024274728	
ZNF575	&1660.829436	&1663.366342	5.073812	0.24744	0.024289912	
HRH3	&2194.120449	&2196.655713	5.070528	0.04043	0.02433597	
GSC	&1065.304721	&1067.834032	5.058622	0.06371	0.024503714	
ZNF569	&3121.86002	&3124.369878	5.019716	0.28399	0.025060279	
RPS23	&645.084016	&647.586878	5.005724	0	0.025263635	
MDM4	&2141.910227	&2144.412159	5.003864	0	0.025290796	
MRPL21	&1129.394373	&1131.895327	5.001908	0.11381	0.025319392	
STX2	&1321.515339	&1324.015111	4.999544	0	0.025353998	
POLR2F	&562.408122	&564.902446	4.988648	0	0.025514136	0.028428094
KRT36	&2449.40721	&2451.87626	4.9381	0.3333	0.0262709	0.028511706
GPRASP2	&4102.927926	&4105.383523	4.911194	0.38512	0.02668319	0.028595318

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
KCNJ9	&1729.805797	&1732.251171	4.890748	0.06362	0.027000986	0.02867893
SCG3	&2152.174153	&2154.615196	4.882086	0.14971	0.027136805	0.028762542
RPL26	&712.678571	&715.105273	4.853404	0.09556	0.027591629	0.028846154
DCTN6	&847.781334	&850.197777	4.832886	0	0.027921854	0.028929766
KRTAP4&7	&1360.289009	&1362.702922	4.827826	0.07694	0.028003921	0.029013378
ANKRD52	&5039.190268	&5041.588555	4.796574	0.50132	0.028516389	0.02909699
FGF2	&1339.764063	&1342.13888	4.749634	0.25805	0.029304527	0.029180602
C11orf80	&563.794925	&566.157849	4.725848	0.62204	0.029712529	
TIAF1	&615.724033	&618.070866	4.693666	999	0.030273991	
ZNF540	&3153.875002	&3156.213959	4.677914	0.35063	0.030552827	
HSD17B3	&1583.237055	&1585.557192	4.640274	0.11496	0.031230016	
FTSJ2	&1311.479015	&1313.791315	4.6246	0.30684	0.031516609	
TACR2	&1978.456722	&1980.768376	4.623308	0.20703	0.031540355	
WDR63	&4324.741845	&4327.030961	4.578232	0.2492	0.032380608	
PTPRCAP	&1095.712928	&1098.001515	4.577174	0.2304	0.032400608	
KLRG2	&2205.196151	&2207.464996	4.53769	0.35845	0.033156307	
IRX6	&2444.185682	&2446.423722	4.47608	0.39931	0.034372472	
SECTM1	&1274.905908	&1277.142717	4.473618	0.46325	0.03442203	
CCDC115	&881.665012	&883.859202	4.38838	0.17193	0.036184679	
C8orf40	&467.375964	&469.566653	4.381378	0	0.036333612	
ZNF20	&2602.714138	&2604.88482	4.341364	0.27303	0.037197112	
SEC13	&1771.147835	&1773.289757	4.283844	0.21285	0.038476239	
C11orf20	&1249.398697	&1251.50131	4.205226	0.48187	0.040299604	
RAB17	&1171.38797	&1173.481921	4.187902	0.27243	0.040713452	
PLB1	&7858.537014	&7860.609026	4.144024	0.54648	0.041781735	
MFSD6L	&8312.340999	&8314.371475	4.060952	0.42674	0.043885752	
CCDC157	&833.78529	&835.797006	4.023432	0.47262	0.044872313	
SDAD1	&548.821808	&550.821286	3.998956	0.61383	0.045528456	
MOAP1	&1705.680979	&1707.660054	3.95815	0.18722	0.04664494	
BLNK	&2338.467391	&2340.427198	3.919614	0.34185	0.047725837	
IL19	&1202.163121	&1204.102741	3.87924	0.19202	0.048886682	
EXPH5	&10700.90713	&10702.83455	3.854842	0.66686	0.049602599	
MSRB2	&999.298774	&1001.22447	3.851392	0.31814	0.049704723	
PPM1E	&3396.564885	&3398.454577	3.779384	0.36248	0.05188776	
BCCIP	&1569.211255	&1571.072627	3.722744	999	0.053676092	
ACOT12	&2905.903393	&2907.763842	3.720898	0.44168	0.053735464	
MTIF3	&1537.933977	&1539.787322	3.70669	0.32071	0.054194763	
MTG1	&1717.904296	&1719.750106	3.69162	0.26736	0.054686477	
SOCS4	&1989.847784	&1991.693548	3.691528	0.16964	0.054689493	
CAPN11	&3812.459973	&3814.295583	3.67122	0.48506	0.055359648	
ADAM29	&4769.677901	&4771.49943	3.643058	0.39903	0.05630343	
C4orf31	&2782.597577	&2784.40711	3.619066	0.32277	0.057120933	
CCDC82	&2745.273131	&2747.078737	3.611212	0.32814	0.05739128	
AMBN	&2391.618669	&2393.393443	3.549548	3.75017	0.059561673	
ZNF561	&3224.141086	&3225.915069	3.547966	0.43678	0.05961849	
KPTN	&2399.631358	&2401.393558	3.5244	0.52816	0.060471709	
OLA1	&1684.835353	&1686.595329	3.519952	0.13701	0.060634203	
INTS6	&4106.031368	&4107.777312	3.491888	0.52733	0.061670214	
DLEC1	&9083.506056	&9085.237454	3.462796	0.57761	0.062764099	
CHRDL2	&2434.932323	&2436.641373	3.4181	0.5182	0.064485191	
EPT1	&1772.737908	&1774.446612	3.417408	0.19148	0.06451223	
CHMP5	&937.877506	&939.568559	3.382106	0	0.065907788	
H2AFB3	&626.069639	&627.749788	3.360298	0.18284	0.066785982	
MBD6	&4425.984616	&4427.642006	3.31478	0.40536	0.06865951	
WISP3	&1792.55294	&1794.197728	3.289576	0.21668	0.069721024	
C1QTNF7	&1370.802466	&1372.439454	3.273976	0.26702	0.070386839	
NPY1R	&1729.9241	&1731.556366	3.264532	0.14695	0.07079322	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
CD2AP	-3055.027802	-3056.656384	3.257164	0.3112	0.071112015	
S100A4	-429.462564	-431.019912	3.114696	0	0.077588956	
RBM7	-1282.4826	-1284.039818	3.114436	0	0.07760134	
HEYL	-1751.475958	-1753.013406	3.074896	0.39664	0.079509679	
CD69	-1045.083477	-1046.608772	3.05059	0.35013	0.080707819	
CMBL	-1196.213798	-1197.709351	2.991106	0.15628	0.083722968	
CYP3A5	-2730.860462	-2732.305153	2.889382	0.40471	0.089165122	
AGGF1	-3402.98927	-3404.422106	2.865672	0.37466	0.09048791	
ELF4	-3306.433388	-3307.859703	2.85263	0.53621	0.091224593	
ADH1A	-2353.708464	-2355.127112	2.837296	0.42699	0.09209908	
ARHGAP19	-2378.698492	-2380.077468	2.757952	0.28211	0.096772049	
PM20D2	-2164.060332	-2165.420236	2.719808	0.28575	0.099109936	
LSM7	-453.364263	-454.721492	2.714458	0	0.099442742	
MAGEB3	-1941.823789	-1943.1692	2.690822	0.48525	0.100927736	
TXNDC11	-4977.89749	-4979.239575	2.68417	0.43479	0.101350022	
LIPH	-2244.444305	-2245.778726	2.668842	0.30256	0.102330454	
TMEM105	-685.820591	-687.146575	2.651968	999	0.103421788	
BROX	-1818.116854	-1819.442037	2.650366	0.22631	0.103526058	
PER3	-6656.460021	-6657.78432	2.648598	0.64949	0.103641266	
GCOM1	-2849.383464	-2850.702477	2.638026	0.30783	0.104333107	
RAE1	-1757.690522	-1758.968256	2.555468	0.22673	0.109913262	
KIAA0562	-4758.3906	-4759.66509	2.54898	0.53101	0.110365486	
GFRAL	-2056.7429	-2057.988728	2.491656	0.45562	0.114451243	
NDP	-595.249727	-596.486803	2.474152	0	0.115731847	
SDSL	-1769.057015	-1770.288517	2.463004	0.40098	0.116555681	
CCDC73	-5510.246464	-5511.44916	2.405392	0.55099	0.120917832	
PLP1	-1162.116469	-1163.303968	2.374998	0	0.123291756	
DNAJC24	-685.154818	-686.334574	2.359512	0.15434	0.124521137	
DCAF4L1	-1946.314085	-1947.472095	2.31602	0.41652	0.128047281	
PNMA1	-1582.808053	-1583.942386	2.268666	0.40398	0.132013492	
GAL3ST4	-2425.386308	-2426.50897	2.245324	0.43162	0.134018835	
PRSS55	-2131.794067	-2132.893363	2.198592	0.56252	0.138136862	
CWC22	-4317.840431	-4318.937569	2.194276	0.47522	0.138524283	
CES5A	-266.000171	-267.08108	2.161818	0.5339	0.141477215	
ITGB3BP	-885.800346	-886.85887	2.117048	999	0.145667073	
RHOB	-856.572076	-857.617308	2.090464	0	0.148221046	
DBX1	-2071.273467	-2072.304866	2.062798	0.37532	0.150932807	
GNAT2	-1602.84573	-1603.848196	2.004932	0.18279	0.156788325	
WSB2	-1863.168036	-1864.147809	1.959546	0.3831	0.161561881	
FGGY	-2753.398865	-2754.374166	1.950602	0.32106	0.162521994	
PPM1K	-1667.544421	-1668.511278	1.933714	0.28255	0.164352687	
ATP5H	-762.096	-763.060906	1.929812	0.27936	0.164779015	
ITGB8	-3615.798355	-3616.740909	1.885108	0.42026	0.169754724	
C11orf40	-1331.10692	-1332.04941	1.88498	1.48214	0.169769216	
CCRL1	-1662.409614	-1663.349017	1.878806	0.19694	0.170469916	
FAM131A	-1320.364544	-1321.274919	1.82075	0.31797	0.177224028	
THY1	-745.381076	-746.276955	1.791758	0.14351	0.180712115	
OR6M1	-1725.575615	-1726.452102	1.752974	2.52795	0.185503296	
ARV1	-1317.461143	-1318.328366	1.734446	0.2101	0.187844097	
PDK3	-1818.785725	-1819.647315	1.72318	0.20879	0.189284223	
ADAT2	-893.320175	-894.161913	1.683476	7.20662	0.194463213	
TTF1	-5078.602798	-5079.443869	1.682142	0.54977	0.194640074	
CASP8	-2454.023345	-2454.838733	1.630776	0.51038	0.20159575	
CISH	-1389.772682	-1390.564715	1.584066	0.44267	0.20817599	
MAGEB17	-1975.036694	-1975.824264	1.57514	0.52708	0.209462128	
DHRS7	-1626.250182	-1627.034916	1.569468	0.22573	0.21028429	
MRPL43	-1379.206314	-1379.989906	1.567184	0.2726	0.210616437	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
C1orf43	&1161.190909	&1161.964769	1.54772	0.2254	0.213472346	
VSIG1	&2093.64345	&2094.401849	1.516798	0.49459	0.218104695	
ZNF30	&3412.830883	&3413.568669	1.475572	0.54906	0.224468611	
HNRNPD	&1488.8624	&1489.597653	1.470506	0.41321	0.225265875	
ADNP2	&5606.312166	&5607.046971	1.46961	0.59389	0.225407237	
WFDC11	&494.031214	&494.759385	1.456342	0.22137	0.227513045	
METAP1D	&1550.451005	&1551.164079	1.426148	0.36762	0.232394117	
LRRC27	&2939.229005	&2939.940743	1.423476	0.67553	0.232832117	
EBI3	&1154.440315	&1155.13501	1.38939	0.35894	0.238508141	
USP18	&2027.551381	&2028.235364	1.367966	0.51002	0.242161661	
LRPPRC	&708.121598	&708.80008	1.356964	0.68268	0.244064341	
GOLGA5	&3484.080772	&3484.749221	1.336898	0.48237	0.247581754	
SLC5A3	&3195.592915	&3196.260947	1.336064	0.37614	0.247729284	
RCN2	&1491.154934	&1491.818491	1.327114	0.32934	0.24931929	
TEKT5	&2688.127337	&2688.76998	1.285286	0.57656	0.256918502	
TFEC	&1628.859975	&1629.479164	1.238378	0.39343	0.265783882	
LYG1	&1103.008294	&1103.624904	1.23322	0.38758	0.266781737	
GLYAT	&1578.31291	&1578.92686	1.2279	0.45981	0.267815827	
TMEM92	&872.321957	&872.934445	1.224976	0.32133	0.268386316	
CCL24	&713.146642	&713.754598	1.215912	0.37414	0.270164418	
COQ3	&1950.817916	&1951.413756	1.19168	0.48359	0.274990942	
FMO6P	&713.115008	&713.709426	1.188836	0.37646	0.275564475	
PRRC1	&2119.456189	&2120.034621	1.156864	0.52168	0.28211687	
SUSD3	&1285.708017	&1286.283288	1.150542	0.40759	0.283435719	
GIMAP2	&1824.041929	&1824.601633	1.119408	0.52688	0.290045963	
IFNA2	&1005.722076	&1006.274189	1.104226	0.52608	0.293340541	
RAD21L1	&2719.729946	&2720.274649	1.089406	0.51089	0.296602858	
C17orf51	&1210.271712	&1210.793882	1.04434	0.68629	0.306814247	
IFI27L1	&554.178013	&554.68614	1.016254	0.49494	0.313409222	
SLC31A1	&859.429576	&859.920063	0.980974	0.36249	0.32195846	
RNF34	&1774.138106	&1774.622103	0.967994	0.42749	0.32518098	
LGALS7	&626.121868	&626.593853	0.94397	0	0.331258946	
FAM165B	&284.951411	&285.42304	0.943258	0.31029	0.331441374	
PMFBP1	&5165.582959	&5166.037151	0.908384	1.42703	0.340543555	
MAT2A	&1788.981639	&1789.41996	0.876642	999	0.349123061	
CNPY1	&412.901421	&413.30485	0.806858	999	0.369050817	
DIRC2	&2213.856049	&2214.248674	0.78525	0.48029	0.375540297	
NSUN3	&1619.45993	&1619.846641	0.773422	0.4078	0.379160507	
EXD1	&2904.329044	&2904.71568	0.773272	1.70881	0.379206732	
ZMYND17	&328.621286	&328.98893	0.735288	0.55398	0.391174493	
CPB2	&2230.639483	&2230.981849	0.684732	0.61958	0.407962024	
PRRG1	&977.752448	&978.094003	0.68311	31.19345	0.40851786	
DNAJC30	&1247.759894	&1248.098297	0.676806	0.59344	0.410688741	
RBCK1	&2214.527664	&2214.864262	0.673196	0.45444	0.41193955	
BET1	&508.096069	&508.426719	0.6613	0.30289	0.416101369	
CEACAM6	&2795.177077	&2795.483374	0.612594	0.82455	0.433812792	
FAAH2	&2753.603257	&2753.90459	0.602666	0.63985	0.43756263	
ZNF157	&2376.112885	&2376.411197	0.596624	9.1413	0.43986903	
VPREB1	&805.789279	&806.084894	0.59123	0.55361	0.441943879	
SLC45A2	&2716.97178	&2717.264017	0.584474	0.64709	0.44456398	
PRKRIP1	&905.180276	&905.47213	0.583708	999	0.444862563	
CEP78	&3500.101521	&3500.3787	0.554358	0.65235	0.456542465	
PIGA	&2362.675786	&2362.949596	0.54762	0.60467	0.459291795	
C12orf5	&1454.656854	&1454.930059	0.54641	0.49489	0.459788288	
TTC29	&2306.846419	&2307.114715	0.536592	0.56013	0.463848554	
NPFF	&606.328942	&606.586563	0.515242	0.48224	0.472878397	
C14orf180	&1004.154603	&1004.396711	0.484216	0.58918	0.486518823	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
CENPT	&3154.651523	&3154.893104	0.483162	0.77018	0.486993541	
OR1N2	&1643.820779	&1644.060221	0.478884	1.55329	0.488928254	
WDR74	&1903.025756	&1903.263035	0.474558	0.65284	0.490897715	
TMEM194A	&2096.328941	&2096.558667	0.459452	0.58799	0.497880193	
TNIP3	&2039.670469	&2039.892236	0.443534	0.64801	0.505421658	
CLEC4E	&1201.370784	&1201.587637	0.433706	3.68877	0.510176051	
DEFB110	&340.304879	&340.52152	0.433282	999	0.5103829	
GP1BA	&4201.395534	&4201.611971	0.432874	0.81683	0.510582079	
FCRL2	&3056.357017	&3056.554504	0.394974	0.70627	0.529696375	
CCDC36	&3125.811168	&3126.006315	0.390294	1.36898	0.532144903	
IL10RA	&3125.733212	&3125.927927	0.38943	0.76067	0.53259917	
DDHD2	&3296.930818	&3297.12292	0.384204	1.8918	0.53536187	
MRGPRD	&1878.922815	&1879.110844	0.376058	0.70343	0.539720515	
LPAR3	&1795.107217	&1795.292317	0.3702	0.60578	0.542895271	
C1orf101	&5590.371996	&5590.544452	0.344912	0.79583	0.557007552	
CCDC69	&1441.945762	&1442.117713	0.343902	0.68333	0.557585526	
C4orf7	&518.868154	&519.033945	0.331582	1.55609	0.564729031	
EPSTI1	&2231.538602	&2231.701352	0.3255	1.60751	0.568320943	
GEMIN7	&641.803239	&641.960744	0.31501	0.44454	0.574621998	
GNG5P2	&353.013951	&353.171395	0.314888	0.44517	0.574696088	
COX5B	&679.239104	&679.396282	0.314356	0.43851	0.57501939	
JAM2	&1441.461888	&1441.615243	0.30671	0.3661	0.579706113	
LAMC2	&5962.150056	&5962.302524	0.304936	0.79775	0.580804412	
NUP88	&3814.470659	&3814.613883	0.286448	0.77655	0.592505779	
OAZ2	&818.975414	&819.115325	0.279822	0.46671	0.596817908	
PSMD9	&1064.892832	&1065.028235	0.270806	0.50319	0.602791613	
C4orf33	&1021.542647	&1021.670257	0.25522	0.62798	0.613423264	
SYNJ2BP	&647.222483	&647.348201	0.251436	0.48699	0.616065756	
C9orf142	&1043.416988	&1043.535593	0.23721	0.69637	0.626228502	
AHSA1	&1500.910852	&1501.021419	0.221134	0.50299	0.638177222	
TMEM139	&1120.603761	&1120.709356	0.21119	1.66594	0.645836289	
ZNF528	&3222.589437	&3222.690963	0.203052	1.28143	0.652268556	
ZBP1	&2567.323312	&2567.401331	0.156038	0.8498	0.692830744	
OAS1	&2334.375844	&2334.450354	0.14902	1.24032	0.699473646	
PINX1	&1711.351708	&1711.423479	0.143542	0.78898	0.70478487	
PAFAH1B1	&1900.211933	&1900.279437	0.135008	0.76593	0.713295055	
TSSK4	&1833.380965	&1833.441257	0.120584	0.83059	0.728401956	
HAUS2	&1108.977087	&1109.034262	0.11435	0.73884	0.735245053	
DLX6	&1107.215871	&1107.272827	0.113912	0.66452	0.735733592	
MRPL55	&877.979853	&878.03391	0.108114	0.6871	0.742301621	
AGAP10	&4366.92048	&4366.970277	0.099594	0.90992	0.752317395	
WFDC6	&441.72506	&441.763715	0.07731	0.78431	0.780976465	
PTTG2	&1129.911312	&1129.949777	0.07693	1.17702	0.781501713	
OR10G3	&1721.77493	&1721.812368	0.074876	1.14066	0.784365293	
SMR3B	&486.809296	&486.845908	0.073224	0.82686	0.786699207	
FXYD3	&495.742006	&495.778232	0.072452	0.74997	0.787799564	
CCDC68	&1603.493482	&1603.528067	0.06917	0.84699	0.792549114	
CDCA2	&5450.488947	&5450.519732	0.06157	0.91494	0.804031481	
ZNF192	&2772.563043	&2772.593709	0.061332	0.85502	0.804402913	
SDHA	&3565.145491	&3565.172921	0.05486	0.93499	0.814812546	
ARHGEF25	&2844.949457	&2844.973714	0.048514	0.8482	0.825669497	
C14orf181	&762.315277	&762.336718	0.042882	0.83764	0.83594762	
PNLIPRP3	&2314.321446	&2314.340941	0.03899	0.85754	0.843468475	
FANCG	&3676.408724	&3676.424973	0.032498	1.03697	0.856939023	
RBP7	&646.807813	&646.823856	0.032086	1.22054	0.857839039	
TBRG1	&1916.4491	&1916.463944	0.029688	0.8071	0.863200065	
LAPTM4B	&2134.03002	&2134.044507	0.028974	1.0679	0.864839083	

Gene	FREE'lnL	FIXED'lnL	2ΔlnL	branch_w	pvalue	k
SH3D21	&4133.622189	&4133.635168	0.025958	1.07071	0.872002932	
RPS12	&632.354243	&632.363511	0.018536	1.12161	0.891705089	
GPHA2	&626.905512	&626.914314	0.017604	0.85559	0.894446408	
DARC	&1863.806538	&1863.814206	0.015336	0.91397	0.901443065	
RGS18	&1078.380891	&1078.38728	0.012778	0.87512	0.909998989	
TSSK2	&1692.40961	&1692.415953	0.012686	0.61167	0.910322199	
USP26	&5057.868971	&5057.875149	0.012356	1.03896	0.911491416	
TAC4	&627.907108	&627.913271	0.012326	1.07921	0.911598489	
CYLC1	&3426.55099	&3426.55685	0.01172	1.04112	0.913790285	
MPV17L	&1180.82299	&1180.827769	0.009558	1.06629	0.922118881	
WDR5B	&1587.507316	&1587.51166	0.008688	1.11302	0.925737174	
IL17RB	&2643.815624	&2643.819791	0.008334	1.05545	0.927261572	
C10orf11	&974.100809	&974.103702	0.005786	1.05451	0.93936678	
ZFP37	&3100.901681	&3100.904424	0.005486	0.96131	0.940956646	
TMEM61	&1208.993989	&1208.994933	0.001888	1.04744	0.965341927	
FAM64A	&1282.278366	&1282.278676	0.00062	1.0205	0.980134887	
DEFB103A	&836.132903	&836.132949	9.2E&05	0	0.992347077	
OR13J1	&1779.142835	&1779.142871	7.2E&05	0	0.993229806	
RNF11	&655.292812	&655.292839	5.4E&05	0	0.994136823	
ZNRD1	&572.059204	&572.059213	1.8E&05	0	0.996614873	
MBNL2	&1567.260764	&1567.260773	1.8E&05	0	0.996614873	
C8orf39	&460.606656	&460.390785	&0.431742	5.87568	#NUM!	
CDC20	&2493.801608	&2296.016641	&395.569934	0	#NUM!	
DNAJC5G	&1275.552333	&1132.671302	&285.762062	0.00985	#NUM!	
MEGF10	&5667.786022	&5535.762088	&264.047868	1.56584	#NUM!	
NXT1	&642.059951	&642.059941	&2E&05	0	#NUM!	
PPP2R2C	&2066.432984	&2061.356754	&10.15246	21.62813	#NUM!	
TMEM106B	&1219.461908	&1217.585811	&3.752194	11.27859	#NUM!	

Macaque

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
APC2	%11985.49169	%12200.77629	430.569196	0.04668	1.22181E%95	
NCOR2	%12224.82905	%12373.36604	297.073978	0.04509	1.42976E%66	
VPS13D	%20744.71275	%20862.22951	235.033524	0.0861	4.76064E%53	
CARD11	%5895.931727	%6011.728454	231.593454	0.00278	2.67819E%52	
SPTB	%11263.35956	%11368.62939	210.539664	0.05249	1.04744E%47	
SLIT1	%7419.404624	%7510.469839	182.13043	0.04553	1.66064E%41	
JAG2	%6290.239731	%6380.131759	179.784056	0.02576	5.40219E%41	
ECEL1	%3724.844261	%3805.537079	161.385636	0.01681	5.63523E%37	
PLCH2	%7498.086527	%7566.641858	137.110662	0.09967	1.14049E%31	
ROR2	%4586.555601	%4654.148557	135.185912	0.01908	3.00657E%31	
PITPNM1	%6235.291956	%6302.487202	134.390492	0.05722	4.48805E%31	
ERC1	%5070.276902	%5137.180955	133.808106	0.00299	6.01798E%31	
SIPA1	%4987.709831	%5052.597033	129.774404	0.04452	4.591E%30	
SEMA6B	%4180.440194	%4241.438603	121.996818	0.02983	2.31208E%28	
TBC1D9	%5832.291886	%5891.647245	118.710718	0	1.21173E%27	
UNC13C	%10554.1062	%10611.90224	115.592074	0.11143	5.83844E%27	
FKRP	%2436.392932	%2492.377655	111.969446	0.0325	3.62859E%26	
EIF2C2	%4030.695748	%4086.161581	110.931666	0	6.12458E%26	
EPHB3	%4499.3223	%4554.469963	110.295326	0.01868	8.44275E%26	
KIDINS220	%8391.731481	%8445.924539	108.386116	0.07121	2.21202E%25	
HRH3	%2185.799307	%2238.406457	105.2143	0.01836	1.09616E%24	
TNS3	%7655.208362	%7706.125544	101.834364	0.13768	6.03639E%24	
ZFP64	%3243.008774	%3293.710778	101.404008	0.00691	7.50119E%24	
KDM5D	%8474.617799	%8522.851904	96.46821	0.25145	9.06883E%23	
SMPD3	%3077.190915	%3125.341472	96.301114	0.02078	9.86745E%23	
PCDH7	%5420.791819	%5468.241781	94.899924	0.03211	2.00258E%22	
ANO1	%4809.584914	%4855.351945	91.534062	0.06153	1.09688E%21	
ZNF574	%4508.63721	%4553.706252	90.138084	0.0335	2.22105E%21	
GRIK3	%4314.665336	%4359.22436	89.118048	0.00748	3.71942E%21	
MEGF10	%5514.056789	%5557.925518	87.737458	0.03492	7.47454E%21	
DCAF12L2	%2607.995447	%2651.850701	87.710508	0.01264	7.57708E%21	
ERCC3	%3772.7096	%3815.209826	85.000452	0.00939	2.98297E%20	
ISYNA1	%2711.990791	%2754.314851	84.64812	0.04334	3.56483E%20	
ARHGAP4	%5874.647864	%5916.971384	84.64704	0.08356	3.56677E%20	
SEC14L5	%3456.932687	%3497.325408	80.785442	0.0746	2.51605E%19	
LDB3	%3929.07208	%3969.266321	80.388482	0.08602	3.07583E%19	
ADNP2	%5608.749512	%5647.997728	78.496432	0.08776	8.01429E%19	
ASCC3	%10025.76736	%10064.68083	77.826932	0.10131	1.12476E%18	
FZR1	%2349.133087	%2387.991179	77.716184	0	1.18963E%18	
PCDHA3	%4895.860768	%4933.251457	74.781378	0.13643	5.25834E%18	
STAT5B	%3675.927839	%3712.553768	73.251858	0.01746	1.14118E%17	
SULF2	%4179.490376	%4215.614083	72.247414	0.05001	1.89839E%17	
ANKRD52	%5041.058016	%5077.113603	72.111174	0	2.03409E%17	
C19orf68	%3315.932341	%3351.412139	70.959596	0.07609	3.64616E%17	
PRKCD	%3136.082468	%3170.945722	69.726508	0.01795	6.81244E%17	
PPP2R2C	%2050.921703	%2085.155093	68.46678	0.00892	1.29033E%16	
TBC1D17	%3152.720533	%3186.63507	67.829074	0.04704	1.78301E%16	
DEF8	%2627.584966	%2661.292104	67.414276	0.01732	2.2005E%16	
GFOD2	%1868.749885	%1901.626853	65.753936	0.01082	5.10884E%16	
USP7	%4826.645211	%4859.398166	65.50591	0.01173	5.794E%16	
BCL9L	%7013.218526	%7045.901324	65.365596	0.08971	6.22156E%16	
ADAMTS8	%4011.90786	%4044.176496	64.537272	0.04894	9.47235E%16	
ZNF335	%6610.491144	%6642.744425	64.506562	0.11538	9.62114E%16	
EPB41L1	%4095.52366	%4127.459896	63.872472	0.03925	1.3274E%15	
YLPM1	%9690.381747	%9722.080056	63.396618	0.11527	1.69008E%15	
SV2B	%3188.672687	%3220.121605	62.897836	0	2.17711E%15	
RAP1GAP2	%3635.460344	%3666.861761	62.802834	0.05636	2.2847E%15	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
UPF2	%5621.386286	%5652.668033	62.563494	0.02343	2.57992E%15	
SMC2	%5402.794593	%5433.986585	62.383984	0.08558	2.82612E%15	
RBBP6	%8239.826012	%8270.85453	62.057036	0.10333	3.33652E%15	
CHST2	%2515.940282	%2546.633207	61.38585	0.04924	4.6917E%15	
TGM1	%4090.195927	%4120.800113	61.208372	0.08646	5.13427E%15	
LEPREL4	%1973.867321	%2004.225681	60.71672	0.02445	6.5908E%15	
KCNJ9	%1725.827856	%1756.047973	60.440234	0	7.58467E%15	
KCNB1	%3940.993722	%3970.883926	59.780408	0.02366	1.06054E%14	
SHPRH	%8159.260814	%8189.106346	59.691064	0.17572	1.10979E%14	
SDHA	%3583.139152	%3612.926869	59.575434	0.06127	1.17695E%14	
ZC3H13	%7601.993561	%7631.697331	59.40754	0.14482	1.28177E%14	
SLC7A14	%3657.479457	%3686.808811	58.658708	0.07078	1.87536E%14	
CYTH1	%1782.277782	%1811.562079	58.568594	0	1.96325E%14	
SLC6A4	%3062.07157	%3090.867544	57.591948	0.0543	3.22543E%14	
WDR33	%6005.788344	%6034.55843	57.540172	0.06148	3.31146E%14	
TUBB	%2145.417268	%2173.943603	57.05267	0.01333	4.24295E%14	
STUB1	%1347.877786	%1376.158476	56.56138	0	5.44712E%14	
MAP4K4	%6064.805339	%6093.013169	56.41566	0.10304	5.86613E%14	
COL5A2	%6699.163565	%6727.202144	56.077158	0.09686	6.9682E%14	
LAMA4	%8660.457424	%8688.39034	55.865832	0.16902	7.75894E%14	
GPT2	%2463.691191	%2491.52565	55.668918	0.02243	8.57636E%14	
RALGDS	%4387.255154	%4414.57625	54.642192	0.08615	1.44598E%13	
RFX7	%6742.19511	%6769.475225	54.56023	0.08359	1.50756E%13	
DLEC1	%9083.82814	%9111.051719	54.447158	0.23176	1.59684E%13	
ZNF592	%5978.968421	%6005.616114	53.295386	0.15065	2.8698E%13	
RABEP1	%3980.310317	%4006.909988	53.199342	0.06793	3.0136E%13	
TTYH1	%2167.830188	%2194.251389	52.842402	0.04496	3.61414E%13	
PLB1	%7859.250369	%7885.664385	52.828032	0.24516	3.64068E%13	
SLC25A23	%2100.65211	%2126.859135	52.41405	0.01558	4.49497E%13	
DENND4B	%7193.980344	%7220.087528	52.214368	0.1367	4.97607E%13	
NR2C2	%2827.844733	%2853.932489	52.175512	0	5.07551E%13	
CHRDL2	%2441.071231	%2467.075809	52.009156	0.04848	5.52424E%13	
SLC22A17	%2376.502906	%2402.482396	51.95898	0.01522	5.66723E%13	
DNAI2	%3180.489533	%3206.38084	51.782614	0.1076	6.19984E%13	
ZNF275	%2173.578421	%2199.454435	51.752028	0.06579	6.29717E%13	
CCDC132	%4368.392306	%4393.846207	50.907802	0.02574	9.6808E%13	
CDC37	%1706.190311	%1731.609428	50.838234	0	1.00301E%12	
SFRP1	%1508.345484	%1533.64943	50.607892	0.02565	1.12791E%12	
GCDH	%2323.533776	%2348.836633	50.605714	0.05225	1.12916E%12	
ALDH1A3	%2494.608197	%2519.790521	50.364648	0.05153	1.27674E%12	
LHX2	%1796.055431	%1821.190436	50.27001	0.01139	1.33982E%12	
OVOL2	%1298.576699	%1323.709779	50.26616	0	1.34245E%12	
LHFPL5	%928.930846	%953.950112	50.038532	0	1.50756E%12	
KANK3	%4441.415793	%4466.420932	50.010278	0.21657	1.52943E%12	
NCKAP1L	%5395.985088	%5420.879244	49.788312	0.09	1.71261E%12	
DACT2	%4063.268155	%4088.119537	49.702764	0.19486	1.78894E%12	
FAM120A	%5415.190279	%5439.793124	49.20569	0.04252	2.30481E%12	
POGK	%2869.400924	%2893.823715	48.845582	0.05548	2.76929E%12	
MLLT6	%4825.701676	%4850.088391	48.77343	0.04205	2.87306E%12	
TBXA2R	%1671.254961	%1695.530659	48.551396	0.06337	3.21745E%12	
HIST1H2AL	%742.895497	%767.125402	48.45981	0.01169	3.37128E%12	
ABCD3	%3241.256737	%3265.407425	48.301376	0.07018	3.65496E%12	
RAE1	%1757.798187	%1781.462887	47.3294	0	6.00054E%12	
MARK2	%3518.437492	%3541.972953	47.070922	0.0404	6.84639E%12	
DHTKD1	%4800.437589	%4823.925313	46.975448	0.15842	7.18816E%12	
PRMT6	%1671.731627	%1695.183962	46.90467	0.0145	7.45249E%12	
TMEM121	%1353.729444	%1377.125355	46.791822	0	7.89421E%12	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
PADI1	%3539.991942	%3563.319179	46.654474	0.15988	8.46734E%12	
CAPN7	%3742.051676	%3765.263355	46.423358	0.04696	9.5273E%12	
TJP2	%6016.212867	%6039.361293	46.296852	0.1454	1.01627E%11	
CDK9	%1676.805972	%1699.725471	45.838998	0	1.28382E%11	
RHOB	%855.688617	%878.526452	45.67567	0	1.39545E%11	
EPB49	%1818.37967	%1841.196977	45.634614	0.01623	1.42501E%11	
ASB1	%1625.042388	%1647.525425	44.966074	0.01777	2.00478E%11	
MAP4K5	%5006.140415	%5028.506496	44.732162	0.05982	2.25916E%11	
PRPF4B	%4587.280492	%4609.395686	44.230388	0.10668	2.91914E%11	
MAP4K3	%4018.485986	%4040.596065	44.220158	0.01688	2.93444E%11	
NLGN3	%3584.956391	%3607.053429	44.194076	0	2.9738E%11	
TMEM43	%2110.14725	%2131.874048	43.453596	0.10707	4.34133E%11	
TSSK2	%1691.106582	%1712.490064	42.766964	0.02843	6.16648E%11	
SLC24A4	%2704.506507	%2725.760065	42.507116	0.05741	7.04255E%11	
RTN4RL2	%1988.103977	%2009.060274	41.912594	0.03239	9.54459E%11	
DBX1	%2069.523595	%2090.447347	41.847504	0.10457	9.86767E%11	
RBCK1	%2218.493961	%2239.149478	41.311034	0.02809	1.29834E%10	
PLXDC2	%2634.484195	%2655.038686	41.108982	0.08808	1.43973E%10	
NPFFR1	%2089.904441	%2110.236668	40.664454	0.08879	1.80745E%10	
DSCR3	%1518.770962	%1538.913311	40.284698	0.03477	2.19522E%10	
PDZD7	%2715.683126	%2735.743787	40.121322	0.13467	2.3867E%10	
ASH2L	%2901.727916	%2921.777659	40.099486	0.05061	2.41352E%10	
SLC5A3	%3191.930472	%3211.932854	40.004764	0	2.53344E%10	
INTS6	%4102.743707	%4122.699681	39.911948	0.03352	2.65673E%10	
PCDHA1	%5051.867146	%5071.735283	39.736274	0.22997	2.90676E%10	
FBXL12	%1532.713985	%1552.48047	39.53297	0.01706	3.22567E%10	
NR1D2	%2649.930765	%2669.630509	39.399488	0.01799	3.45388E%10	
SLC16A8	%2346.347361	%2366.033733	39.372744	0.10402	3.50151E%10	
PIAS1	%2898.905163	%2918.482211	39.154096	0	3.91641E%10	
CNTN6	%5057.210225	%5076.634114	38.847778	0.14562	4.58175E%10	
GALNT12	%3048.381866	%3067.619704	38.475676	0.0984	5.54404E%10	
S1PR3	%1732.182096	%1751.334559	38.304926	0.05442	6.05097E%10	
HM13	%1874.073919	%1893.198594	38.24935	0.01903	6.22578E%10	
SUV39H1	%1814.111902	%1833.232543	38.241282	0	6.25158E%10	
PPIG	%3503.072582	%3522.178908	38.212652	0.05741	6.34397E%10	
GCOM1	%2843.071365	%2862.150277	38.157824	0.06238	6.52476E%10	
TEKT5	%2695.182088	%2714.189493	38.01481	0.11178	7.02097E%10	
SQSTM1	%2439.382493	%2458.221365	37.677744	0.08087	8.34513E%10	
DMGDH	%4202.810802	%4221.64231	37.663016	0.13511	8.40837E%10	
CPT1B	%3719.797671	%3738.609937	37.624532	0.15323	8.57591E%10	
VPS52	%3325.900617	%3344.634682	37.46813	0.08188	9.29189E%10	
RNF208	%1198.599151	%1217.297326	37.39635	0.03323	9.64024E%10	
SMC5	%5108.662991	%5127.331865	37.337748	0.11546	9.9343E%10	
PPP1R12A	%4525.912161	%4544.470251	37.11618	0.04911	1.11296E%09	
ZBTB38	%5739.670027	%5758.213145	37.086236	0.14581	1.13019E%09	
HNRPLL	%2492.373142	%2510.885492	37.0247	0.05028	1.16642E%09	
HIST1H2AJ	%620.35151	%638.552263	36.401506	0	1.60579E%09	
TOP3A	%5198.701499	%5216.843293	36.283588	0.17761	1.70594E%09	
MAP2	%8748.976903	%8766.971861	35.989916	0.2396	1.98341E%09	
PNKP	%2843.659538	%2861.275139	35.231202	0.0974	2.92795E%09	
ATG16L1	%2891.804311	%2909.292876	34.97713	0.08262	3.33601E%09	
ZNF570	%2393.55381	%2410.78927	34.47092	0.0416	4.32667E%09	
LPAR3	%1795.660205	%1812.5993	33.87819	0.08561	5.86728E%09	
EIF2C4	%3719.55317	%3736.315165	33.52399	0	7.03904E%09	
CDK13	%6756.519549	%6773.199802	33.360506	0.0895	7.65631E%09	
NUP88	%3813.876661	%3830.50174	33.250158	0.17026	8.10332E%09	
LTK	%4352.005606	%4368.06238	32.113548	0.19793	1.4542E%08	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
KIAA0562	%4759.270429	%4775.30762	32.074382	0.1735	1.48381E%08	
PCDHB5	%4602.153015	%4618.139784	31.973538	0.22913	1.56287E%08	
CDT1	%2995.285801	%3011.265555	31.959508	0.15263	1.5742E%08	
HMGCR	%4419.307748	%4435.175818	31.73614	0.13716	1.76605E%08	
SREK1	%2712.628697	%2728.432008	31.606622	0.05864	1.88785E%08	
KLHDC4	%2857.906306	%2873.387139	30.961666	0.15634	2.63175E%08	
ATAD2	%6458.456202	%6473.933425	30.954446	0.2206	2.64156E%08	
FAM126B	%2581.799716	%2597.13093	30.662428	0	3.07054E%08	
TMC8	%3631.310488	%3646.502037	30.383098	0.10116	3.54604E%08	
CDC20	%2295.395193	%2310.573319	30.356252	0.01632	3.59546E%08	
ZNF569	%3121.668458	%3136.8311	30.325284	0.08025	3.65333E%08	
HES5	%658.160072	%673.303317	30.28649	0.02949	3.72713E%08	
PLCB1	%5509.78584	%5524.925874	30.280068	0.14219	3.73949E%08	
CDC23	%2708.105034	%2723.205433	30.200798	0.08178	3.89549E%08	
C19orf47	%2054.35647	%2069.188532	29.664124	0.09653	5.13769E%08	
DCAF4L1	%1946.063968	%1960.835195	29.542454	0.07713	5.47052E%08	
NPY5R	%1990.06401	%2004.826733	29.525446	0.04402	5.51874E%08	
ADRA1B	%2496.960146	%2511.690002	29.459712	0.03182	5.70912E%08	
KIAA0947	%12218.7513	%12233.41792	29.333244	0.44034	6.09412E%08	
TBCB	%1152.67801	%1167.258835	29.16165	0.02159	6.65842E%08	
ADAM9	%3866.359605	%3880.905599	29.091988	0.17621	6.90218E%08	
DCAF5	%4503.828695	%4518.335633	29.013876	0.16566	7.18617E%08	
IRF8	%2086.136499	%2100.544553	28.816108	0.04341	7.95864E%08	
ACCN1	%2708.658014	%2723.003219	28.69041	0.06896	8.49232E%08	
CHL1	%6210.286067	%6224.530958	28.489782	0.28888	9.41943E%08	
DGAT1	%2575.228072	%2589.390687	28.32523	0.16158	1.02551E%07	
GUCA1B	%890.171845	%904.141094	27.938498	0	1.25233E%07	
C4orf31	%2784.093125	%2798.050772	27.915294	0.12383	1.26744E%07	
PSMD4	%1696.934305	%1710.84438	27.82015	0.02809	1.33132E%07	
AGPAT2	%1422.098976	%1435.932757	27.667562	0.05964	1.44058E%07	
MIER1	%1902.089653	%1915.879203	27.5791	0	1.50799E%07	
SHMT2	%2375.357946	%2389.07495	27.434008	0.0684	1.62547E%07	
TXNDC11	%4977.371673	%4991.084394	27.425442	0.23695	1.63269E%07	
DNAJC17	%1458.147407	%1471.720369	27.145924	0.09149	1.88663E%07	
PLS3	%2741.925214	%2755.428317	27.006206	0	2.02803E%07	
MRGPRE	%1603.323932	%1616.792324	26.936784	0.09801	2.1022E%07	
PAX9	%1574.409682	%1587.823798	26.828232	0.04235	2.22365E%07	
POFUT2	%2134.204767	%2147.490363	26.571192	0.02623	2.54003E%07	
HIST1H3F	%761.424527	%774.708548	26.568042	0	2.54418E%07	
TMCC3	%2203.604853	%2216.86764	26.525574	0.02324	2.60072E%07	
CNTFR	%1738.530573	%1751.755846	26.450546	0.08413	2.70372E%07	
ATP10D	%7192.544001	%7205.768293	26.448584	0.3338	2.70647E%07	
HIST1H3G	%641.629555	%654.656059	26.053008	0	3.32171E%07	
MBTPS2	%2424.127314	%2437.140333	26.026038	0.05437	3.36844E%07	
ABCB11	%6822.341426	%6835.29021	25.897568	0.32049	3.60022E%07	
RNF216	%4385.54448	%4398.450394	25.811828	0.20345	3.76375E%07	
ZNF324B	%3117.506421	%3130.398581	25.78432	0.20355	3.81777E%07	
ROBO4	%5267.287287	%5280.163837	25.7531	0.29075	3.88003E%07	
CAPN11	%3812.490543	%3825.183302	25.385518	0.22542	4.69429E%07	
ME2	%2646.487635	%2659.136857	25.298444	0.05057	4.91105E%07	
TMEM178	%1341.818114	%1354.457034	25.27784	0	4.96379E%07	
C11orf84	%2724.930231	%2737.540757	25.221052	0.05202	5.11211E%07	
C7orf60	%1790.238423	%1802.751077	25.025308	0	5.65827E%07	
PAFAH1B1	%1899.936711	%1912.3467	24.819978	0.05389	6.29417E%07	
DRAP1	%962.0844	%974.445134	24.721468	0	6.62422E%07	
SDSL	%1769.645414	%1781.996902	24.702976	0.14903	6.68808E%07	
GPR89A	%1485.556238	%1497.878645	24.644814	0.03178	6.893E%07	

Gene	Free&lnL	Fixed&lnL	2ΔlnL	branch_w	pvalue	k
BROX	-1817.356634	-1829.596135	24.479002	0.05172	7.51241E-07	
DUSP1	-1011.279256	-1023.481648	24.404784	0	7.80746E-07	
ZFYVE20	-3771.07742	-3783.204928	24.255016	0.11812	8.4387E-07	
DIRC2	-2215.303525	-2227.377794	24.148538	0.06088	8.91838E-07	
SLC4A4	-4931.787403	-4943.760698	23.94659	0.14289	9.90456E-07	
WSB2	-1864.062748	-1876.034849	23.944202	0	9.91685E-07	
GCK	-2424.796694	-2436.731957	23.870526	0.17299	1.03037E-06	
PSMD9	-1064.676705	-1076.59457	23.83573	0.07932	1.04917E-06	
ACOT12	-2906.217324	-2918.112249	23.78985	0.16971	1.07448E-06	
GCGR	-2923.872417	-2935.740312	23.73579	0.24062	1.10508E-06	
LSM7	-452.879052	-464.566279	23.374454	0	1.33338E-06	
KPTN	-2401.194832	-2412.868058	23.346452	0.15313	1.35293E-06	
TRIM39	-2365.867043	-2377.54009	23.346094	0.03279	1.35318E-06	
C1orf43	-1158.630337	-1170.295206	23.329738	0	1.36474E-06	
CCDC157	-3832.66778	-3844.331264	23.326968	0.26133	1.3667E-06	
YTHDC1	-3081.206912	-3092.811932	23.21004	0.02849	1.45237E-06	
ITGB8	-3617.57554	-3629.123784	23.096488	0.1217	1.54072E-06	
FGGY	-2753.678554	-2765.224822	23.092536	0.16764	1.54389E-06	
SOCS4	-1990.062178	-2001.60607	23.087784	0.0988	1.54771E-06	
JAM2	-1437.035755	-1448.520174	22.968838	0	1.64649E-06	
PGAM1	-1122.093737	-1133.35674	22.526006	0	2.07318E-06	
CXCR5	-1773.930412	-1785.170557	22.48029	0.10326	2.12311E-06	
ZC3H12D	-2708.205859	-2719.433907	22.456096	0.22272	2.15002E-06	
FLT3	-4939.088155	-4950.268821	22.361332	0.28088	2.25876E-06	
CEP78	-3498.491154	-3509.630282	22.278256	0.17353	2.35862E-06	
GPR176	-2457.060005	-2468.171672	22.223334	0.10702	2.42706E-06	
CPA5	-2349.074346	-2360.129314	22.109936	0.15275	2.57474E-06	
OR13J1	-1777.817397	-1788.816273	21.997752	0.29934	2.7297E-06	
CORO1C	-2136.167603	-2146.933867	21.532528	0.02849	3.47878E-06	
TBR1	-2894.492573	-2905.219292	21.453438	0.02744	3.62525E-06	
PTPRCAP	-1093.195319	-1103.91758	21.444522	0.05139	3.64215E-06	
ELF4	-3310.101123	-3320.796658	21.39107	0.13986	3.74511E-06	
MAP3K7	-2660.30639	-2670.95247	21.29216	0	3.94341E-06	
UBLCP1	-1380.588699	-1391.183089	21.18878	0	4.16194E-06	
ABHD4	-1660.984522	-1671.516301	21.063558	0.06003	4.44298E-06	
C21orf59	-1401.195066	-1411.647974	20.905816	0.03044	4.82428E-06	
GJA4	-1636.684488	-1647.122076	20.875176	0.08311	4.90206E-06	
GUCY2F	-5372.248239	-5382.615012	20.733546	0.25533	5.27832E-06	
THY1	-744.689521	-755.053899	20.728756	0	5.29154E-06	
MED19	-1132.103883	-1142.422494	20.637222	0	5.55064E-06	
TMEM38B	-1444.451535	-1454.719594	20.536118	0.08228	5.85166E-06	
LRRTM3	-2555.637446	-2565.889276	20.50366	0	5.95173E-06	
RNF34	-1773.899623	-1784.093092	20.386938	0.07357	6.32601E-06	
SEC13	-1770.823521	-1780.955707	20.264372	0.05884	6.74449E-06	
TSPAN15	-1376.804556	-1386.871096	20.13308	0.10043	7.22364E-06	
SLC35C1	-1828.652974	-1838.685148	20.064348	0.12351	7.48796E-06	
FAAH2	-2751.633996	-2761.633463	19.998934	0.18146	7.74853E-06	
ORC2	-2609.503316	-2619.361949	19.717266	0.13414	8.97865E-06	
ZNF575	-1658.656147	-1668.482105	19.651916	0.11163	9.29101E-06	
NPY1R	-1730.450023	-1740.229757	19.559468	0.03912	9.75162E-06	
DCTN6	-847.232997	-856.999162	19.53233	0	9.89114E-06	
CYP4F11	-2990.918995	-3000.647893	19.457796	0.33945	1.02847E-05	
SCN1B	-1018.930298	-1028.594309	19.328022	0.07016	1.10079E-05	
MBLAC2	-1292.764638	-1302.350993	19.17271	0.03855	1.19408E-05	
TMEM106B	-1217.191979	-1226.717332	19.050706	0.05899	1.27291E-05	
EFS	-2802.264784	-2811.769677	19.009786	0.28174	1.3005E-05	
NXT1	-642.059909	-651.546674	18.97353	0	1.32545E-05	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
CWC22	%4319.319334	%4328.722091	18.805514	0.24009	1.44748E%05	
EXPH5	%10700.35785	%10709.75024	18.784774	0.47803	1.46331E%05	
PNMA1	%1585.417161	%1594.75388	18.673438	0.03599	1.55129E%05	
TAGLN	%884.376929	%893.645897	18.537936	0.03081	1.66556E%05	
MAT2A	%1792.410416	%1801.619163	18.417494	0.08182	1.77422E%05	
ZNF652	%2778.283274	%2787.469624	18.3727	0.06179	1.81642E%05	
POU2F2	%2165.5159	%2174.676357	18.320914	0.07853	1.86647E%05	
GNAT2	%1603.271173	%1612.426887	18.311428	0.03844	1.87579E%05	
SLC45A2	%2718.197131	%2727.215721	18.03718	0.22394	2.16633E%05	
B4GALT5	%1750.569191	%1759.469558	17.800734	0	2.45289E%05	
ARCN1	%2281.612198	%2290.487116	17.749836	0.08667	2.51939E%05	
PNPT1	%3659.534112	%3668.332051	17.595878	0.20953	2.7318E%05	
GSC	%1064.359553	%1073.12901	17.538914	0	2.81487E%05	
SIX6	%1100.538108	%1109.305671	17.535126	0.05931	2.82049E%05	
TACR2	%1978.266516	%1986.891212	17.249392	0.1544	3.27802E%05	
KRTAP4%7	%1361.02997	%1369.614429	17.168918	0.22291	3.41986E%05	
GOLGA5	%3484.384894	%3492.814742	16.859696	0.22859	4.02472E%05	
LGALS7	%626.286113	%634.661139	16.750052	0.05061	4.26411E%05	
CD2AP	%3055.069648	%3063.298028	16.45676	0.26403	4.97724E%05	
RABGGTA	%2637.839425	%2646.057763	16.436676	0.17414	5.03025E%05	
ZNF30	%3411.101723	%3419.226298	16.24915	0.30587	5.55345E%05	
SCG3	%2151.309069	%2159.27516	15.932182	0.18871	6.56529E%05	
GAL3ST4	%2423.894402	%2431.785305	15.781806	0.25534	7.10828E%05	
IRX6	%2443.404215	%2451.239523	15.670616	0.23008	7.53863E%05	
CHM	%3029.010529	%3036.816112	15.611166	0.22768	7.77938E%05	
TMED4	%1062.323882	%1070.083281	15.518798	0.08876	8.16889E%05	
OR6X1	%1668.675298	%1676.412071	15.473546	0.20602	8.36681E%05	
SOAT2	%2726.117991	%2733.838289	15.440596	0.2549	8.51395E%05	
TNFAIP8L3	%1464.92835	%1472.626581	15.396462	0.21735	8.71513E%05	
GPR179	%14282.50836	%14290.19862	15.380532	0.67012	8.78892E%05	
FBL	%1605.801511	%1613.450234	15.297446	0.16127	9.18406E%05	
C1orf187	%1762.23698	%1769.866531	15.259102	0.16971	9.3724E%05	
DCAF7	%1557.671294	%1565.299258	15.255928	0.04282	9.38816E%05	
DDHD2	%3298.128582	%3305.667618	15.078072	0.20549	0.000103155	
CA10	%1497.387011	%1504.921224	15.068426	0	0.000103683	
PIP4K2C	%1757.574893	%1765.109005	15.068224	0.14631	0.000103694	
MED7	%980.949481	%988.479749	15.060536	0	0.000104117	
ZNF528	%3226.584526	%3234.078901	14.98875	0.31431	0.000108154	
SDAD1	%3554.792295	%3562.273089	14.961588	0.13837	0.000109722	
FANCG	%3675.707909	%3683.178008	14.940198	0.26164	0.000110973	
ALOX15	%3885.730728	%3893.178069	14.894682	0.34612	0.000113683	
RBM7	%1282.882928	%1290.27483	14.783804	0.13135	0.000120567	
RPL23A	%865.342656	%872.732535	14.779758	0	0.000120826	
CHMP5	%937.877506	%945.258399	14.761786	0	0.000121983	
OR10G3	%1721.774888	%1729.131982	14.714188	0.22333	0.000125101	
FOSB	%1437.306546	%1444.651897	14.690702	0.04806	0.00012667	
DEFB103A	%334.510415	%341.830373	14.639916	0	0.000130129	
G6PC	%1732.891826	%1740.191134	14.598616	0.12401	0.000133012	
COPS4	%1959.417805	%1966.419229	14.002848	0.14177	0.000182534	
OR2J3	%1696.134038	%1703.112082	13.956088	0.22318	0.000187131	
GPRASP2	%4102.754709	%4109.676573	13.843728	0.32717	0.000198659	
CDCA2	%5452.85998	%5459.707678	13.695396	0.41715	0.000214981	
ARHGEF25	%2845.781505	%2852.6287	13.69439	0.27912	0.000215096	
LAMC2	%5963.057442	%5969.854218	13.593552	0.36987	0.000226964	
AGGF1	%3402.601549	%3409.397795	13.592492	0.23617	0.000227092	
BLNK	%2338.415676	%2345.186772	13.542192	0.19306	0.00023326	
KRT36	%2449.883104	%2456.63676	13.507312	0.19492	0.000237636	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
MSRB2	%997.233968	%1003.964693	13.46145	0.04841	0.000243515	
FOLR2	%1277.959678	%1284.682181	13.445006	0.16763	0.000245659	
MOAP1	%1705.561035	%1712.223826	13.325582	0.17342	0.00026181	
DERL1	%1106.286993	%1112.946987	13.319988	0.04825	0.000262592	
SYNPO2L	%4886.999337	%4893.613187	13.2277	0.32468	0.000275842	
IL17REL	%1708.77021	%1715.364856	13.189292	0.25691	0.000281553	
ASPH	%3783.590262	%3790.170651	13.160778	0.35133	0.00028587	
RPS12	%638.377031	%644.895596	13.03713	0	0.000305376	
ZC4H2	%923.282245	%929.778756	12.993022	0	0.000312654	
ARHGAP19	%2378.67061	%2385.148069	12.954918	0.21675	0.000319082	
C1QTNF7	%1370.997386	%1377.461378	12.927984	0.09218	0.000323706	
NDP	%594.742057	%601.19398	12.903846	0	0.000327908	
LAPTM4B	%2135.485164	%2141.834282	12.698236	0.19982	0.000366001	
GPR39	%2381.191027	%2387.534618	12.687182	0.26287	0.000368171	
IL10RA	%3126.164121	%3132.444861	12.56148	0.35022	0.00039378	
PRKRIP1	%906.438103	%912.690769	12.505332	0.13061	0.000405792	
CHST4	%1995.985982	%2002.23561	12.499256	0.25381	0.000407114	
RPS23	%645.084014	%651.325343	12.482658	0	0.000410747	
ATAD5	%9296.037788	%9302.274933	12.47429	0.47818	0.000412591	
CEBPZ	%5167.224037	%5173.457021	12.465968	0.40522	0.000414434	
ZNF192	%2770.569083	%2776.650323	12.16248	0.15997	0.000487605	
S100A4	%429.462564	%435.53548	12.145832	0	0.000491977	
PDK3	%1819.118482	%1825.151096	12.065228	0	0.00051371	
OR6M1	%1726.926886	%1732.952835	12.051898	0.28884	0.000517397	
PRSS55	%2131.633955	%2137.655222	12.042534	0.29225	0.000520002	
ZFP57	%2766.29444	%2772.280291	11.971702	0.32117	0.000540146	
PMFBP1	%5169.306896	%5175.251824	11.889856	0.40433	0.000564405	
AHSA1	%1500.536491	%1506.474307	11.875632	0.05474	0.000568732	
USP18	%2027.104874	%2032.999893	11.790038	0.29711	0.000595485	
ZMYND17	%2327.831386	%2333.707106	11.75144	0.31721	0.000607962	
DDB2	%2011.483521	%2017.3591	11.751158	0.15425	0.000608054	
MBD6	%4426.106758	%4431.960521	11.707526	0.25042	0.000622478	
PRRC1	%2120.504833	%2126.248947	11.488228	0.20701	0.000700384	
PM20D2	%2164.071966	%2169.795032	11.446132	0.2362	0.00071643	
CCNB1	%1925.843486	%1931.548113	11.409254	0.09749	0.000730792	
MOCS3	%2332.738481	%2338.364312	11.251662	0.34385	0.000795518	
MRPL20	%881.731737	%887.312099	11.160724	0.12661	0.000835473	
WDR74	%1904.294319	%1909.824999	11.06136	0.18912	0.000881455	
ZNF157	%2378.739596	%2384.265312	11.051432	0.23884	0.000886187	
MRGPRD	%1879.417203	%1884.934472	11.034538	0.36122	0.0008943	
ILKAP	%1840.756763	%1846.210724	10.907922	0.12991	0.000957539	
C20orf160	%2425.212831	%2430.632395	10.839128	0.44794	0.000993775	
HSD17B3	%1583.585426	%1588.856453	10.542054	0.25669	0.001166887	
HELB	%5542.977005	%5548.245639	10.537268	0.43583	0.001169912	
HSPB2	%812.082764	%817.337596	10.509664	0	0.001187518	
TMEM208	%764.303606	%769.521473	10.435734	0.06104	0.001236004	
ARV1	%1316.239195	%1321.442126	10.405862	0.13611	0.001256159	
PPM1K	%1667.985149	%1673.145126	10.319954	0.13946	0.001315996	
C22orf41	%894.036759	%899.181814	10.29011	0	0.001337451	
SUSD3	%1285.932418	%1291.06665	10.268464	0.22544	0.001353234	
MSL2	%2520.671756	%2525.774375	10.205238	0	0.001400423	
MPHOSPH9	%4893.236212	%4898.326186	10.179948	0.3871	0.001419762	
HLF	%1269.463425	%1274.52357	10.12029	0	0.001466459	
RBBP7	%2093.713966	%2098.771869	10.115806	0.13175	0.001470031	
PLEKHB2	%1116.113455	%1121.072181	9.917452	0.17038	0.001637189	
PPM1E	%3396.373168	%3401.261682	9.777028	0.18849	0.001767057	
SNRPA1	%1117.342391	%1122.206529	9.728276	0	0.001814546	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
ADAT2	%896.005678	%900.832313	9.65327	0.11076	0.001890148	
PRRG1	%978.247492	%983.051549	9.608114	0	0.001937195	
ZNF235	%3660.941822	%3665.74537	9.607096	0.37854	0.001938269	
ANGEL2	%2366.566476	%2371.367167	9.601382	0.16305	0.00194431	
FAM55B	%2830.312327	%2835.059239	9.493824	0.34176	0.002061647	
POLR2F	%561.966813	%566.696307	9.458988	0	0.00210117	
EPT1	%1772.752716	%1777.48124	9.457048	0.14991	0.002103393	
EXD1	%2905.083399	%2909.771311	9.375824	0.35429	0.002198659	
ARL6IP1	%939.876896	%944.541471	9.32915	0.07009	0.002255369	
ADAM29	%4769.01733	%4773.679408	9.324156	0.52723	0.002261525	
CISH	%1389.742431	%1394.266187	9.047512	0.25923	0.002630525	
TMEM194A	%2095.994732	%2100.503952	9.01844	0.25644	0.002672694	
SDC2	%947.423036	%951.923358	9.000644	0.11549	0.002698845	
C9orf9	%840.434107	%844.867265	8.866316	0.1466	0.002904808	
RPL26	%711.204562	%715.624212	8.8393	0	0.002948122	
FTSJ2	%1311.412925	%1315.818018	8.810186	0.22534	0.002995535	
PER3	%6656.988748	%6661.388217	8.798938	0.52188	0.003014059	
MAGEB17	%1973.92884	%1978.278669	8.699658	0.29591	0.003182698	
WDFY2	%1824.152827	%1828.477962	8.65027	0.12195	0.003270129	
GNAO1	%2114.570742	%2118.862601	8.583718	0	0.003391821	
CCDC115	%881.706805	%885.934563	8.455516	0.21188	0.00363938	
MRPL43	%1378.514431	%1382.674354	8.319846	0.20412	0.003921424	
ZCCHC17	%1049.458281	%1053.613009	8.309456	0.06933	0.00394392	
NSUN3	%1618.843655	%1622.974723	8.262136	0.1883	0.004048047	
GNPAT	%3338.206047	%3342.275827	8.13956	0.29628	0.004330979	
CES5A	%3265.510698	%3269.538311	8.055226	0.34548	0.004537258	
KLRG2	%2204.687031	%2208.675632	7.977202	0.41047	0.00473701	
DNAJC24	%684.990966	%688.978349	7.974766	0.19887	0.004743389	
MRPL21	%1129.722931	%1133.670634	7.895406	0.33284	0.004956051	
RD3	%982.68588	%986.518594	7.665428	0.14299	0.005628891	
EBI3	%1154.563742	%1158.330673	7.533862	0.25632	0.006054997	
OLA1	%1684.069834	%1687.766785	7.393902	0	0.006544536	
SH3D21	%4135.312485	%4139.004011	7.383052	0.52794	0.006584134	
HNRNPD	%1490.51827	%1494.169146	7.301752	0	0.006888741	
MFSD6L	%3312.34382	%3315.943752	7.199864	0.46668	0.007290911	
C10orf11	%974.495568	%978.072961	7.154786	0.13846	0.007476421	
ENOPH1	%1175.699119	%1179.245592	7.092946	0.21334	0.007738793	
CAPS2	%2949.965422	%2953.508816	7.086788	0.37484	0.00776543	
VCX2	%903.121161	%906.617604	6.992886	0.30221	0.00818343	
NUDCD1	%2710.054796	%2713.526408	6.943224	0.25627	0.008413733	
UGT1A3	%2747.432375	%2750.894392	6.924034	0.47577	0.008504492	
RCN2	%1491.652668	%1495.09716	6.888984	0.10181	0.008672855	
DLX6	%1105.748702	%1109.161022	6.82464	0	0.008990868	
GADD45A	%732.548331	%735.939482	6.782302	0.07937	0.009206608	
IL17RB	%2645.240483	%2648.595862	6.710758	0.38558	0.009583298	
C8orf40	%467.375964	%470.697685	6.643442	0	0.009952147	
FBXO22	%1930.614615	%1933.918899	6.608568	0.27388	0.010148924	
PINX1	%1711.945562	%1715.144749	6.398374	0.37131	0.011422493	
C9orf46	%559.576468	%562.678473	6.20401	0.08488	0.012746122	
WDR5B	%1588.638385	%1591.719937	6.163104	0.27935	0.013044211	
RAB17	%1171.410879	%1174.480601	6.139444	0.29613	0.013219887	
C1orf27	%2081.121824	%2084.112978	5.982308	0.32063	0.01445008	
C12orf5	%1453.722768	%1456.690989	5.936442	0.32142	0.014830929	
DNAJC30	%1248.117648	%1250.977229	5.719162	0.38342	0.016780738	
IDO2	%2229.870649	%2232.697976	5.654654	0.43147	0.017409109	
TBRG1	%1916.754059	%1919.557088	5.606058	0.33464	0.017898484	
GPHA2	%627.460338	%630.217671	5.514666	0.22858	0.018857674	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
ICT1	%1154.836147	%1157.577989	5.483684	0.2798	0.019194764	0.037956811
C9orf142	%1043.842112	%1046.577899	5.471574	0.24679	0.019328211	
ABHD10	%1500.896444	%1503.494767	5.196646	0.26029	0.022630514	
COQ3	%1949.797416	%1952.380028	5.165224	0.39549	0.023043486	
GOLGA6C	%5060.926301	%5063.398942	4.945282	0.67379	0.026161971	
ACSM1	%3134.54617	%3136.983171	4.874002	0.58481	0.027264202	
NR1I3	%1719.194897	%1721.620998	4.852202	0.34275	0.027610862	
MTG1	%1716.937479	%1719.313051	4.751144	0.43469	0.029278823	
HAUS2	%1109.477258	%1111.825292	4.696068	0.29211	0.030231705	
USP26	%5055.567807	%5057.905462	4.67531	0.58343	0.03059918	0.038704319
MBNL2	%1567.197245	%1569.534456	4.674422	0.12198	0.030615003	0.038787375
TMEM61	%1209.503908	%1211.835558	4.6633	0.42006	0.030813914	0.038870432
FMO6P	%713.102505	%715.432619	4.660228	0.32929	0.030869092	0.038953488
CCL24	%713.13396	%715.463279	4.658638	0.32939	0.030897692	0.039036545
CDCA3	%1245.967299	%1248.293171	4.651744	0.26284	0.031022014	0.039119601
WISP3	%1792.269231	%1794.591451	4.64444	0.35368	0.0311543	0.039202658
CASP8	%2453.836331	%2456.108069	4.543476	0.50025	0.033044425	0.039285714
TMEM232	%3271.73811	%3274.007379	4.538538	0.50496	0.033139885	0.039368771
ZNF20	%2603.192657	%2605.449118	4.512922	0.47837	0.033639726	0.039451827
LETM2	%2523.133585	%2525.382623	4.498076	0.58118	0.033933013	0.039534884
CCDC69	%1442.218616	%1444.372902	4.308572	0.31018	0.037920781	0.03961794
EPSTI1	%2232.301943	%2234.4504	4.296914	0.4796	0.038181596	0.039700997
PFDN6	%550.585522	%552.724769	4.278494	0	0.038597532	0.039784053
GFRAL	%2052.074075	%2054.183092	4.218034	3.64335	0.039996478	0.03986711
ADH1A	%2353.576403	%2355.649804	4.146802	0.48093	0.041713235	
USP1	%3479.240727	%3481.309657	4.13786	0.38623	0.041934151	
APOBEC1	%1256.990455	%1259.019258	4.057606	0.34534	0.043972798	
ZNF561	%3224.14955	%3226.054054	3.809008	0.45659	0.050977634	
CCDC36	%3125.684594	%3127.561273	3.753358	0.51328	0.052701535	
FAM165B	%284.149876	%286.000483	3.701214	0	0.054372893	
MRPL55	%878.006465	%879.781723	3.550516	0.40994	0.059526936	
CEACAM6	%2791.872227	%2793.630817	3.51718	2.43666	0.060735705	
CLEC4E	%1201.749802	%1203.484309	3.469014	0.49528	0.062528572	
DARC	%1863.907248	%1865.612254	3.410012	0.54034	0.064801975	
ATP5H	%762.089943	%763.787469	3.395052	0.30585	0.065392301	
GP1BA	%4201.38729	%4203.063699	3.352818	0.64941	0.067090069	
TRAIP	%2304.894243	%2306.56404	3.339594	0.42416	0.067631295	
OR5AS1	%1664.240047	%1665.872056	3.264018	0.48752	0.07081541	
CAV1	%809.483356	%811.112639	3.258566	0	0.071051235	
RAD21L1	%2719.27487	%2720.900506	3.251272	0.46677	0.071368053	
CPB2	%2230.652046	%2232.273986	3.24388	0.55324	0.071690673	
MPZL2	%1008.144149	%1009.713242	3.138186	0.22621	0.076478824	
RGS8	%884.748687	%886.289641	3.081908	0.1956	0.079167603	
CLK4	%2165.177918	%2166.71368	3.071524	0.30122	0.079674747	
FAM103A1	%520.705329	%522.208174	3.00569	0	0.082972642	
LSM10	%586.345102	%587.805041	2.919878	0.20774	0.087494479	
SYNJ2BP	%647.16897	%648.62681	2.91568	0.28854	0.087722428	
CCDC68	%1602.987455	%1604.442727	2.910544	0.43503	0.088002186	
TSSK4	%1833.716507	%1835.094139	2.755264	0.47515	0.096934815	
MPV17L	%1181.750731	%1183.076793	2.652124	0.48226	0.10341164	
HEYL	%1750.587675	%1751.884601	2.593852	0.49681	0.107279146	
AGAP10	%4366.199297	%4367.469044	2.539494	0.71197	0.111030363	
C8orf39	%460.662939	%461.919413	2.512948	999	0.112914527	
PLAU	%2337.515337	%2338.752581	2.474488	0.56745	0.115707116	
TTF1	%5077.901196	%5079.11198	2.421568	0.71221	0.119675088	
GMNN	%1034.368436	%1035.568169	2.399466	0.38258	0.121376676	
TSPAN8	%1578.586478	%1579.743863	2.31477	1.92016	0.128150255	

Gene	Free&nL	Fixed&nL	2ΔlnL	branch_w	pvalue	k
LHFPL2	%1092.013672	%1093.167288	2.307232	0.32791	0.128773185	
METAP1D	%1550.471821	%1551.617834	2.292026	0.32426	0.13004008	
C4orf7	%518.312456	%519.4504	2.275888	3.83975	0.131399844	
GEMIN7	%641.781954	%642.885845	2.207782	0.36302	0.137315972	
RGS18	%1078.675495	%1079.775778	2.200566	0.28307	0.137960073	
DHRS7	%1625.569967	%1626.661627	2.18332	0.50031	0.139513221	
OAS1	%2332.23369	%2333.32263	2.17788	0.60245	0.140007202	
WDR63	%4322.978617	%4324.039578	2.121922	0.63063	0.145204223	
VSIG1	%2093.679801	%2094.711375	2.063148	0.54922	0.150898152	
TMEM139	%1119.952528	%1120.979252	2.053448	2.34775	0.151861926	
ZNF540	%3153.682788	%3154.698819	2.032062	0.56658	0.15401153	
C11orf20	%1250.459581	%1251.468317	2.017472	0.44036	0.155497834	
TNIP3	%2039.588884	%2040.584964	1.99216	0.6262	0.158115216	
H2AFB3	%626.181273	%627.145381	1.928216	0.42064	0.164953756	
SMR3B	%486.36828	%487.316332	1.896104	0.46402	0.168515054	
MAGEB3	%1942.196988	%1943.144029	1.894082	0.59374	0.16874223	
TTC29	%2306.835411	%2307.768618	1.866414	0.55068	0.171886354	
NDUFA6	%804.102358	%805.024129	1.843542	0.46434	0.17453637	
CD69	%1044.947844	%1045.858831	1.821974	0.54412	0.177078486	
CCDC73	%5510.579033	%5511.471844	1.785622	0.70701	0.18146049	
BCCIP	%1571.18332	%1572.048784	1.730928	0.41182	0.188292427	
LIPH	%2243.786386	%2244.570657	1.568542	0.59269	0.210418877	
GLYAT	%1578.177767	%1578.942534	1.529534	0.60789	0.216182397	
CMBL	%1195.134128	%1195.847939	1.427622	0.55293	0.232152922	
STX2	%1321.218151	%1321.926349	1.416396	0.36609	0.233997516	
IFNA2	%1005.566095	%1006.272695	1.4132	0.54015	0.234525901	
TFEC	%1628.607585	%1629.285907	1.356644	0.5205	0.244119953	
FCRL2	%3056.335435	%3057.010927	1.350984	0.74714	0.245106166	
DEFB110	%339.853171	%340.491864	1.277386	999	0.258385631	
STH	%711.395576	%711.929284	1.067416	1.81991	0.30152984	
BET1	%506.186153	%506.716573	1.06084	999	0.303023679	
C1orf101	%5584.983966	%5585.489731	1.01153	1.24209	0.314536577	
KMO	%2493.938487	%2494.422179	0.967384	0.7104	0.325333469	
LYG1	%1103.184062	%1103.666948	0.965772	0.57898	0.325736898	
GNG5P2	%352.746854	%353.225676	0.957644	0.43799	0.327781185	
FAM64A	%1282.482248	%1282.954499	0.944502	0.64461	0.331122726	
C14orf180	%1004.02853	%1004.496236	0.935412	0.70002	0.333460558	
AMBN	%2392.830381	%2393.292026	0.92329	1.39548	0.336612606	
MTIF3	%1537.781795	%1538.2363	0.90901	1.45546	0.340377231	
PNLIPRP3	%2311.394653	%2311.827109	0.864912	1.58362	0.352367744	
MS4A7	%1300.157131	%1300.579122	0.843982	0.65733	0.358260395	
CNPY1	%412.901289	%413.304806	0.807034	999	0.368998605	
C4orf33	%1021.605238	%1021.995862	0.781248	0.49512	0.376759729	
LRRC2	%1793.803242	%1794.183025	0.759566	0.62973	0.383464376	
FXYD3	%495.740711	%496.052062	0.622702	0.45543	0.430044975	
RBP7	%647.184713	%647.452754	0.536082	0.5751	0.464061024	
PTTG2	%1129.448065	%1129.710309	0.524488	1.58522	0.468933482	
DDTL	%774.163838	%774.412007	0.496338	0.76813	0.481113608	
TNFSF9	%1174.218332	%1174.448806	0.460948	0.41645	0.497181257	
DNAJC5G	%1132.454236	%1132.679874	0.451276	0.63994	0.501729624	
CCRL1	%1661.379096	%1661.602727	0.447262	0.7101	0.503638063	
ZNRD1	%571.029156	%571.25099	0.443668	4.03788	0.50535736	
ZNF117	%3441.795631	%3442.001656	0.41205	0.76411	0.520930836	
CCDC82	%2745.132541	%2745.302589	0.340096	0.82722	0.559773814	
PLP1	%1160.80004	%1160.96698	0.33388	0.43474	0.563383286	
OR14A2	%1605.940187	%1606.097597	0.31482	0.76864	0.574737393	
NPFF	%606.901231	%607.056266	0.31007	1.44114	0.577637234	

Gene	Free lnL	Fixed lnL	2ΔlnL	branch_w	pvalue	k
CYP3A5	-2729.008899	-2729.146996	0.276194	0.85087	0.599206725	
ZBP1	-2566.361965	-2566.485931	0.247932	1.17649	0.618534999	
TIAF1	-617.444741	-617.541432	0.193382	1.28603	0.660116589	
IFI27L1	-553.952742	-554.036188	0.166892	1.3824	0.682888887	
VPREB1	-805.477026	-805.542463	0.130874	0.77216	0.717527561	
LAIR1	-1743.692533	-1743.752564	0.120062	1.12551	0.728967255	
CENPT	-3154.557542	-3154.611235	0.107386	0.889	0.743139992	
METTL6	-1400.863356	-1400.900393	0.074074	0.86132	0.785494852	
ITGB3BP	-886.961787	-886.997317	0.07106	1.23045	0.789799628	
WFDC11	-493.221064	-493.254277	0.066426	1.17493	0.796613424	
COX5B	-678.818419	-678.845783	0.054728	1.14987	0.815031432	
FAM111A	-3300.254178	-3300.277001	0.045646	1.07016	0.830820594	
IL19	-1203.258226	-1203.274326	0.0322	0.90812	0.857589411	
HSPBP1	-1502.934495	-1502.946406	0.023822	0.01307	0.877338686	
PIGA	-2361.222071	-2361.23288	0.021618	1.06871	0.88310786	
TMEM92	-872.072275	-872.077554	0.010558	0.9332	0.9181597	
CD300C	-1372.113123	-1372.116945	0.007644	0.9643	0.930329746	
RESP18	-1251.443795	-1251.446961	0.006332	0.96346	0.936576182	
SLC31A1	-858.540008	-858.542421	0.004826	0.9214	0.944615975	
GIMAP2	-1823.438289	-1823.439749	0.00292	1.0239	0.956905666	
CYLC1	-3426.531004	-3426.532351	0.002694	1.01429	0.958605381	
LRPPRC	-7706.101882	-7706.103136	0.002508	0.99124	0.960058688	
CACNG6	-1273.229382	-1273.229775	0.000786	1.02327	0.977633685	
TMEM105	-687.214621	-687.215011	0.00078	1.02312	0.977719193	
RNF11	-655.292812	-655.293201	0.000778	0	0.97774777	
PLK2	-3091.218565	-3091.21862	0.00011	0	0.99163187	
CLCN4	-3692.496974	-3613.341632	-158.310684	33.57554	#NUM!	
FAM131A	-1505.426042	-1331.093121	-348.665842	0	#NUM!	
L3MBTL1	-3976.057645	-3976.05723	-0.00083	0	#NUM!	
OAZ2	-820.725354	-820.725343	-2.2E-05	0	#NUM!	
RC3H1	-5713.838493	-5147.174413	-1133.32816	0	#NUM!	
ZFP37	-3102.256558	-3100.974348	-2.56442	0.80329	#NUM!	

Human-Chimp Ancestor

Gene	lnL_free	lnL_fixed	2ΔlnL	branch_w	pvalue	k
GNAO1	-2115.091208	-2133.571392	36.960368	0	1.20555E-09	
UNC13C	-10554.27004	-10571.62212	34.704158	0.07085	3.83811E-09	
SEMA6B	-4181.097838	-4195.242104	28.288532	0.01843	1.04513E-07	
VPS13D	-20748.18924	-20761.65837	26.938274	0.14678	2.10058E-07	
SMPD3	-3077.880073	-3090.44672	25.133294	0.02912	5.35011E-07	
ERC1	-5076.954182	-5089.189601	24.470838	0.03236	7.54431E-07	
SLIT1	-7418.808109	-7429.86411	22.112002	0	2.57197E-06	
NCOR2	-12225.44978	-12235.23968	19.57979	0	9.64844E-06	
PRKCD	-3135.65905	-3144.924042	18.529984	0	1.67252E-05	
ACCN1	-2708.453216	-2717.119536	17.33264	0	3.13751E-05	
PCDHA1	-5051.64786	-5059.621927	15.948134	0.14569	6.51019E-05	
COL5A2	-6697.950638	-6705.758709	15.616142	0	7.75894E-05	
POFUT2	-2133.873503	-2141.567298	15.38759	0	8.75615E-05	
FZR1	-2351.306176	-2358.62605	14.639748	0	0.000130141	
PITPNM1	-6235.110506	-6242.309713	14.398414	0	0.000147927	
S1PR3	-1731.166255	-1738.212404	14.092298	0	0.000174055	
ERCC3	-3775.847615	-3782.801969	13.908708	0	0.000191907	
ATAD2	-6457.628634	-6464.544865	13.832462	0.10529	0.000199853	
ZC3H13	-7600.366067	-7607.190212	13.64829	0	0.000220442	
ZNF561	-3219.880878	-3226.266051	12.770346	0	0.000352158	
ADNP2	-5610.225166	-5616.600005	12.749678	0	0.00035607	
ATP10D	-7191.496821	-7197.532463	12.071284	0.12126	0.000512044	
ARHGAP4	-5882.654538	-5888.644234	11.979392	0.04361	0.000537921	
STAT5B	-3676.220385	-3681.810636	11.180502	0	0.000826614	
RALGDS	-4386.300318	-4391.82727	11.053904	0	0.000885006	
EPHB3	-4499.076015	-4504.602734	11.053438	0	0.000885229	
PLEKHA5	-4834.462898	-4839.955254	10.984712	0.09147	0.000918666	
FGGY	-2752.047509	-2757.39831	10.701602	0	0.001070428	
RBBP7	-2092.123799	-2097.436242	10.624886	0	0.001115758	
ZNF540	-3151.562822	-3156.804853	10.484062	0.09728	0.001204087	0.002388535
EIF2C4	-3719.55317	-3724.656459	10.206578	0	0.001399406	0.002468153
PLCH2	-7498.310721	-7503.405582	10.189722	0.06696	0.001412256	0.002547771
MTG1	-1716.223724	-1721.194052	9.940656	0.05663	0.001616679	0.002627389
ISYNA1	-2711.263761	-2716.012318	9.497114	0	0.002057953	0.002707006
ELF4	-3309.176044	-3313.688377	9.024666	0	0.002663606	0.002786624
GCOM1	-2848.818456	-2853.330049	9.023186	0.13989	0.002665763	0.002866242
SPTB	-11267.84216	-11272.2016	8.718894	0.05605	0.00314929	0.00294586
CAPN11	-3811.291113	-3815.545837	8.509448	0	0.003533072	0.003025478
LDB3	-3931.072567	-3935.317072	8.48901	0	0.003572982	0.003105096
CHST4	-1994.104399	-1998.316706	8.424614	0	0.003701752	0.003184713
KLRG2	-2204.361442	-2208.547933	8.372982	0.14051	0.003808402	
DLEC1	-9084.950102	-9089.128077	8.35595	0.1035	0.003844264	
ZNF275	-2173.004139	-2177.134308	8.260338	0	0.004052058	
HMGCR	-4419.481798	-4423.489469	8.015342	0	0.004638271	
KDM5D	-8473.291133	-8477.27016	7.958054	0	0.004787386	
UPF2	-5623.164372	-5627.102695	7.876646	0	0.005007727	
ANO1	-4808.876371	-4812.808919	7.865096	0	0.005039815	
EIF2C2	-4034.31954	-4038.235199	7.831318	0	0.005134864	
ASCC3	-10025.13645	-10029.01741	7.76192	0	0.005335921	
HEYL	-1749.884684	-1753.713014	7.65666	0	0.005656312	0.003980892
ZBTB38	-5738.76161	-5742.523998	7.524776	0	0.006085612	
MBLAC2	-1292.484472	-1296.246116	7.523288	0	0.006090641	
SDAD1	-3554.679622	-3558.42624	7.493236	0	0.006193117	
CDCA2	-5452.418983	-5456.152059	7.466152	0.29227	0.006286979	
NPFFR1	-2089.197286	-2092.922602	7.450632	0	0.006341418	
TBC1D9	-5834.179969	-5837.85647	7.353002	0	0.006695087	
OLA1	-1684.083125	-1687.755907	7.345564	0	0.006722844	
PNPLA7	-6801.934227	-6805.59517	7.321886	0.08966	0.006811989	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
CCDC157	&3833.587919	&3837.215635	7.255432	0.22721	0.007068687	
SIX6	&1100.548839	&1104.164863	7.232048	0.06246	0.007161347	0.00477707
CHL1	&6211.294096	&6214.870874	7.153556	0	0.00748155	
ADRA1B	&2497.561152	&2501.115676	7.109048	0	0.007669583	
C1orf43	&1160.788754	&1164.343052	7.108596	0	0.007671517	
C11orf20	&1248.523569	&1252.0717	7.096262	0	0.007724488	
ZNF570	&2394.670808	&2398.115204	6.888792	0.08463	0.008673787	
ADAMTS8	&4014.106481	&4017.534539	6.856116	0.06023	0.008833836	
TMEM43	&2109.417419	&2112.765747	6.696656	0	0.009659391	
HM13	&1873.91276	&1877.246051	6.666582	0	0.009823741	
TEKT5	&2694.252199	&2697.554433	6.604468	0	0.010172319	
KLHDC4	&2857.177678	&2860.422036	6.488716	0	0.010856136	0.005573248
DCAF12L2	&2617.412848	&2620.652217	6.478738	0	0.010917247	
HSD17B3	&1582.241081	&1585.467014	6.451866	0	0.011083587	
CCDC132	&4369.877	&4373.100339	6.446678	0	0.011116	
PRMT6	&1671.86089	&1675.054495	6.38721	0	0.011494556	
SUSD3	&1284.588209	&1287.677214	6.17801	0	0.012934767	
TMED4	&1062.012389	&1065.098059	6.17134	0	0.012983623	
ITGB8	&3616.816794	&3619.888908	6.144228	0	0.013184171	
SYNPO2L	&4885.619878	&4888.676771	6.113786	0	0.013413151	
H2AFB3	&625.918604	&628.963827	6.090446	0.21037	0.013591477	
TRIM39	&2366.464346	&2369.505261	6.08183	0	0.013657922	0.006369427
APC2	&11996.24921	&11999.24779	5.997168	0.13919	0.014328861	
CWC22	&4318.980885	&4321.973006	5.984242	0.09391	0.014434244	
RPL26	&711.825225	&714.786646	5.922842	0	0.014945832	
RPL23A	&867.721742	&870.667393	5.891302	0	0.015215847	
PRPF4B	&4588.239205	&4591.17488	5.87135	0	0.015389246	
KCNB1	&3940.827989	&3943.758842	5.861706	0	0.015473789	
ZFP64	&3248.177403	&3251.107984	5.861162	0	0.015478572	
LAMA4	&660.37432	&663.297152	5.845664	0.09033	0.01561548	
CAV1	&809.394837	&812.292772	5.79587	0	0.016063864	
ZNF652	&779.4035	&782.254085	5.70117	0	0.016953608	
PNPT1	&658.559003	&661.391984	5.665962	0	0.017297228	
HIST1H3G	&641.629555	&644.459334	5.659558	0	0.017360498	
GAL3ST4	&2424.654993	&2427.469571	5.629156	0.15709	0.017664134	
MAP4K3	&4020.941599	&4023.746818	5.610438	0	0.0178538	
INTS6	&4109.48468	&4112.285853	5.602346	0	0.017936444	
RNF216	&4385.915151	&4388.695998	5.561694	0.18411	0.018357642	
SLC24A4	&2704.227066	&2707.001993	5.549854	0	0.018482229	
C4orf33	&1019.832452	&1022.525616	5.386328	0	0.020295135	
SDHA	&589.956724	&592.639699	5.36595	0.09483	0.020533601	
CA5A	&1403.520234	&1406.196158	5.351848	0.35869	0.020700319	0.007961783
PCDHB5	&4602.472929	&4605.148045	5.350232	0.21748	0.020719514	
MYL6B	&176.14654	&178.820487	5.347894	0	0.020747316	
JAM2	&1428.794393	&1431.457335	5.325884	999	0.021010948	
HIST1H2AL	&744.284595	&746.941525	5.31386	0	0.021156432	
DENND4B	&7194.301997	&7196.956248	5.308502	0.09231	0.021221596	
ZNF574	&4509.221017	&4511.857078	5.272122	0	0.021669582	
SDSL	&1769.096335	&1771.72141	5.25015	0	0.021944879	
CD300C	&1370.279145	&1372.903069	5.247848	0	0.021973931	
SMC5	&5110.722148	&5113.31525	5.186204	0	0.022766893	
NLGN3	&586.287036	&588.865348	5.156624	0	0.02315787	
BCL9L	&7012.735279	&7015.302578	5.134598	0	0.023453518	
ACOT12	&2906.073381	&2908.597655	5.048548	0	0.024646584	
ANKRD52	&5052.532517	&5055.053613	5.042192	0	0.02473717	
C1orf101	&5588.718742	&5591.238313	5.039142	0.21823	0.024780761	
KRT36	&2448.806811	&2451.298278	4.982934	0	0.025598534	
ASH2L	&2901.661925	&2904.125451	4.927052	0	0.026439385	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
GPRASP2	&4101.617008	&4104.061548	4.88908	0	0.027027085	
COL20A1	&6579.366131	&6581.794879	4.857496	0	0.027526259	
SLC16A8	&2346.279237	&2348.70448	4.850486	0.14667	0.027638344	
ZNF324B	&3116.807712	&3119.226433	4.837442	0	0.027848174	
PPM1K	&1667.461629	&1669.872003	4.820748	0	0.02811914	
PADI1	&3540.013989	&3542.415914	4.80385	0	0.028396213	
PIAS1	&2899.330693	&2901.715492	4.769598	0	0.028966589	
ABCB11	&6821.481691	&6823.836092	4.708802	0	0.030008557	
CEACAM6	&2793.487861	&2795.841039	4.706356	0.24948	0.030051286	
FBL	&1605.452718	&1607.746839	4.588242	0	0.032192017	
PINX1	&1711.168781	&1713.438606	4.53965	0.10908	0.033118363	
CES5A	&3264.558086	&3266.817419	4.518666	0	0.033526963	
OR1N2	&1644.068584	&1646.260316	4.383464	0	0.036289176	
CPA5	&2349.018093	&2351.16623	4.296274	0.10508	0.038195969	
MPHOSPH9	&4893.106572	&4895.229368	4.245592	0.23261	0.039352348	
USP1	&3480.626348	&3482.746136	4.239576	0.24471	0.039492029	
YLPM1	&9690.612744	&9692.7199	4.214312	0.11764	0.040084319	
KRTAP4&7	&1360.370495	&1362.463903	4.186816	0.06294	0.040739544	
AGGF1	&3402.570505	&3404.663063	4.185116	0.11305	0.040780422	
CDC23	&2708.16235	&2710.200534	4.076368	0.1247	0.043487039	
GLYAT	&1577.315636	&1579.336172	4.041072	0.12031	0.044405606	
RTN4RL2	&1990.393587	&1992.410015	4.032856	0	0.04462234	
RNF34	&1774.172591	&1776.182805	4.020428	0	0.044952304	0.011066879
SCG3	&2151.628149	&2153.495441	3.734584	0	0.053296937	
CHRDL2	&2444.949508	&2446.809657	3.720298	0	0.053754776	
LRPPRC	&7706.803342	&7708.639529	3.672374	0.13622	0.055321335	
APOBEC1	&1256.806463	&1258.638103	3.66328	0.23322	0.055624028	
STUB1	&1347.877786	&1349.702881	3.65019	0	0.056062816	
LAMC2	&5962.805698	&5964.593018	3.57464	0.1316	0.058668164	
VPS52	&3325.604316	&3327.390406	3.57218	0	0.05875513	
TNS3	&7655.693569	&7657.474399	3.56166	0.10848	0.05912858	
KCNG2	&1850.91312	&1852.660877	3.495514	0.01893	0.061535303	
DHTKD1	&4800.582103	&4802.317429	3.470652	0	0.062466684	
C21orf59	&1400.614463	&1402.34753	3.466134	0.17086	0.062637544	
PER3	&6656.955396	&6658.670438	3.430084	0.46039	0.064018845	
SFRP1	&1508.883116	&1510.552643	3.339054	0	0.067653495	
SIPA1	&4987.226607	&4988.894677	3.33614	0.22043	0.067773426	
PPIG	&3510.666321	&3512.292113	3.251584	0	0.07135447	
MPZL2	&1008.25044	&1009.858763	3.216646	0.15063	0.072892844	
RD3	&982.389044	&983.993498	3.208908	0	0.073238348	
CXCR5	&1773.79027	&1775.394253	3.207966	0	0.073280528	
RBCK1	&2218.800396	&2220.404109	3.207426	0	0.07330472	
FTSJ2	&1310.792867	&1312.382887	3.18004	0	0.074542905	
RBM7	&1282.92319	&1284.512365	3.17835	0.19172	0.074620046	
GMNN	&1034.468981	&1036.03369	3.129418	0	0.076891186	
DUSP1	&1011.279256	&1012.794154	3.029796	0	0.081748294	
KIDINS220	&8391.906885	&8393.408381	3.002992	0.13769	0.083110901	
GCK	&2425.11164	&2426.581942	2.940604	0	0.086378428	
TTLL9	&2360.75581	&2362.222931	2.934242	0	0.08671936	
MPV17L	&1180.748645	&1182.163665	2.83004	0	0.092516055	
C12orf5	&1453.67416	&1455.076922	2.805524	0	0.093940147	
SOCS4	&1989.987166	&1991.386139	2.797946	0	0.09438515	
WDR74	&1904.461011	&1905.852483	2.782944	0.14417	0.095272893	
PDK3	&1819.535863	&1820.89715	2.722574	0	0.09893835	
CCDC36	&3124.960084	&3126.315252	2.710336	999	0.09969999	
SV2B	&3191.070308	&3192.424331	2.708046	0	0.09984322	
PLAU	&2338.289175	&2339.64232	2.70629	0	0.099953202	
PPP1R12A	&4527.081565	&4528.423584	2.684038	0	0.101358421	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
TMEM38B	&1445.850141	&1447.184637	2.668992	0	0.10232081	
CD69	&1044.372996	&1045.706093	2.666194	0	0.102500878	
TMC8	&631.72058	&633.04931	2.65746	0	0.103065199	
PMFBP1	&5168.022887	&5169.348604	2.651434	999	0.103456532	
ARCN1	&2281.851204	&2283.167293	2.632178	0	0.104717977	
RPS12	&640.044881	&641.342915	2.596068	0	0.107129203	
COPS4	&1959.594894	&1960.882726	2.575664	0	0.108518557	
SHMT2	&2376.199073	&2377.483675	2.569204	0	0.108962548	
KANK3	&4441.64247	&4442.920156	2.555372	0	0.109919939	
FAM120A	&5421.951889	&5423.227436	2.551094	0	0.110217913	
PPP2R2C	&2051.300447	&2052.575861	2.550828	0	0.11023647	
TFEC	&1628.150893	&1629.423373	2.54496	0	0.110646713	
JAG2	&6296.818531	&6298.089945	2.542828	0.05991	0.110796181	
CLK4	&2165.807159	&2167.078157	2.541996	0	0.11085457	
MOAP1	&1705.252134	&1706.521945	2.539622	0	0.111021362	
WSB2	&1866.430396	&1867.693385	2.525978	0	0.111985331	
PNLIPRP3	&2313.482903	&2314.739846	2.513886	0	0.112847354	
CA10	&1497.578032	&1498.821035	2.486006	0	0.114862883	
FKRP	&2437.461534	&2438.698398	2.473728	0	0.115763062	
PSMD9	&1065.178029	&1066.39958	2.443102	0	0.118042588	
GIMAP2	&1823.167429	&1824.387107	2.439356	0	0.118324795	
PSMD4	&1696.878378	&1698.094903	2.43305	0	0.118801547	
HELB	&5540.58964	&5541.80466	2.43004	999	0.119029861	
ALOX15	&885.326763	&886.541183	2.42884	0	0.119121019	
PIP4K2C	&1757.262238	&1758.473771	2.423066	0	0.119560719	
GPT2	&464.09337	&465.302703	2.418666	0	0.119896993	
ZNF30	&412.576643	&413.780494	2.407702	0.23103	0.120739491	
ZNF592	&978.958728	&980.159395	2.401334	0	0.121231831	
ANGEL2	&366.276063	&367.468825	2.385524	0	0.122463823	
ILKAP	&841.340164	&842.532912	2.385496	0	0.122466017	
CPT1B	&719.948023	&721.138975	2.381904	0.15345	0.12274786	
NR2C2	&829.805036	&830.995794	2.381516	0	0.122778347	
ATG16L1	&891.718501	&892.906812	2.376622	0	0.123163614	
C1orf187	&762.049298	&763.233371	2.368146	0	0.123834043	
EPSTI1	&231.676446	&232.859004	2.365116	0	0.12407469	
RABGGTA	&637.490934	&638.66014	2.338412	0	0.126218164	
GP1BA	&4200.551149	&4201.71722	2.332142	0	0.126727389	
ADAT2	&96.33273	&97.494644	2.323828	0	0.127406147	
CMBL	&1195.910714	&1197.057467	2.293506	0	0.129916165	
ALDH1A3	&496.624487	&497.768914	2.288854	0	0.130306104	
IL10RA	&126.734981	&127.874479	2.278996	0.45973	0.13113674	
PRRG1	&979.184937	&980.324292	2.27871	0	0.131160927	
MED19	&1132.891245	&1134.028263	2.274036	0	0.131556903	
TACR2	&978.068775	&979.194744	2.251938	0	0.133447183	
MBNL2	&1567.0871	&1568.195885	2.21757	0	0.136447673	
SLC7A14	&657.68187	&658.784311	2.204882	0	0.137574421	
OR6M1	&1728.3494	&1729.440856	2.182912	0	0.139550202	
SEMA4B	&997.909377	&998.996197	2.17364	0	0.140393578	
GCDH	&327.709609	&328.795314	2.17141	0	0.140597271	
PLXDC2	&635.067175	&636.150212	2.166074	0	0.14108602	
EPB41L1	&4096.503579	&4097.584596	2.162034	0	0.141457332	
AHSA1	&1500.733348	&1501.810359	2.154022	0	0.14219696	
DEF8	&632.037661	&633.108604	2.141886	0.11866	0.143325593	
ASPH	&783.18443	&784.24968	2.1305	0	0.144393649	
GJA4	&1636.802056	&1637.854589	2.105066	0	0.146812009	
IL19	&1202.613172	&1203.663521	2.100698	0	0.147231913	
C14orf181	&761.093706	&762.141887	2.096362	0.1758	0.147650082	
CCNB1	&1927.038119	&1928.0808	2.085362	0.26869	0.148716965	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
LYG1	&1102.121289	&1103.161125	2.079672	999	0.149272249	
PM20D2	&2164.027267	&2165.04248	2.030426	0.31617	0.154177386	
FAM111A	&3299.684291	&3300.693832	2.019082	999	0.155333025	
DEFB103A	&335.977395	&336.977522	2.000254	0	0.15727285	
SULF2	&4179.648766	&4180.608788	1.920044	0	0.16585181	
RNF208	&1198.660948	&1199.619694	1.917492	0	0.166133405	
ADH1A	&2353.514298	&2354.465351	1.902106	0.19425	0.16784278	
CYP3A5	&2730.347626	&2731.297433	1.899614	0	0.168121531	
PCDHA3	&4893.198093	&4894.14385	1.891514	999	0.169031256	
EFS	&2801.90263	&2802.818137	1.831014	0	0.176007824	
CENPT	&3153.534855	&3154.441881	1.814052	999	0.178022918	
TTF1	&5078.200013	&5079.093393	1.78676	0.1949	0.181321424	
OR5H6	&1745.760707	&1746.639343	1.757272	0.15234	0.184965146	
GPR179	&14281.46644	&14282.31981	1.706758	279.57328	0.191406544	
DGAT1	&2575.954955	&2576.803494	1.697078	0	0.192670555	
USP18	&2027.668141	&2028.502512	1.668742	0.41892	0.196427118	
C11orf84	&2731.012922	&2731.839158	1.652472	0.18634	0.198622812	
DNAI2	&3181.345013	&3182.137245	1.584464	0.17727	0.20811886	
ARHGAP19	&2378.934189	&2379.708134	1.54789	0.22898	0.213447205	
BCCIP	&1570.765331	&1571.522943	1.515224	999	0.218343678	
AMBN	&2391.795442	&2392.552257	1.51363	0.22958	0.218586015	
CAPS2	&2949.467907	&2950.222648	1.509482	0	0.219218146	
DCAF4L1	&1947.504122	&1948.256325	1.504406	0.35811	0.219994669	
C4orf7	&518.378046	&519.108051	1.46001	999	0.22692853	
C1QTNF7	&1368.156398	&1368.884575	1.456354	16.78766	0.22751113	
GCGR	&2923.870035	&2924.595775	1.45148	0.26666	0.228290622	
C4orf31	&2783.978862	&2784.699319	1.440914	0.22513	0.229991493	
NPFF	&606.315829	&607.035892	1.440126	999	0.230118952	
DBX1	&2071.455486	&2072.15236	1.393748	0	0.237773171	
CHM	&3027.616086	&3028.309497	1.386822	999	0.238942522	
ZNF235	&3660.874872	&3661.563514	1.377284	0	0.240564323	
ZNF20	&2603.166697	&2603.854362	1.37533	0.39162	0.240898223	
OR1N1	&1422.260294	&1422.939633	1.358678	999	0.243766727	
SLC25A23	&2100.440751	&2101.110868	1.340234	0.17517	0.246992706	
ROBO4	&5267.422725	&5268.089116	1.332782	0.34472	0.2483109	
MARVELD3	&1939.564542	&1940.222596	1.316108	999	0.251291739	
MAGEB17	&1973.892307	&1974.541451	1.298288	999	0.254526177	
ARHGEF25	&2845.951741	&2846.593897	1.284312	0.43391	0.257098829	
MTIF3	&1538.822821	&1539.448348	1.251054	999	0.263351264	
ZFP57	&2765.607977	&2766.227484	1.239014	999	0.265661165	
ADAM9	&864.03718	&864.644713	1.215066	95.16792	0.270331129	
TNIP3	&2038.710125	&2039.313059	1.205868	59.71003	0.272152001	
TTYH1	&2169.117291	&2169.692032	1.149482	0.20258	0.283657611	
C19orf47	&2051.910498	&2052.485035	1.149074	999	0.283743078	
COQ3	&1950.060444	&1950.633435	1.145982	999	0.28439184	
AGAP10	&4365.893287	&4366.464795	1.143016	1.64374	0.285015932	
CDT1	&2995.161656	&2995.727373	1.131434	0.2698	0.287469671	
RESP18	&1250.908634	&1251.47242	1.127572	999	0.288293829	
LTK	&4350.685181	&4351.248089	1.125816	999	0.288669556	
HIST1H3F	&761.424527	&761.984014	1.118974	0	0.290139486	
DACT2	&4064.983918	&4065.532616	1.097396	0.39058	0.294838284	
MRPL20	&882.156704	&882.69826	1.083112	0	0.298002422	
LETM2	&522.2911	&522.826157	1.070114	999	0.300919697	
FAM55B	&2830.764502	&2831.288181	1.047358	0.41929	0.306116349	
ZC3H12D	&2708.405165	&2708.892099	0.973868	0.22677	0.323717402	
MBD6	&4425.09935	&4425.579865	0.96103	999	0.326927506	
GPR39	&2381.340044	&2381.804728	0.929368	0.23121	0.335027204	
MS4A7	&1299.62578	&1300.048443	0.845326	999	0.357877961	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
TMEM139	&1120.300863	&1120.708159	0.814592	999	0.366766098	
PDZD7	&2715.583255	&2715.98063	0.79475	0.25305	0.372667683	
CDCA3	&1245.984978	&1246.376144	0.782332	0	0.376428879	
NT5M	&973.009834	&973.400394	0.78112	0.13851	0.376798823	
LHFPL5	&930.235403	&930.622986	0.775166	0	0.378623638	
TIAF1	&617.319593	&617.705035	0.770884	999	0.379943719	
OAS1	&2334.06276	&2334.436485	0.74745	999	0.387284779	
RABEP1	&979.264265	&979.621093	0.713656	999	0.398232774	
IFI27L1	&554.267369	&554.617911	0.701084	0.50137	0.402419694	
MAGEB3	&1942.075798	&1942.42221	0.692824	999	0.405205491	
RAB17	&1170.575145	&1170.921495	0.6927	999	0.405247526	
FAAH2	&2753.416426	&2753.76004	0.687228	999	0.407108844	
CCDC68	&1603.127352	&1603.465271	0.675838	999	0.411023589	
CYP4F11	&2992.977458	&2993.313756	0.672596	0.26305	0.412147985	
TMEM92	&871.960459	&872.29296	0.665002	999	0.414799583	
RBP7	&647.092422	&647.423308	0.661772	0.30354	0.415935057	
DDB2	&2010.177342	&2010.505053	0.655422	999	0.418180817	
PTTG2	&1130.000091	&1130.326211	0.65224	0.52692	0.419312958	
USP26	&5057.706216	&5058.031754	0.651076	0.42527	0.419728244	
FLT3	&4938.253517	&4938.569798	0.632562	999	0.42641711	
ROR2	&4589.329667	&4589.643683	0.628032	0.20933	0.428078109	
STX2	&1320.779601	&1321.092741	0.62628	268.0164	0.428723127	
SLC5A3	&3196.571844	&3196.884746	0.625804	999	0.428898625	
RAD21L1	&2719.695516	&2720.005994	0.620956	0.31691	0.430692252	
SEC13	&1770.09537	&1770.395523	0.600306	999	0.438461297	
CEBPZ	&5166.627957	&5166.926704	0.597494	84.04842	0.439535779	
PNKP	&2844.044506	&2844.340202	0.591392	0.25662	0.441881345	
TRAIP	&2304.273211	&2304.568676	0.59093	34.99832	0.442059719	
LHFPL2	&1092.006558	&1092.300933	0.58875	999	0.442902893	
GNPAT	&3338.206377	&3338.499332	0.58591	0.44518	0.444005069	
RAP1GAP2	&3635.459307	&3635.750293	0.581972	0.30786	0.445540396	
CCDC82	&2745.561522	&2745.847143	0.571242	999	0.4497658	
GALNT12	&3049.405211	&3049.689913	0.569404	999	0.450495848	
GOLGA5	&3483.761731	&3484.045515	0.567568	999	0.45122695	
CISH	&1389.147974	&1389.429033	0.562118	5.47806	0.453408125	
FXYD3	&495.695252	&495.975182	0.55986	0.32943	0.454316656	
BROX	&1817.065536	&1817.33925	0.547428	999	0.45937052	
ZNF117	&3441.582524	&3441.8561	0.547152	999	0.459483726	
NUDCD1	&2710.034863	&2710.305741	0.541756	0.33886	0.461705893	
ZNF335	&6610.053089	&6610.320738	0.535298	0.43571	0.464387947	
LIPH	&2243.962383	&2244.227261	0.529756	999	0.46670946	
L3MBTL1	&3975.333574	&3975.589817	0.512486	999	0.474064662	
ADAM29	&4769.215793	&4769.466421	0.501256	999	0.478948766	
GPHA2	&626.850089	&627.09914	0.498102	999	0.480335276	
SECTM1	&1274.584363	&1274.825759	0.482792	369.29669	0.48716037	
WDR5B	&1588.821342	&1589.060006	0.477328	0.36502	0.489635122	
C20orf160	&2424.832004	&2425.070602	0.477196	1.57476	0.489695166	
TOP3A	&5199.892071	&5200.130384	0.476626	0.34313	0.489954588	
PLEKHB2	&1115.085506	&1115.321588	0.472164	999	0.491993308	
IFI44	&2283.058512	&2283.293406	0.469788	999	0.493084715	
DCAF5	&4503.990134	&4504.215557	0.450846	0.37305	0.501933476	
SQSTM1	&2440.432236	&2440.657104	0.449736	0.33642	0.50246035	
TGM1	&4088.80902	&4089.032568	0.447096	999	0.503717253	
SH3D21	&4135.291753	&4135.501879	0.420252	0.37763	0.516811328	
MRGPRD	&1879.09737	&1879.305858	0.416976	116.16057	0.518449831	
GFOD2	&1868.181908	&1868.388688	0.41356	0.32873	0.520168098	
TXNDC11	&4978.128413	&4978.332201	0.407576	0.3931	0.523202403	
RFX7	&6744.044293	&6744.246216	0.403846	0.39056	0.525109677	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
GRIK3	&4315.394329	&4315.596138	0.403618	0	0.525226661	
PTPRCAP	&1095.627978	&1095.825675	0.395394	0.39882	0.529477626	
IL17RB	&2645.306916	&2645.504435	0.395038	0.40094	0.529663031	
KCNJ9	&1729.745028	&1729.941916	0.393776	0	0.530321224	
PIGA	&2362.640411	&2362.833187	0.385552	0.39718	0.534646775	
PLB1	&7860.541194	&7860.727795	0.373202	0.52072	0.541264056	
LAIR1	&1743.597491	&1743.777454	0.359926	1.42976	0.548547336	
CNTN6	&5057.791791	&5057.971535	0.359488	0.39014	0.548790725	
TJP2	&6016.66355	&6016.842958	0.358816	0.38568	0.549164535	
KMO	&2495.454183	&2495.628979	0.349592	0.41494	0.55434418	
NSUN3	&1619.468181	&1619.639755	0.343148	0.43021	0.558017748	
GPR89A	&1484.143481	&1484.311229	0.335496	0.43226	0.562440626	
ECEL1	&8726.614854	&8726.778221	0.326734	999	0.567588585	
HRH3	&2193.166306	&2193.325811	0.31901	812.58385	0.572203207	
CAPN7	&8742.563227	&8742.722559	0.318664	999	0.57241164	
MAP2	&8749.62696	&8749.785583	0.317246	0.56106	0.573267418	
OR5AS1	&1664.239869	&1664.397638	0.315538	0	0.574301564	
KIAA0562	&4759.565356	&4759.723116	0.31552	0.65542	0.574312482	
SLC35C1	&1828.303251	&1828.46096	0.315418	999	0.574374359	
MRGPRE	&1602.311526	&1602.467673	0.312294	999	0.576275895	
TMEM61	&1209.070843	&1209.213483	0.28528	999	0.593261217	
LRRC2	&1794.279894	&1794.4133	0.266812	0.47528	0.605478371	
WFDC6	&441.656817	&441.78939	0.265146	0.44209	0.606606622	
UGT1A3	&2747.916444	&2748.045725	0.258562	0.45144	0.611109806	
MIER1	&1901.459218	&1901.583286	0.248136	999	0.618390646	
SEC14L5	&8456.649112	&8456.772528	0.246832	999	0.61931465	
CYLC1	&8426.411935	&8426.521568	0.219266	1.30261	0.63959976	
TMEM105	&687.131697	&687.236044	0.208694	2.16394	0.647792965	
ABCD3	&8242.758057	&8242.857561	0.199008	0	0.655522754	
VCX2	&904.830757	&904.920349	0.179184	1.68053	0.672075438	
FAM165B	&284.464755	&284.553788	0.178066	0.64602	0.673040585	
CCDC73	&5510.577903	&5510.666795	0.177784	0.57734	0.673284593	
GOLGA6C	&5060.831146	&5060.914399	0.166506	0.81777	0.68323589	
GUCY2F	&5371.948435	&5372.019772	0.142674	0.61794	0.705637034	
ZNF528	&8226.349278	&8226.416455	0.134354	0.71224	0.713959699	
KIAA0947	&12218.85769	&12218.9244	0.133426	0.72666	0.71490596	
LRRC27	&2939.37391	&2939.423821	0.099822	0.7396	0.752043346	
DARC	&1864.001354	&1864.047472	0.092236	0.64269	0.76135356	
SCT	&525.146919	&525.186443	0.079048	0	0.778591701	
SCN1B	&1019.185063	&1019.223427	0.076728	0	0.781781492	
LPAR3	&1796.170113	&1796.206437	0.072648	0.71034	0.787519606	
PAX9	&1574.295182	&1574.327815	0.065266	999	0.798358481	
FCRL2	&8056.35679	&8056.387021	0.060462	0.75284	0.805767215	
IRX6	&2443.467779	&2443.49703	0.058502	1.32566	0.80887945	
TMEM194A	&2095.58885	&2095.607294	0.036888	0.87057	0.847693257	
ZFYVE20	&8771.420627	&8771.438358	0.035462	0.78398	0.85063085	
PRSS55	&2132.107381	&2132.116163	0.017564	0.8335	0.894565695	
EXPH5	&10701.22764	&10701.23624	0.017214	0.85798	0.895615408	
CASP8	&2454.041737	&2454.047332	0.01119	2.15631	0.915754687	
OR13J1	&1778.883619	&1778.888803	0.010368	0.88015	0.91889687	
C11orf80	&8563.685039	&8563.690105	0.010132	1.1295	0.919822083	
EBI3	&1154.072012	&1154.075636	0.007248	0.85606	0.932153917	
MLXIPL	&8536.737288	&8536.740753	0.00693	0.24058	0.933655443	
IDO2	&2230.098491	&2230.10139	0.005798	0.90369	0.939304058	
ARL6IP1	&939.558112	&939.560375	0.004526	207.83281	0.946362339	
SLC4A4	&4931.993535	&4931.995535	0.004	0	0.949570971	
CARD11	&5919.132599	&5919.134239	0.00328	0	0.954329095	
C19orf68	&8320.049954	&8320.051335	0.002762	0	0.958086685	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
C17orf51	&1210.510423	&1210.511725	0.002604	1.05602	0.959302091	
NUP88	&3817.046408	&3817.047581	0.002346	0	0.961369148	
TMEM232	&3272.151622	&3272.152756	0.002268	0	0.962016284	
SLC6A4	&3062.301389	&3062.302455	0.002132	0	0.963171896	
MLLT6	&4826.511905	&4826.512759	0.001708	0	0.967034446	
MAP4K5	&5020.275066	&5020.275901	0.00167	0	0.967403015	
ABHD4	&1660.994394	&1660.995214	0.00164	0	0.967696968	
PLCB1	&5510.573869	&5510.574635	0.001532	0	0.968778155	
ZNF157	&2379.433983	&2379.434736	0.001506	0	0.969044092	
CDK13	&6756.597766	&6756.598492	0.001452	0	0.969603871	
TSPAN8	&1578.640012	&1578.640594	0.001164	0	0.972783498	
ZNF192	&2773.180244	&2773.180818	0.001148	0	0.972971128	
CDC37	&1707.086323	&1707.086849	0.001052	0	0.97412551	
DHRS7	&1626.309857	&1626.310371	0.001028	0	0.974422257	
G6PC	&1733.835289	&1733.835798	0.001018	0	0.974546924	
ZNF575	&1660.838958	&1660.839364	0.000812	0	0.977266866	
EXD1	&2906.588425	&2906.588786	0.000722	0	0.978563375	
MAP3K7	&2660.905167	&2660.905496	0.000658	0	0.9795353	
LAPTM4B	&2137.507358	&2137.507686	0.000656	0	0.979566418	
SMC2	&5402.889178	&5402.889498	0.00064	0	0.979817093	
ZBP1	&2567.330081	&2567.330399	0.000636	0	0.97988025	
RBBP6	&8240.593348	&8240.593648	0.0006	0	0.980457854	
ZNF302	&2362.241409	&2362.241689	0.00056	0	0.981120367	
OR51F2	&1557.560046	&1557.560317	0.000542	0	0.981426212	
FGF2	&1339.770921	&1339.771184	0.000526	0	0.981702369	
PPM1E	&3396.768092	&3396.768301	0.000418	0	0.983688348	
HES5	&658.879445	&658.87964	0.00039	0	0.984244067	
SOAT2	&2726.300451	&2726.300637	0.000372	0	0.984611914	
TBC1D17	&3152.761375	&3152.761536	0.000322	0	0.985683242	
ZNF569	&3122.819688	&3122.819848	0.00032	0	0.985727768	
ALKBH3	&1306.239688	&1306.239847	0.000318	0	0.985772434	
MRPL55	&878.061482	&878.061626	0.000288	0	0.9864601	
DDTL	&774.799386	&774.799523	0.000274	0	0.986793264	
NR1D2	&2651.174757	&2651.174893	0.000272	0	0.986841547	
FBXL12	&1532.754325	&1532.754455	0.00026	0	0.987135056	
LEPREL4	&1976.363692	&1976.363821	0.000258	0	0.987184627	
POU2F2	&2166.079504	&2166.079632	0.000256	0	0.987234392	
TAC4	&627.99489	&627.995008	0.000236	0	0.987743147	
RCN2	&1491.694128	&1491.694243	0.00023	0	0.987899945	
CCL24	&713.149783	&713.149897	0.000228	0	0.987952665	
FMO6P	&713.11874	&713.118854	0.000228	0	0.987952665	
SUMF1	&1881.996088	&1881.996202	0.000228	0	0.987952665	
OR2J3	&1698.407857	&1698.40797	0.000226	0	0.988005617	
TUBB	&2154.245572	&2154.245677	0.00021	0	0.988437959	
OVOL2	&1302.354606	&1302.35471	0.000208	0	0.988493144	
LHX2	&1796.598767	&1796.59887	0.000206	0	0.988548595	
MSRB2	&999.36647	&999.366572	0.000204	0	0.988604316	
RGS18	&1078.748923	&1078.749024	0.000202	0	0.988660311	
PLK2	&3091.218554	&3091.218652	0.000196	0	0.988829981	
CYTH1	&1782.949154	&1782.949251	0.000194	0	0.988887113	
PRRC1	&2120.586891	&2120.586985	0.000188	0	0.989060301	
TBXA2R	&1671.256651	&1671.256743	0.000184	0	0.989177299	
LSM7	&453.51219	&453.51228	0.00018	0	0.989295576	
ME2	&2646.488508	&2646.488596	0.000176	0	0.989415176	
MBTPS2	&2424.127336	&2424.127422	0.000172	0	0.989536142	
DNAJC5G	&1132.628472	&1132.628557	0.00017	0	0.989597153	
GSC	&1065.457454	&1065.457539	0.00017	0	0.989597153	
RHOB	&856.699882	&856.699966	0.000168	0	0.989658524	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
ZCCHC17	&1050.546673	&1050.546753	0.00016	0	0.989907739	
HNRPLL	&2492.6402	&2492.640278	0.000156	0	0.990034684	
SUV39H1	&1814.111869	&1814.111946	0.000154	0	0.990098767	
DLX6	&1107.77776	&1107.777834	0.000148	0	0.990293555	
CDK9	&1677.649241	&1677.649313	0.000144	0	0.990425615	
ITGB3BP	&887.421805	&887.421874	0.000138	0	0.990627194	
TMEM42	&680.488313	&680.488382	0.000138	0	0.990627194	
UBLCP1	&1381.406973	&1381.407042	0.000138	0	0.990627194	
CCRL1	&1662.592932	&1662.592993	0.000122	0	0.991187256	
FOLR2	&1278.385347	&1278.385404	0.000114	0	0.991481086	
DERL1	&1106.312857	&1106.312913	0.000112	0	0.991556141	
RAE1	&1759.923538	&1759.923591	0.000106	0	0.991785421	
CHMP5	&937.877506	&937.877558	0.000104	0	0.991863283	
YTHDC1	&3081.268473	&3081.268522	9.8E&05	0	0.992101475	
C9orf9	&840.437387	&840.437434	9.4E&05	0	0.992264343	
DMGDH	&4203.956754	&4203.9568	9.2E&05	0	0.992347077	
TMEM18	&652.610728	&652.610774	9.2E&05	0	0.992347077	
IRF8	&2086.868892	&2086.868937	9E&05	0	0.992430716	
MSL2	&2521.142295	&2521.14234	9E&05	0	0.992430716	
TSSK2	&1694.098684	&1694.098728	8.8E&05	0	0.992515289	
GPR176	&2457.061547	&2457.06159	8.6E&05	0	0.992600829	
DIRC2	&2215.782118	&2215.782159	8.2E&05	0	0.992774947	
METAP1D	&1550.472561	&1550.4726	7.8E&05	0	0.992953366	
RNF11	&655.292812	&655.29285	7.6E&05	0	0.993044292	
DNAJC24	&685.156696	&685.156733	7.4E&05	0	0.993136422	
WISP3	&1792.582005	&1792.582042	7.4E&05	0	0.993136422	
CD2AP	&3055.097345	&3055.097382	7.4E&05	0	0.993136422	
MED7	&980.949485	&980.949521	7.2E&05	0	0.993229806	
PRKRIP1	&906.450117	&906.450153	7.2E&05	0	0.993229806	
B4GALT5	&1751.845412	&1751.845447	7E&05	0	0.993324497	
FAM167A	&1035.199304	&1035.199339	7E&05	0	0.993324497	
TAGLN	&885.165761	&885.165796	7E&05	0	0.993324497	
TMCC3	&2204.330259	&2204.330293	6.8E&05	0	0.99342055	
NPY1R	&1730.458241	&1730.458273	6.4E&05	0	0.993616992	
ORC2	&2609.560098	&2609.560127	5.8E&05	0	0.993923551	
C9orf46	&559.674775	&559.674804	5.8E&05	0	0.993923551	
GUCA1B	&890.171812	&890.17184	5.6E&05	0	0.994029234	
ZFP37	&3100.920717	&3100.920744	5.4E&05	0	0.994136823	
C10orf11	&975.762908	&975.762935	5.4E&05	0	0.994136823	
HIST1H2AJ	&620.351488	&620.351515	5.4E&05	0	0.994136823	
FBXO22	&1930.720812	&1930.720838	5.2E&05	0	0.994246422	
ICT1	&1155.089212	&1155.089238	5.2E&05	0	0.994246422	
VPREB1	&805.815411	&805.815437	5.2E&05	0	0.994246422	
CPB2	&2230.708687	&2230.708711	4.8E&05	0	0.994472138	
PNMA1	&1586.9628	&1586.962823	4.6E&05	0	0.994588525	
TNFAIP8L3	&1465.138268	&1465.138291	4.6E&05	0	0.994588525	
CACNG6	&1274.568042	&1274.568065	4.6E&05	0	0.994588525	
EPT1	&1772.758409	&1772.758431	4.4E&05	0	0.994707471	
TMEM179	&904.10152	&904.101542	4.4E&05	0	0.994707471	
POLR2F	&562.780971	&562.780992	4.2E&05	0	0.994829153	
NDP	&595.33534	&595.33536	4E&05	0	0.994953769	
C1orf27	&2081.132271	&2081.132291	4E&05	0	0.994953769	
DCAF7	&1558.92311	&1558.923129	3.8E&05	0	0.99508154	
RGS8	&885.363464	&885.363483	3.8E&05	0	0.99508154	
MAGEA8	&1513.628707	&1513.628726	3.8E&05	0	0.99508154	
MRPL21	&1129.843944	&1129.843962	3.6E&05	0	0.995212721	
TTC29	&2306.847532	&2306.847549	3.4E&05	0	0.9953476	
DRAP1	&964.998803	&964.99882	3.4E&05	0	0.9953476	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
SMR3B	&486.84025	&486.840267	3.4E&05	0	0.9953476	
CORO1C	&2136.312124	&2136.312141	3.4E&05	0	0.9953476	
SNRPA1	&1117.342329	&1117.342346	3.4E&05	0	0.9953476	
METTL6	&1402.772109	&1402.772124	3E&05	0	0.995629828	
OR14A2	&1605.945376	&1605.945391	3E&05	0	0.995629828	
WFDC11	&494.399787	&494.399801	2.8E&05	0	0.995778011	
ZNRD1	&572.059202	&572.059216	2.8E&05	0	0.995778011	
SLC45A2	&2718.501206	&2718.501219	2.6E&05	0	0.995931589	
CCDC69	&1442.396532	&1442.396545	2.6E&05	0	0.995931589	
ASB1	&1625.070218	&1625.07023	2.4E&05	0	0.996091196	
CHST2	&2516.659292	&2516.659304	2.4E&05	0	0.996091196	
LRRTM3	&2556.673976	&2556.673988	2.4E&05	0	0.996091196	
NR1I3	&1719.752585	&1719.752597	2.4E&05	0	0.996091196	
STH	&712.60433	&712.604342	2.4E&05	0	0.996091196	
TSSK4	&1833.803054	&1833.803066	2.4E&05	0	0.996091196	
SLC22A17	&2376.654799	&2376.65481	2.2E&05	0	0.996257603	
TMEM208	&764.313317	&764.313328	2.2E&05	0	0.996257603	
OR6X1	&1673.053249	&1673.05326	2.2E&05	0	0.996257603	
MOCS3	&2332.974214	&2332.974224	2E&05	0	0.996431764	
GEMIN7	&641.842101	&641.842111	2E&05	0	0.996431764	
GNAT2	&1603.34031	&1603.34032	2E&05	0	0.996431764	
ZC4H2	&923.282204	&923.282214	2E&05	0	0.996431764	
C14orf180	&1004.156928	&1004.156937	1.8E&05	0	0.996614873	
C8orf40	&467.375964	&467.375973	1.8E&05	0	0.996614873	
FAM103A1	&520.816492	&520.816501	1.8E&05	0	0.996614873	
IFNA2	&1006.051632	&1006.051641	1.8E&05	0	0.996614873	
C9orf142	&1044.044013	&1044.044021	1.6E&05	0	0.99680847	
COX5B	&679.311418	&679.311426	1.6E&05	0	0.99680847	
NDUFA6	&805.108293	&805.108301	1.6E&05	0	0.99680847	
THY1	&745.905301	&745.905309	1.6E&05	0	0.99680847	
PFDN6	&550.824183	&550.82419	1.4E&05	0	0.997014596	
HLF	&1269.765225	&1269.765232	1.4E&05	0	0.997014596	
TMEM106B	&1217.607899	&1217.607906	1.4E&05	0	0.997014596	
CNPY1	&413.535209	&413.535215	1.2E&05	0	0.997236052	
FOSB	&1438.019208	&1438.019214	1.2E&05	0	0.997236052	
HNRNPD	&1491.679038	&1491.679044	1.2E&05	0	0.997236052	
DNAJC17	&1458.535917	&1458.535922	1E&05	0	0.997476872	
BET1	&508.096101	&508.096106	1E&05	0	0.997476872	
S100A4	&429.46254	&429.462545	1E&05	0	0.997476872	
FAM64A	&1282.482651	&1282.482656	1E&05	0	0.997476872	
HAUS2	&1109.529254	&1109.529259	1E&05	0	0.997476872	
MDM4	&2142.535366	&2142.535371	1E&05	0	0.997476872	
AGPAT2	&1422.236606	&1422.23661	8E&06	0	0.997743245	
DEFB110	&340.49901	&340.499014	8E&06	0	0.997743245	
GNG5P2	&353.079636	&353.07964	8E&06	0	0.997743245	
VSIG1	&2093.71478	&2093.714784	8E&06	0	0.997743245	
RPS23	&645.084004	&645.084007	6E&06	0	0.998045592	
PGAM1	&1123.194261	&1123.194264	6E&06	0	0.998045592	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
ATP5H	&762.138313	&762.138314	2E&06	0	0.998871621	
C22orf41	&894.97054	&894.970541	2E&06	0	0.998871621	
DCTN6	&847.906571	&847.906571	0	0	1	
NXT1	&642.059909	&642.059909	0	0	1	
PLS3	&2743.014314	&2743.014314	0	0	1	
ABHD10	&1500.948167	&1500.948148	&3.8E&05	0	#NUM!	
ARV1	&1317.520583	&1317.520561	&4.4E&05	0	#NUM!	
ATAD5	&9298.161842	&9296.379697	&3.56429	85.1273	#NUM!	
BLNK	&2338.664863	&2338.664601	&0.000524	0	#NUM!	
C11orf40	&1331.198557	&1331.198442	&0.00023	0	#NUM!	
C7orf60	&1897.635709	&1791.770797	&211.729824	0	#NUM!	
C8orf39	&460.662943	&460.66294	&6E&06	0	#NUM!	
CCDC115	&881.708195	&881.708107	&0.000176	0	#NUM!	
CDC20	&2511.834628	&2292.43512	&438.799016	0	#NUM!	
CEP78	&3500.900133	&3500.900072	&0.000122	0	#NUM!	
CLEC4E	&1202.006962	&1202.006957	&1E&05	0	#NUM!	
DDHD2	&3298.987578	&3298.987021	&0.001114	0	#NUM!	
DNAJC30	&1248.118556	&1248.118393	&0.000326	0	#NUM!	
DSCR3	&1519.806963	&1519.806957	&1.2E&05	0	#NUM!	
ENOPH1	&1178.249991	&1178.24998	&2.2E&05	0	#NUM!	
EPB49	&1818.38214	&1818.382135	&1E&05	0	#NUM!	
FAM126B	&2587.999087	&2587.998747	&0.00068	0	#NUM!	
FAM131A	&1505.714846	&1321.308695	&368.812302	0	#NUM!	
FANCG	&3680.959494	&3680.959486	&1.6E&05	0	#NUM!	
GADD45A	&733.845815	&733.845806	&1.8E&05	0	#NUM!	
GFRAL	&2057.282264	&2057.282237	&5.4E&05	0	#NUM!	
KPTN	&2402.789052	&2402.788779	&0.000546	0	#NUM!	
LSM10	&597.904068	&586.6729	&22.462336	0.10826	#NUM!	
MAP4K4	&6065.313196	&6065.298835	&0.028722	0	#NUM!	
MAT2A	&1792.739565	&1792.739324	&0.000482	0	#NUM!	
MEGF10	&5515.705644	&5515.705535	&0.000218	0	#NUM!	
MFSD6L	&3312.353011	&3312.352576	&0.00087	0	#NUM!	
MRPL43	&1379.251502	&1379.251489	&2.6E&05	0	#NUM!	
NCKAP1L	&5397.166142	&5397.166014	&0.000256	0	#NUM!	
NPY5R	&2009.450533	&1990.417926	&38.065214	0	#NUM!	
OAZ2	&820.725354	&820.725343	&2.2E&05	0	#NUM!	
OR10G3	&1724.388195	&1724.38818	&3E&05	0	#NUM!	
OR1A2	&1764.083024	&1540.316512	&447.533024	0	#NUM!	
PAFAH1B1	&1902.931105	&1902.931086	&3.8E&05	0	#NUM!	
PLP1	&1162.283125	&1162.283105	&4E&05	0	#NUM!	
POGK	&2869.754602	&2869.754599	&6E&06	0	#NUM!	
PYGO2	&1791.658471	&1791.658431	&8E&05	0	#NUM!	
RC3H1	&5132.544852	&5132.544831	&4.2E&05	0	#NUM!	
SDC2	&947.716091	&947.716088	&6E&06	0	#NUM!	
SHPRH	&8159.357533	&8159.356365	&0.002336	0	#NUM!	
SLC31A1	&859.479825	&859.479754	&0.000142	0	#NUM!	
SPIB	&1131.721229	&1095.852575	&71.737308	0	#NUM!	
SREK1	&2924.686733	&2713.300435	&422.772596	0	#NUM!	
SYNJ2BP	&724.447072	&647.257628	&154.378888	0	#NUM!	
TBCB	&1153.229238	&1153.229233	&1E&05	0	#NUM!	
TBR1	&3035.125571	&2895.650034	&278.951074	0	#NUM!	
TBRG1	&1916.754365	&1916.754363	&4E&06	0	#NUM!	
TSPAN15	&1377.409713	&1377.409477	&0.000472	0	#NUM!	
USP7	&5101.739955	&4826.663192	&550.153526	0	#NUM!	
WDFY2	&2004.964725	&1824.215586	&361.498278	0	#NUM!	
WDR33	&6521.260181	&6005.821727	&1030.876908	0	#NUM!	
WDR63	&4327.07081	&4325.137253	&3.867114	126.62538	#NUM!	
ZMYND17	&2328.698889	&2328.698543	&0.000692	0	#NUM!	

Stem-African Branch

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
NCOR2	&12226.76119	&12255.48136	57.440354	0.04126	3.48386E&14	
TBC1D17	&3149.808429	&3172.181383	44.745908	0	2.24335E&11	
COL20A1	&6578.609415	&6597.937171	38.655512	0.11948	5.05603E&10	
APC2	&11995.98568	&12015.29922	38.627094	0.05514	5.13018E&10	
ANO1	&4808.807642	&4827.517367	37.41945	0.0225	9.52673E&10	
SIPA1	&4988.243183	&5004.138056	31.789746	0.03736	1.71797E&08	
CARD11	&5916.43749	&5931.5106	30.14622	0	4.00667E&08	
ROR2	&4587.959533	&4603.009644	30.100222	0	4.10284E&08	
ISYNA1	&2711.539466	&2726.499007	29.919082	0.02048	4.50458E&08	
ERCC3	&3774.788535	&3789.588997	29.600924	0	5.30796E&08	
GFOD2	&1868.499389	&1882.412927	27.827076	0	1.32657E&07	
GALNT12	&3045.606703	&3059.346869	27.480332	0	1.587E&07	
GPT2	&2462.812155	&2475.976071	26.327832	0	2.88107E&07	
TNS3	&7653.246782	&7666.12531	25.757056	0.02751	3.87209E&07	
JAG2	&6296.359299	&6308.542877	24.367156	0.03936	7.96145E&07	
TGM1	&4089.963702	&4102.110126	24.292848	0.04721	8.27457E&07	
DEF8	&2630.693066	&2642.804933	24.223734	0.02121	8.57688E&07	
SHPRH	&157.22595	&169.256035	24.06017	0.03045	9.33718E&07	
GRIK3	&4314.72352	&4326.608045	23.76905	0	1.08615E&06	
RALGDS	&4387.358051	&4399.158803	23.601504	0.0914	1.18495E&06	
LDB3	&929.626955	&941.322404	23.390898	0	1.32203E&06	
SULF2	&4178.048464	&4189.474514	22.8521	0	1.74958E&06	
SQSTM1	&2438.58601	&2449.810739	22.449458	0.02906	2.15746E&06	
KIDINS220	&391.88038	&403.099968	22.439176	0.06098	2.16904E&06	
PITPNM1	&6236.475966	&6247.637874	22.323816	0.09473	2.30332E&06	
ASCC3	&10025.81575	&10036.35066	21.069816	0.08323	4.42849E&06	
KRT36	&2447.987451	&2458.444064	20.913226	0.07262	4.80565E&06	
NCKAP1L	&5394.395103	&5404.827523	20.86484	0	4.92859E&06	
CCDC132	&4368.569278	&4378.923501	20.708446	0	5.34796E&06	
TJP2	&6016.286143	&6026.584522	20.596758	0.11889	5.6692E&06	
DCAF12L2	&2616.682882	&2626.908674	20.451584	0.02633	6.11589E&06	
SCG3	&2149.29243	&2159.480649	20.376438	0	6.36082E&06	
ZFP64	&3247.115997	&3257.237596	20.243198	0	6.81955E&06	
GUCY2F	&5370.884863	&5380.666735	19.563744	0.1075	9.72982E&06	
PPP2R2C	&2050.833813	&2060.517554	19.367482	0	1.07828E&05	
KIAA0947	&12216.28179	&12225.91181	19.260042	0.1378	1.14069E&05	
SLIT1	&7420.092485	&7429.712644	19.240318	0.02595	1.15253E&05	
ARHGAP4	&5882.357809	&5891.96544	19.215262	0.08164	1.16776E&05	
C19orf68	&3316.664051	&3326.256106	19.18411	0	1.18697E&05	
ITGB8	&3615.066507	&3624.589277	19.04554	0	1.27636E&05	
PLCH2	&7497.036966	&7506.223178	18.372424	0.2046	1.81668E&05	
ASPH	&3779.265783	&3788.273015	18.014464	0	2.19233E&05	
GJA4	&1635.681086	&1644.681433	18.000694	0	2.20824E&05	
PLK2	&3091.217087	&3100.019942	17.60571	0.09359	2.71771E&05	
GSC	&1064.351766	&1073.14961	17.595688	0	2.73207E&05	
RAP1GAP2	&3635.013946	&3643.7967	17.565508	0.0057	2.77578E&05	
SPTB	&11267.94849	&11276.7153	17.533618	0.0865	2.82272E&05	
RABEP1	&979.264031	&987.989805	17.451548	0	2.94724E&05	
BCL9L	&7012.657057	&7021.322653	17.331192	0.03523	3.1399E&05	
ZNF335	&6610.616322	&6619.065339	16.898034	0.15553	3.94424E&05	
ZNF574	&4509.463711	&4517.854105	16.780788	0.04005	4.19559E&05	
EXPH5	&10697.4749	&10705.62485	16.2999	0.19645	5.40668E&05	
PRKCD	&3136.353756	&3144.491498	16.275484	0.03314	5.4768E&05	
PRRC1	&2117.177895	&2125.211882	16.067974	0	6.11088E&05	
ZNF275	&2173.630682	&2181.613382	15.9654	0.05436	6.45108E&05	
PDZD7	&2715.534572	&2723.333265	15.597386	0.09684	7.83628E&05	
SEMA4B	&998.306695	&4005.905886	15.198382	0.15057	9.67863E&05	
CDC37	&1706.866037	&1714.456596	15.181118	0	9.76752E&05	
KCNB1	&940.558299	&947.778691	14.440784	0	0.000144636	
ADNP2	&611.924025	&619.113529	14.379008	0.19857	0.000149459	
SV2B	&190.637306	&197.683976	14.09334	0	0.000173959	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
CDT1	&2995.125444	&3002.127182	14.003476	0.11372	0.000182473	
SLC22A17	&2376.307116	&2383.208488	13.802744	0	0.000203039	
GCK	&2423.274594	&2430.137897	13.726606	0	0.000211438	
C11orf84	&2727.28602	&2734.007289	13.442538	0	0.000245983	
EIF2C2	&4034.142667	&4040.832145	13.378956	0	0.000254463	
ALOX15	&3885.356229	&3892.016612	13.320766	0.15	0.000262483	
CHL1	&6212.605801	&6219.236117	13.260632	0.1906	0.000271038	
MAP4K5	&5016.277273	&5022.838367	13.122188	0.04451	0.000291819	
EPB41L1	&4096.554715	&4103.078163	13.046896	0.04452	0.000303787	
ZC3H13	&7601.464352	&7607.875697	12.82269	0.04748	0.000342441	
PPP1R12A	&4525.893269	&4532.274843	12.763148	0	0.000353515	
ANKRD52	&5051.439927	&5057.79629	12.712726	0	0.000363176	
RPS23	&645.084014	&651.427258	12.686488	0	0.000368307	
RBBP6	&8240.559246	&8246.862008	12.605524	0.16151	0.000384608	
COL5A2	&6699.087788	&6705.390548	12.60552	0.05721	0.000384609	
FLT3	&4937.746612	&4944.02023	12.547236	0.09491	0.000396793	
LHFPL2	&1091.865304	&1098.055106	12.379604	0	0.000434049	
ECEL1	&3728.282553	&3734.460359	12.355612	0.0329	0.000439663	
SLC25A23	&2100.449928	&2106.602643	12.30543	0	0.000451642	
SEC14L5	&3456.796632	&3462.801335	12.009406	0.10546	0.000529327	
MEGF10	&5515.701478	&5521.601364	11.799772	0.06653	0.00059238	
TBR1	&2895.527645	&2901.396749	11.738208	0	0.0006123	
TBXA2R	&1670.259789	&1675.950278	11.380978	0	0.000742	
TUBB	&2152.516081	&2158.206093	11.380024	0	0.000742382	
DENND4B	&7194.430631	&7200.116962	11.372662	0.14591	0.00074533	
GUCA1B	&890.171812	&895.820231	11.296838	0	0.000776392	
AGGF1	&3401.252241	&3406.833448	11.162414	0.06786	0.000834712	
DCAF7	&1558.772538	&1564.350562	11.156048	0	0.000837582	
GNAT2	&1602.68592	&1608.2293	11.08676	0	0.000869463	
ABCB11	&6821.947899	&6827.446758	10.997718	0.15502	0.000912241	
CYTH1	&1782.854203	&1788.346201	10.983996	0	0.000919021	
PNPT1	&3659.259013	&3664.738242	10.958458	0.12285	0.000931773	
ZC3H12D	&2708.142612	&2713.581217	10.87721	0.12119	0.000973548	
HMGCR	&4418.932641	&4424.261344	10.657406	0	0.00109631	
ZNF302	&2358.944869	&2364.167823	10.445908	0.03333	0.001229215	
WDR5B	&1587.008329	&1592.194036	10.371414	0	0.001279815	
SMC2	&5402.84935	&5407.962123	10.225546	0.07279	0.001385087	
CPA5	&2348.86732	&2353.886784	10.038928	0.10082	0.001532664	
SEC13	&1770.295111	&1775.243785	9.897348	0	0.001655171	
L3MBTL1	&975.982017	&980.927646	9.891258	0.31033	0.001660658	
KIAA0562	&4759.947326	&4764.869964	9.845276	0.14233	0.001702684	
PLCB1	&5510.056541	&5514.899483	9.685884	0	0.00185689	
MRGPRD	&1877.798272	&1882.59662	9.596696	0.12435	0.001949278	
RC3H1	&5132.519696	&5137.293045	9.546698	0.11409	0.002003094	
PNPLA7	&6802.432818	&6807.198518	9.5314	0.17443	0.00201986	
MLLT6	&4826.495325	&4831.210825	9.431	0.06346	0.002133479	
ZNF235	&659.374531	&664.010601	9.27214	0.05247	0.002326657	
FAM167A	&1034.761007	&1039.278242	9.03447	0.05187	0.002649359	
VPS52	&325.160935	&329.673391	9.024912	0	0.002663247	
FZR1	&2351.474308	&2355.938634	8.928652	0	0.002807315	
GNAO1	&2114.322465	&2118.781968	8.919006	0	0.002822181	
TSSK4	&1830.95065	&1835.361014	8.820728	0.06736	0.002978278	
USP7	&4826.56136	&4830.942813	8.762906	0	0.003074188	
C1orf101	&5587.584583	&5591.943392	8.717618	0.2613	0.003151495	
CDK9	&1677.483095	&1681.78625	8.60631	0	0.003350003	
FBXL12	&1532.524412	&1536.770874	8.492924	0	0.003565304	
SLC6A4	&3061.66891	&3065.90812	8.47842	0	0.003593841	
HNRPLL	&2492.318825	&2496.499446	8.361242	0	0.003833085	
MDM4	&142.266916	&146.429777	8.325722	0.06962	0.00390876	
SHMT2	&2376.288015	&2380.408522	8.241014	0.07308	0.004095425	
CWC22	&4318.549364	&4322.631608	8.164488	0.06515	0.004271853	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
FOLR2	&1277.346789	&1281.39236	8.091142	0	0.004448212	
DCAF5	&4504.264498	&4508.289341	8.049686	0.12016	0.004551154	
PLB1	&7860.635949	&7864.554938	7.837978	0.35031	0.00511598	
TEKT5	&2693.8045	&2697.67228	7.73556	0	0.005414377	
KDM5D	&8474.873112	&8478.700672	7.65512	0.24703	0.005661143	
POFUT2	&2134.606796	&2138.366207	7.518822	0.16983	0.00610576	
FKRP	&2437.646236	&2441.404721	7.51697	0.05127	0.00611204	
DGAT1	&2575.722343	&2579.452768	7.46085	0.07896	0.006305523	
TBC1D9	&5834.1755	&5837.880969	7.410938	0	0.006482851	
HEYL	&1751.002518	&1754.67059	7.336144	0.12508	0.006758165	
PCDHA3	&4896.608826	&4900.247439	7.277226	0.21668	0.00698343	
SLC24A4	&2703.995431	&2707.623212	7.255562	0	0.007068175	
PDK3	&1819.353725	&1822.970883	7.234316	0	0.007152305	
THY1	&745.800046	&749.401829	7.203566	0.06175	0.007275886	
CISH	&1388.20683	&1391.768459	7.123258	0	0.007609031	
KPTN	&2402.354421	&2405.915568	7.122294	0.14889	0.007613123	
GPR179	&14282.19716	&14285.73686	7.079398	0.50479	0.00779752	
NPY1R	&1730.160164	&1733.69718	7.074032	0	0.007820906	
ATG16L1	&2891.913076	&2895.404163	6.982174	0.08154	0.008232554	
C19orf47	&2054.588303	&2058.079389	6.982172	0.11996	0.008232564	
ALDH1A3	&2496.575281	&2499.995583	6.840604	0.18522	0.008910871	
GCGR	&2923.560561	&2926.952272	6.783422	0.13911	0.009200833	
PCDHB5	&4601.997775	&4605.376579	6.757608	0.12167	0.009334881	
ZNF157	&2377.787385	&2381.127054	6.679338	0	0.009753684	
BLNK	&2337.367671	&2340.697782	6.660222	0	0.009858863	
DLEC1	&9085.9397	&9089.2361	6.5928	0.26538	0.0102392	
SLC31A1	&857.86755	&861.132328	6.529556	0	0.010609644	
MAP2	&8749.797656	&8753.052094	6.508876	0.29123	0.010733733	0.014534884
TMEM43	&2110.109353	&2113.349538	6.48037	0.13254	0.010907228	
CXCR5	&1774.073775	&1777.279492	6.411434	0.05916	0.011338781	
WDR63	&4324.477182	&4327.665508	6.376652	0.21471	0.011563136	
CYP4F11	&2992.920926	&2996.089138	6.336424	0.19435	0.011828311	
ILKAP	&1841.003292	&1844.151914	6.297244	0.14038	0.012092583	
CHRDL2	&2445.551485	&2448.684117	6.265264	0.16736	0.012312782	
GCDH	&2327.814361	&2330.925383	6.222044	0.06379	0.012616937	
MRPL55	&876.080449	&879.163052	6.165206	0	0.01302872	
ROBO4	&5267.419965	&5270.470384	6.100838	0.30722	0.013511779	
HIST1H2AJ	&620.351488	&623.368323	6.03367	0	0.014035522	0.015503876
DNAJC24	&684.160553	&687.176184	6.031262	0	0.014054681	0.015600775
DUSP1	&1011.279256	&1014.283759	6.009006	0	0.014233043	0.015697674
FBXO22	&1930.475905	&1933.462392	5.972974	0.1223	0.014526761	0.015794574
ASH2L	&2901.967916	&2904.946206	5.95658	0.0887	0.014662456	0.015891473
ZNF592	&5979.199189	&5982.136192	5.874006	0.15807	0.015366046	0.015988372
SLC35C1	&1829.437693	&1832.356887	5.838388	0.10367	0.015680186	0.016085271
WDR74	&1903.316399	&1906.229986	5.827174	0	0.015780454	0.016182171
RABGGTA	&2637.657361	&2640.568393	5.822064	0.09739	0.015826363	0.01627907
COQ3	&1948.919865	&1951.777577	5.715424	0.09059	0.016816503	0.016375969
HM13	&1873.924375	&1876.758864	5.668978	0	0.017267513	0.016472868
RGS8	&884.7928	&887.615546	5.645492	0	0.017500305	
LHX2	&1796.376747	&1799.199463	5.645432	0	0.017500904	
TTLL9	&2360.065156	&2362.881841	5.63337	0	0.017621722	
CYP3A5	&2729.862733	&2732.663172	5.600878	0.19751	0.017951479	
PRPF4B	&4588.307034	&4591.08852	5.562972	0	0.018344247	
EPB49	&1818.272964	&1821.053551	5.561174	0	0.018363096	
TSPAN15	&1376.987117	&1379.758065	5.541896	0	0.018566457	
SFRP1	&1508.535455	&1511.294835	5.51876	0	0.01881359	
PNMA1	&1586.264908	&1589.010128	5.49044	0	0.01912073	
CHMP5	&937.877506	&940.621842	5.488672	0	0.019140076	0.01744186
GPR176	&2456.498268	&2459.240593	5.48465	0	0.01918416	
TNFAIP8L3	&1464.257273	&1466.982221	5.449896	0	0.019569492	
CLK4	&2165.424532	&2168.149308	5.449552	0	0.019573345	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
CHST4	&1994.834067	&1997.541507	5.41488	0	0.019965826	
RAE1	&1759.736998	&1762.439895	5.405794	0	0.020070017	
ANGEL2	&2366.541023	&2369.213426	5.344806	0.1139	0.020784096	
ADAT2	&895.709578	&898.378842	5.338528	0	0.020859079	
WSB2	&1866.171108	&1868.838197	5.334178	0	0.020911199	
DBX1	&2071.850915	&2074.504846	5.307862	0.17184	0.021229394	
NR2C2	&2829.705586	&2832.348628	5.286084	0	0.021496506	0.018410853
DHTKD1	&4801.258406	&4803.888242	5.259672	0.25017	0.021825132	
ASB1	&1622.422412	&1625.041306	5.237788	0.1551	0.022101358	
GNPAT	&338.380248	&340.979491	5.198486	0.20097	0.02260657	
ARCN1	&2281.701136	&2284.287068	5.171864	0	0.022955572	
TAGLN	&885.064143	&887.633996	5.139706	0	0.023384608	
MRPL43	&1378.354732	&1380.923414	5.137364	0.09061	0.023416177	
TFEC	&1627.403313	&1629.967846	5.129066	0	0.023528385	
STAT5B	&676.464606	&679.009114	5.089016	0	0.02407785	
STX2	&1321.506402	&1324.034396	5.055988	0	0.024540986	
HLF	&1269.627584	&1272.152311	5.049454	0	0.0246337	
LRRC27	&2937.594661	&2940.104048	5.018774	0.31842	0.025073916	
C1orf187	&1761.509517	&1763.99222	4.965406	0	0.025859244	
SMC5	&5111.536909	&5113.985109	4.8964	0.13152	0.026912744	
STUB1	&1347.877786	&1350.321824	4.888076	0	0.027042807	
OR10G3	&1723.345982	&1725.765316	4.838668	0.10991	0.027828382	
TACR2	&1978.446946	&1980.864386	4.83488	0.17182	0.027889582	
NR1D2	&2651.064183	&2653.478278	4.82819	0.09868	0.027998009	
SOAT2	&2725.985335	&2728.394092	4.817514	0.08607	0.028171949	
RNF11	&655.292812	&657.699443	4.813262	0	0.028241538	
MSRB2	&998.568917	&1000.959039	4.780244	0	0.028788041	
WDFY2	&1823.803854	&1826.189155	4.770602	0	0.028949701	
PADI1	&3540.796888	&3543.154574	4.715372	0.23128	0.029894097	
C4orf31	&2783.594686	&2785.948682	4.707992	0	0.0300227	
CPT1B	&3719.874415	&3722.225896	4.702962	0.18079	0.030110682	
SLC45A2	&2718.210854	&2720.558875	4.696042	0.14404	0.030232162	
TMEM179	&903.220619	&905.531791	4.622344	0	0.031558085	
DIRC2	&2215.358648	&2217.663697	4.610098	0	0.031784217	
SLC7A14	&657.520959	&659.82493	4.607942	0	0.031824204	
PAX9	&1574.297569	&1576.584075	4.573012	0.06545	0.032479412	
OR2J3	&1697.457688	&1699.736592	4.557808	0.10838	0.032768988	
OR13J1	&1779.01786	&1781.290805	4.54589	0.4518	0.032997864	
INTS6	&4110.332484	&4112.596797	4.528626	0.10676	0.03333237	
ATP5H	&760.950704	&763.211177	4.520946	0	0.033482313	
ADRA1B	&2497.74981	&2499.979519	4.459418	0	0.034709322	
MBNL2	&1566.895818	&1569.114677	4.437718	0	0.035153205	
UPF2	&623.280634	&625.485385	4.409502	0.17047	0.035739273	
ABCD3	&242.834856	&245.032951	4.39619	0.11038	0.036019314	
ADAM9	&866.409321	&868.606479	4.394316	0.17292	0.036058921	
PPIG	&510.995345	&513.167577	4.344464	0.09542	0.037129453	
SDAD1	&556.279205	&558.439246	4.320082	0.17456	0.037665107	
TMEM232	&271.843361	&273.96356	4.240398	0.24684	0.039472913	
ITGB3BP	&885.768422	&887.839728	4.142612	0.12504	0.041816598	
SDSL	&1770.027088	&1772.071709	4.089242	0.1981	0.043156992	
ZFYVE20	&771.999709	&774.015273	4.031128	0.25805	0.044668066	
MOCS3	&332.639448	&334.611706	3.944516	0.12452	0.047024379	
C4orf33	&1020.749913	&1022.711428	3.92303	0.12443	0.047628963	
TMEM139	&1117.603916	&1119.548371	3.88891	0.13899	0.04860596	
IRX6	&444.197248	&446.134711	3.874926	0.28213	0.04901247	0.023062016
DDB2	&2011.682245	&2013.586436	3.808382	0.1499	0.05099669	
MIER1	&1903.192741	&1905.093826	3.80217	0	0.051186205	
CEBPZ	&5167.185601	&5169.071993	3.772784	0.29078	0.052092861	
MAGEA8	&1513.411152	&1515.291638	3.760972	0.18886	0.052462073	
WDR33	&6005.658963	&6007.528476	3.739026	0.13313	0.053155422	
TTF1	&5078.364978	&5080.210358	3.69076	0.44741	0.05471468	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
DRAP1	&964.490515	&966.335361	3.689692	0	0.054749725	
IL17RB	&2645.110713	&2646.929535	3.637644	0.29275	0.056486816	
GIMAP2	&1821.52182	&1823.329102	3.614564	999	0.057275733	
PIP4K2C	&1757.072071	&1758.868861	3.59358	0	0.058003162	
FAM120A	&5421.670418	&5423.456096	3.571356	0	0.05878429	
SYNPO2L	&4887.076374	&4888.858635	3.564522	0.26498	0.059026733	
AGPAT2	&1421.366598	&1423.12675	3.520304	0.19432	0.060621327	
OR1N2	&1644.669438	&1646.419959	3.501042	0.13203	0.06133023	
FBL	&1605.54403	&1607.29346	3.49886	0	0.061411089	
LSM7	&453.438633	&455.187682	3.498098	0	0.061439353	
ZBTB38	&5739.888227	&5741.63312	3.489786	0.18893	0.061748567	
TSSK2	&1693.87585	&1695.60041	3.44912	0.17415	0.063285456	
ZNF569	&3122.785357	&3124.467668	3.364622	0.18511	0.066610869	
TOP3A	&5199.857765	&5201.488504	3.261478	0.19783	0.070925173	
TMC8	&3631.211265	&3632.823151	3.223772	0.34475	0.072576212	
SCN1B	&1018.988122	&1020.596253	3.216262	0	0.072909948	
C1orf27	&2080.271307	&2081.877163	3.211712	0	0.073112946	
C9orf9	&840.428963	&842.0318	3.205674	0.17086	0.073383267	
CAPN7	&3743.364867	&3744.958873	3.188012	0.18291	0.074180172	
HELB	&5542.955037	&5544.496463	3.082852	0.39664	0.079121671	
OAS1	&2332.927117	&2334.459673	3.065112	999	0.07998965	
YLPM1	&9689.053015	&9690.584398	3.062766	0.36139	0.080105201	
ZNF30	&3412.537134	&3414.055732	3.037196	0.25238	0.081376369	
KLHDC4	&2857.635405	&2859.149062	3.027314	0.35604	0.08187345	
RGS18	&1077.893322	&1079.381992	2.97734	0	0.084437939	
PIAS1	&2899.345263	&2900.827782	2.965038	0	0.085082459	
CCRL1	&1662.365009	&1663.824475	2.918932	0.22964	0.08754579	
SLC4A4	&4931.835887	&4933.290119	2.908464	0.20137	0.088115759	
ARHGAP19	&2378.538188	&2379.988375	2.900374	0	0.088559003	
LSM10	&586.272302	&587.696438	2.848272	0	0.091472205	
RFX7	&6744.244888	&6745.632704	2.775632	0.14073	0.095708872	
PNKP	&2843.975482	&2845.360535	2.770106	0.21659	0.096039801	
GADD45A	&733.785643	&735.152967	2.734648	0	0.098193135	
METTL6	&1402.520144	&1403.875865	2.711442	0.22068	0.099630895	
TSPAN8	&1578.03094	&1579.36247	2.66306	9.3244	0.102702982	
CD2AP	&3055.068063	&3056.383175	2.630224	0.29434	0.104846921	
GPR39	&2381.335551	&2382.630675	2.590248	0.24244	0.107523499	
GOLGA5	&3484.579142	&3485.867369	2.576454	0.27547	0.108464398	
C1QTNF7	&1370.911859	&1372.198711	2.573704	0	0.108653056	
TBRG1	&1916.118641	&1917.400325	2.563368	0	0.109365368	
MED7	&980.949476	&982.225624	2.552296	0	0.110134101	
DNAJC17	&1458.231705	&1459.505197	2.546984	0	0.110505022	
ELF4	&3310.474087	&3311.744817	2.54146	0	0.110892204	
TTYH1	&2169.230665	&2170.496097	2.530864	0.1383	0.111639073	
FOSB	&1437.961291	&1439.2254	2.528218	0	0.111826441	
MBTPS2	&2423.7272	&2424.984908	2.515416	0.16437	0.112737879	
ZNF192	&2773.055183	&2774.297785	2.485204	0.33227	0.114921447	
NLGN3	&3586.356417	&3587.595426	2.478018	0	0.115447653	
CAPN11	&3813.383721	&3814.622094	2.476746	0.22806	0.115541074	
PSMD4	&1696.877268	&1698.113765	2.472994	0	0.115817122	
CA10	&1497.578193	&1498.811317	2.466248	0	0.116315284	
SNRPA1	&1117.342391	&1118.571653	2.458524	0	0.116888574	
CES5A	&3265.709112	&3266.930131	2.442038	0.23325	0.118122669	
CORO1C	&2136.201749	&2137.42214	2.440782	0	0.118217279	
PLAU	&2338.76687	&2339.985784	2.437828	0.15385	0.118440122	
DCTN6	&847.845639	&849.060446	2.429614	0	0.119062213	
MAP4K3	&4021.379795	&4022.592898	2.426206	0.15542	0.11932138	
LPAR3	&1796.69187	&1797.902838	2.421936	0	0.119646981	
SUMF1	&1881.957131	&1883.151823	2.389384	0.23005	0.122161757	
C1orf43	&1161.238612	&1162.415757	2.35429	0	0.124938758	
ABHD10	&1500.940457	&1502.112971	2.345028	0.24706	0.125683303	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
VPREB1	&805.369235	&806.531746	2.325022	0.16265	0.127308421	
POGK	&2869.312185	&2870.470234	2.316098	0.20653	0.128040859	
KCNJ9	&1729.755897	&1730.908396	2.304998	0	0.128958447	
JAM2	&1441.105686	&1442.253198	2.295024	0	0.129789205	
NDP	&595.250279	&596.379014	2.25747	0	0.132971141	
CDC20	&2289.935983	&2291.06268	2.253394	0.17028	0.133321706	
NUDCD1	&2710.000158	&2711.116127	2.231938	0.15825	0.135184192	
DNAI2	&3181.302325	&3182.417162	2.229674	0.20504	0.13538241	
STH	&711.378038	&712.491339	2.226602	0.24776	0.13565189	
OVOL2	&1301.218682	&1302.329904	2.222444	0.19747	0.136017591	
C7orf60	&1791.19202	&1792.30203	2.22002	0.16827	0.136231295	
ENOPH1	&1178.058508	&1179.162275	2.207534	0	0.137338053	
TMCC3	&2204.085877	&2205.183841	2.195928	0.16259	0.138375849	
ABHD4	&1659.164076	&1660.256127	2.184102	0.27341	0.139442373	
TXNDC11	&4977.418215	&4978.503065	2.1697	0.5132	0.14075369	
FAM126B	&2588.142864	&2589.21974	2.153752	0.14692	0.142221961	
MFSD6L	&3312.352872	&3313.423162	2.14058	0.4564	0.143447648	
CCDC68	&1602.784757	&1603.854904	2.140294	0	0.143474393	
TMEM92	&870.688491	&871.752536	2.12809	999	0.144620865	
TMEM18	&652.609005	&653.672102	2.126194	0.17184	0.144799903	
RAB17	&1171.322155	&1172.363981	2.083652	0.2053	0.148883597	
PFDN6	&550.716156	&551.755126	2.07794	0	0.149441739	
ZNF570	&2394.463307	&2395.494552	2.06249	0	0.15096331	
MPV17L	&1181.576703	&1182.60089	2.048374	0.32598	0.152368844	
ZBP1	&2566.703173	&2567.711694	2.017042	0.44749	0.155541885	
DEFB103A	&335.976813	&336.980862	2.008098	0	0.156461368	
LAPTM4B	&2137.464148	&2138.465288	2.00228	0.38266	0.157062798	
RNF34	&1774.720402	&1775.696761	1.952718	0.2562	0.162294261	
FXYD3	&494.141224	&495.100545	1.918642	999	0.166006443	
CNTN6	&5056.479683	&5057.430471	1.901576	0.46624	0.167902021	
GPRASP2	&4102.848541	&4103.789982	1.882882	0.25513	0.170006951	
YTHDC1	&3081.203371	&3082.132083	1.857424	0	0.172922402	
NSUN3	&1619.400461	&1620.324917	1.848912	0.20007	0.173909988	
RPL23A	&868.801682	&869.721116	1.838868	0	0.175083683	
LTK	&4352.381311	&4353.281669	1.800716	0.32093	0.179625958	
CCDC115	&878.598048	&879.489937	1.783778	999	0.181686093	
ZFP57	&2764.922343	&2765.772607	1.700528	999	0.192218941	
DACT2	&4064.563142	&4065.406982	1.68768	0.45529	0.193907079	
CDCA3	&1245.692068	&1246.51773	1.651324	0	0.198778823	
LETM2	&522.59625	&523.421679	1.650858	0	0.198842193	
FCRL2	&3055.911105	&3056.736351	1.650492	0.30043	0.19889198	
MAGEB17	&1973.611841	&1974.369479	1.515276	999	0.218335777	
DDTL	&774.414565	&775.165218	1.501306	0.23989	0.220470522	
NPFF	&606.309584	&607.036973	1.454778	999	0.227762827	
HSD17B3	&1581.696781	&1582.418155	1.442748	999	0.229695171	
NPFFR1	&2089.465014	&2090.184636	1.439244	0.31843	0.230261717	
CAV1	&809.418945	&810.138464	1.439038	0	0.230295076	
DNAJC30	&1248.075977	&1248.781918	1.411882	0.28407	0.234744222	
C11orf20	&1250.467047	&1251.16872	1.403346	0.16455	0.236164144	
NR1I3	&1717.604027	&1718.301242	1.39443	152.71434	0.237658401	
CCDC69	&1442.389581	&1443.080828	1.382494	0.37378	0.239676785	
CENPT	&3154.357344	&3155.048201	1.381714	0.51788	0.239809406	
CNPY1	&413.068525	&413.756496	1.375942	0.24618	0.240793584	
IRF8	&2086.167599	&2086.846089	1.35698	0.29669	0.24406156	
CASP8	&2453.988113	&2454.66576	1.355294	0.24779	0.244354741	
PYGO2	&1791.564724	&1792.242184	1.35492	0.24375	0.244419834	
KANK3	&4441.969097	&4442.612547	1.2869	0.44441	0.256620028	
ACOT12	&2907.0945	&2907.728759	1.268518	0.30724	0.260044886	
FAM64A	&1282.150404	&1282.780872	1.260936	0.2277	0.261473993	
METAP1D	&1550.471683	&1551.094313	1.24526	0.30345	0.264459726	
DDHD2	&3298.801188	&3299.410087	1.217798	0.45847	0.269793229	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
MAGEB3	&1942.178195	&1942.755468	1.154546	0.34129	0.282599531	
GMNN	&1034.971197	&1035.544294	1.146194	0.34312	0.284347298	
SUSD3	&1285.931245	&1286.479833	1.097176	0.15622	0.294886691	
ZNF575	&1660.835931	&1661.379673	1.087484	0.24102	0.297029346	
MRGPRE	&1602.596434	&1603.135672	1.078476	0.28731	0.299038735	
PMFBP1	&5170.179794	&5170.699393	1.039198	0.62695	0.308008069	
FGF2	&1339.726841	&1340.244059	1.034436	0.35893	0.309119051	
NDUFA6	&805.107427	&805.60655	0.998246	0.24547	0.317735297	
ZNRD1	&571.804632	&572.298998	0.988732	0.35817	0.320052482	
CCDC73	&5510.487093	&5510.948278	0.92237	0.56435	0.336853456	
RHOB	&856.634946	&857.093096	0.9163	0	0.338448351	
PNLIPRP3	&2314.311667	&2314.766319	0.909304	0.37442	0.340299155	
TMEM38B	&1444.946074	&1445.388304	0.88446	999	0.346983024	
PLEKHB2	&1116.031585	&1116.460666	0.858162	0.28	0.354253554	
CMBL	&1196.427373	&1196.85639	0.858034	0.38163	0.354289448	
C8orf39	&460.662939	&461.082962	0.840046	999	0.359383615	
SMR3B	&486.294831	&486.70261	0.815558	999	0.366482112	
ICT1	&1155.081358	&1155.473439	0.784162	0.42993	0.375871267	
AHSA1	&1499.552728	&1499.937353	0.76925	999	0.380449171	
GEMIN7	&640.874043	&641.256364	0.764642	999	0.381879713	
DHRS7	&1626.29769	&1626.671928	0.748476	0.39916	0.386959168	
GNG5P2	&52.5628	&52.935421	0.745242	999	0.387986836	
MRPL21	&1128.899367	&1129.265134	0.731534	69.89112	0.392386411	
ADAM29	&4769.529787	&4769.887623	0.715672	0.6118	0.397567252	
COX5B	&678.855045	&679.208605	0.70712	999	0.400401563	
LIPH	&2244.498647	&2244.82853	0.659766	0.49588	0.416642566	
LRRC2	&1794.282913	&1794.609776	0.653726	0.43898	0.418783679	
ZNF324B	&3116.971509	&3117.298034	0.65305	0.43911	0.419024331	
OR6X1	&1673.013997	&1673.340413	0.652832	0.61092	0.419101982	
TMEM106B	&1217.237018	&1217.560532	0.647028	0.3056	0.421177255	
WFDC11	&493.930356	&494.250459	0.640206	999	0.423636211	
ME2	&2645.729487	&2646.046358	0.633742	0.31255	0.425986037	
C10orf11	&974.846691	&975.162941	0.6325	10.5551	0.426439778	
PPM1E	&3396.756071	&3397.05711	0.602078	0.34467	0.437786272	
PLXDC2	&2634.424455	&2634.722472	0.596034	0.47494	0.440095248	
C12orf5	&1454.595934	&1454.891269	0.59067	0.31928	0.442160151	
C22orf41	&892.996832	&893.282055	0.570446	999	0.450081742	
C9orf142	&1043.96172	&1044.241473	0.559506	0.48736	0.454459351	
CHST2	&2515.010631	&2515.278212	0.535162	999	0.464444696	
B4GALT5	&1751.070253	&1751.334744	0.528982	0.34645	0.467035162	
RESP18	&1251.111925	&1251.372503	0.521156	0.59027	0.470348981	
CLEC4E	&1201.993781	&1202.252354	0.517146	0.50593	0.472061663	
OR14A2	&1605.832887	&1606.086076	0.506378	0.55355	0.47671101	
S1PR3	&1731.413283	&1731.663658	0.50075	0.38768	0.479170764	
ZNF561	&3224.397348	&3224.64506	0.495424	0	0.481517707	
GP1BA	&4200.41929	&4200.666692	0.494804	1.41843	0.48179214	
C14orf180	&1003.783107	&1004.02878	0.491346	443.82227	0.483327498	
LRPPRC	&7708.183163	&7708.422076	0.477826	0.71261	0.489408703	
ATAD5	&9296.010971	&9296.240883	0.459824	0.64731	0.497706238	
ZFP37	&3100.768989	&3100.998733	0.459488	0.56661	0.497863354	
GFRAL	&2057.23122	&2057.460588	0.458736	0.52811	0.498215298	
TMED4	&1060.835388	&1061.063253	0.45573	999	0.499626354	
LYG1	&1103.14866	&1103.369606	0.441892	999	0.506210678	
HAUS2	&1108.967313	&1109.186765	0.438904	129.13762	0.507651923	
PIGA	&2362.632055	&2362.850673	0.437236	0.39095	0.508459546	
BCCIP	&1571.703919	&1571.91381	0.419782	0.67995	0.517045842	
RNF208	&1197.361871	&1197.566864	0.409986	0.32402	0.521976611	
TNIP3	&2039.701191	&2039.89135	0.380318	0.55649	0.537433097	
NUP88	&3816.465073	&3816.653062	0.375978	0.6415	0.539763642	
PTPRCAP	&1095.595884	&1095.78155	0.371332	0.42228	0.542279108	
RCN2	&1491.397699	&1491.578145	0.360892	0.45695	0.548011258	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
PRSS55	&2132.18439	&2132.353791	0.338802	0.58092	0.560521548	
EFS	&2799.62367	&2799.791918	0.336496	1.58389	0.561858814	
LAMC2	&5963.14969	&5963.317668	0.335956	0.69782	0.562172849	
CEP78	&3500.694022	&3500.860665	0.333286	0.58124	0.563730549	
RTN4RL2	&1990.793454	&1990.955532	0.324156	0	0.569120681	
AMBN	&2392.595222	&2392.756553	0.322662	0.43232	0.570012255	
FAM111A	&3300.510234	&3300.666774	0.31308	1.30064	0.575796296	
MED19	&1131.405187	&1131.536676	0.262978	0.47304	0.608081571	
FAM103A1	&520.749265	&520.868163	0.237796	0	0.625802511	
ARV1	&1315.819526	&1315.938079	0.237106	1.68555	0.626304172	
USP26	&5057.700729	&5057.818934	0.23641	1.2666	0.626811111	
MAT2A	&1792.672433	&1792.787676	0.230486	0	0.631163701	
HIST1H3F	&761.424944	&761.529603	0.209318	0	0.647302474	
DMGDH	&4203.549109	&4203.648717	0.199216	0.57156	0.655354414	
ATP10D	&7191.85971	&7191.957957	0.196494	0.71617	0.657565797	
TRIM39	&2366.995021	&2367.086769	0.183496	999	0.668385889	
SH3D21	&4135.214401	&4135.30021	0.171618	0.74067	0.678677825	
IFNA2	&1005.824553	&1005.907079	0.165052	1.55078	0.684547221	
FANCG	&3680.959357	&3681.038792	0.15887	0.70859	0.690199018	
ZNF117	&3441.591863	&3441.663529	0.143332	1.51023	0.704990768	
EXD1	&2905.863907	&2905.933908	0.140002	1.35149	0.708279024	
CEACAM6	&2795.166039	&2795.234963	0.137848	0.48982	0.710429834	
FAAH2	&2753.890605	&2753.955594	0.129978	0.71262	0.71845485	
TRAIP	&2304.831532	&2304.893675	0.124286	0.64123	0.724431679	
ZMYND17	&2328.505801	&2328.556988	0.102374	0.7429	0.748999129	
CCDC82	&2745.905659	&2745.954934	0.09855	0.8049	0.753576678	
DNAJC5G	&1132.611474	&1132.651484	0.08002	0.77785	0.777270309	
OR6M1	&1728.613941	&1728.653565	0.079248	1.3751	0.778319096	
CD300C	&1372.265467	&1372.286771	0.042608	1.16574	0.836465151	

Stem Hominoid

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
PITPNM1	'6236.428714	'6247.350182	21.842936	0.06422	2.95904E'06	
GRIK3	'4314.692476	'4325.246054	21.107156	0	4.34303E'06	
HRH3	'2191.358357	'2201.631773	20.546832	0	5.819E'06	
SEC14L5	'3454.651231	'3464.291504	19.280546	0	1.1285E'05	
APC2	'11995.05853	'12004.40795	18.698838	0.01961	1.53076E'05	
SDHA	'3586.288283	'3595.607649	18.638732	0	1.57978E'05	
LDB3	'3928.967932	'3938.2329	18.529936	0	1.67257E'05	
PCDH7	'5420.252426	'5428.622196	16.73954	0	4.2878E'05	
NCOR2	'12226.9759	'12235.2342	16.51659	0.03515	4.82263E'05	
ANO1	'4809.493627	'4817.108066	15.228878	0.04264	9.52359E'05	
BCL9L	'7012.69209	'7020.174386	14.964592	0.03586	0.000109548	
DHTKD1	'4798.446059	'4805.496139	14.10016	0	0.000173329	
PRKRIP1	'904.406577	'911.361164	13.909174	0	0.00019186	
SHPRH	'8157.173804	'8164.126134	13.90466	0	0.000192321	
SLIT1	'7419.887999	'7426.74585	13.715702	0	0.000212669	
TEKT5	'2694.528975	'2701.385505	13.71306	0.04896	0.000212968	
ROR2	'4589.502094	'4596.078623	13.153058	0.08032	0.00028705	
KIAA0947	'12217.43264	'12223.94679	13.028286	0.16078	0.000306821	
STUB1	'1347.877786	'1353.964741	12.17391	0	0.000484626	
ZNF528	'3223.543661	'3229.493961	11.9006	0	0.000561159	
KRTAP4'7	'1359.719722	'1365.612506	11.785568	0.09929	0.000596917	
GNPAT	'3336.079204	'3341.925652	11.692896	0	0.000627392	
C11orf84	'2727.18232	'2732.814946	11.265252	0	0.000789715	
SEC13	'1770.090298	'1775.686678	11.19276	0	0.000821171	
TXNDC11	'4975.413068	'4980.839849	10.853562	0	0.000986059	
KIDINS220	'8390.903815	'8396.221447	10.635264	0	0.001109514	
FZR1	'2351.312394	'2356.572308	10.519828	0	0.001181005	
STAT5B	'3676.230084	'3681.29558	10.130992	0	0.001457969	
CDC37	'1706.879886	'1711.914404	10.069036	0	0.001507819	
NLGN3	'3586.145051	'3591.082463	9.874824	0	0.001675556	0.002712477
C21orf59	'1400.825532	'1405.593879	9.536694	0	0.002014042	0.002802893
MAP4K5	'5017.034687	'5021.683373	9.297372	0	0.002294828	0.002893309
ASCC3	'10025.77886	'10030.38925	9.220784	0.06096	0.002392831	0.002983725
ACOT12	'2905.076162	'2909.684896	9.217468	0	0.002397168	0.003074141
ECEL1	'3727.16151	'3731.74405	9.16508	0	0.002466769	0.003164557
PDZD7	'2714.159388	'2718.612958	8.90714	0	0.002840578	0.003254973
CAPN11	'3812.608999	'3816.89937	8.580742	0.13445	0.003397369	0.003345389
TTYH1	'2169.204716	'2173.347838	8.286244	0.05716	0.003994653	0.003435805
TBC1D9	'5834.146457	'5838.251743	8.210572	0	0.004164702	0.003526221
ADRA1B	'2497.368768	'2501.459465	8.181394	0	0.004232222	0.003616637
CYLC1	'3422.589497	'3426.639942	8.10089	0.0208	0.004424353	
SPTB	'11267.4216	'11271.42359	8.003986	0.16887	0.004667449	
CLCN4	'3597.202706	'3601.185305	7.965198	0	0.004768527	
ZNF324B	'3115.388005	'3119.32323	7.87045	0	0.005024915	
HMGCR	'4419.520868	'4423.436876	7.832016	0	0.005132882	
ADNP2	'5611.698018	'5615.565308	7.73458	0.07313	0.005417316	
ZNF569	'3121.655267	'3125.48553	7.660526	0	0.005644205	
FBL	'1604.999583	'1608.657669	7.316172	0	0.006833682	
PCDHB5	'4601.652297	'4605.25394	7.203286	0.08182	0.007277021	
DENND4B	'7193.183159	'7196.73472	7.103122	0	0.00769498	0.004520796
EPB41L1	'4096.022818	'4099.368414	6.691192	0	0.00968904	
PRPF4B	'4588.093043	'4591.432008	6.67793	0	0.009761392	
NR2C2	'2829.65821	'2832.968678	6.620936	0	0.010078685	
SLC4A4	'4931.291699	'4934.583375	6.583352	0	0.010293687	
SLC45A2	'2718.068093	'2721.280938	6.42569	0.13557	0.01124812	
PER3	'6655.982584	'6659.171478	6.377788	0.21617	0.011555737	
TSPAN15	'1376.914284	'1380.102767	6.376966	0	0.01156109	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
FAM131A	'1320.895702	'1324.079238	6.367072	0	0.011625726	
C1orf187	'1762.244767	'1765.411426	6.333318	0.12633	0.011849043	
TBR1	'2895.567462	'2898.733456	6.331988	0	0.011857932	
MLLT6	'4826.5121	'4829.631153	6.238106	0.07694	0.012503012	
FAM120A	'5421.110719	'5424.18933	6.157222	0	0.01308766	
C1QTNF7	'1370.454297	'1373.520817	6.13304	0	0.013267854	
ARCN1	'2281.584406	'2284.630278	6.091744	0	0.013581496	
ABCD3	'3242.024227	'3245.026827	6.0052	0	0.014263777	
ACCN1	'2710.551335	'2713.527384	5.952098	0	0.014699781	
TSSK2	'1694.097417	'1697.070911	5.946988	0.10707	0.014742455	
TJP2	'6015.552953	'6018.51675	5.927594	0	0.014905579	
TGM1	'4090.232238	'4093.147295	5.830114	0.06632	0.015754103	
ZNF592	'5979.219905	'5982.114554	5.789298	0.14451	0.016124027	
FTSJ2	'1310.171536	'1313.063162	5.783252	0	0.016179579	
MIER1	'1903.075894	'1905.965935	5.780082	0	0.016208785	
BCCIP	'1569.14429	'1572.012891	5.737202	0	0.016609231	
VPS52	'3325.340608	'3328.151515	5.621814	0	0.01773828	
LPAR3	'1796.874421	'1799.668395	5.587948	0.08115	0.01808447	
SLC7A14	'3657.426201	'3660.211188	5.569974	0	0.018271032	
RABEP1	'3980.381153	'3983.082871	5.403436	0	0.020097148	
ADH1A	'2352.696804	'2355.353963	5.314318	0.0944	0.021150871	
CES5A	'3264.714349	'3267.340495	5.252292	0.07743	0.021917882	
RBM7	'1282.14124	'1284.739376	5.196272	0	0.022635384	
MARK2	'3519.66125	'3522.227894	5.133288	0	0.023471224	
GUCA1B	'890.171812	'892.725586	5.107548	0	0.023821965	
RBCK1	'2218.634528	'2221.17635	5.083644	0	0.024152557	
CYP4F11	'2992.199517	'2994.731019	5.063004	0.05051	0.024441837	
SQSTM1	'2439.610725	'2442.139343	5.057236	0	0.024523319	
RAE1	'1759.714488	'1762.229166	5.029356	0	0.024921163	
ASH2L	'2901.61363	'2904.125376	5.023492	0	0.025005691	
PLXDC2	'2634.595963	'2637.09977	5.007614	0	0.025236066	
DUSP1	'1011.279256	'1013.77207	4.985628	0	0.025558707	
OLA1	'1684.355233	'1686.792196	4.873926	0	0.027265403	
EPT1	'1772.29401	'1774.727324	4.866628	0	0.027380953	
JAG2	'6295.524274	'6297.949811	4.851074	0	0.027628924	
GFRAL	'2055.218824	'2057.643531	4.849414	0	0.027655526	
SMC2	'5402.395133	'5404.776871	4.763476	0	0.029069784	
GJA4	'1636.619833	'1638.982089	4.724512	0	0.02973562	
PLS3	'2742.848916	'2745.201648	4.705464	0	0.030066885	
MEGF10	'5515.683729	'5517.917934	4.46841	0.09218	0.034527107	
CCDC73	'5508.793385	'5511.00718	4.42759	0.06786	0.035362406	
FGGY	'2752.986023	'2755.17779	4.383534	0	0.036287686	
ASB1	'1624.95826	'1627.125472	4.334424	0	0.037349051	
USP7	'4826.609714	'4828.774263	4.329098	0	0.037466095	
ZBTB38	'5739.067854	'5741.229223	4.322738	0	0.037606366	
WDR33	'6005.48455	'6007.620112	4.271124	0	0.03876528	
TBC1D17	'3152.698938	'3154.833691	4.269506	0.08007	0.038802209	
DSCR3	'1519.431286	'1521.532592	4.202612	0	0.040361765	
WISP3	'1791.694453	'1793.787072	4.185238	0	0.040777487	
HIST1H3F	'761.424527	'763.500033	4.151012	0	0.041609649	
RFX7	'6744.190296	'6746.258864	4.137136	0.10653	0.041952091	
CDK13	'6756.16595	'6758.220098	4.108296	0	0.042673337	
ZFYVE20	'3771.293824	'3773.315078	4.042508	0	0.044367839	
CDCA2	'5452.433521	'5454.435844	4.004646	0.19898	0.045375025	
PNKP	'2844.10181	'2846.057815	3.91201	0.16569	0.047942226	
ZNF30	'3411.51693	'3413.454797	3.875734	0	0.048988885	
PPP2R2C	'2051.172836	'2053.094253	3.842834	0	0.049959011	0.010307414

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
DARC	'1862.720989	'1864.639086	3.836194	0	0.050157255	
RNF216	'4385.27114	'4387.186232	3.830184	0	0.050337407	
CARD11	'5919.079713	'5920.98503	3.810634	0.0509	0.05092817	
GNAT2	'1603.110287	'1605.012072	3.80357	0	0.051143429	
B4GALT5	'1751.584629	'1753.439112	3.708966	0	0.054120908	
CDK9	'1677.537091	'1679.34172	3.609258	0	0.05745875	
ZMYND17	'2327.578558	'2329.371509	3.585902	0	0.058271774	
ZNF335	'6610.637977	'6612.426366	3.576778	0.1687	0.058592693	
POFUT2	'2135.251943	'2137.015578	3.52727	0.09793	0.060367108	
SHMT2	'2376.518529	'2378.279781	3.522504	0.12826	0.060540917	
MAP2	'8749.700333	'8751.459858	3.51905	0.21304	0.060667212	
GOLGA6C	'5060.435179	'5062.17782	3.485282	0.44063	0.061916811	
NUDCD1	'2709.231822	'2710.968706	3.473768	0	0.062349134	
CPB2	'2229.466586	'2231.202017	3.470862	0	0.062458755	
ARHGAP19	'2378.426909	'2380.153076	3.452334	0	0.063162518	
ERC1	'5076.925868	'5078.636015	3.420294	0	0.064399543	
PDK3	'1819.492025	'1821.189494	3.394938	0	0.065396822	
YLPM1	'9690.612745	'9692.218265	3.21104	0.11689	0.073142978	
NR1I3	'1719.660651	'1721.241248	3.161194	0.14495	0.075408012	
AMBN	'2391.742722	'2393.3104	3.135356	4.72965	0.076611659	
ORC2	'2609.047093	'2610.610356	3.126526	0	0.077027722	
RC3H1	'5132.108682	'5133.653427	3.08949	0	0.078799502	
UBLCP1	'1381.310112	'1382.83558	3.050936	0	0.080690627	
MAT2A	'1792.546972	'1794.065336	3.036728	0	0.081399837	
SDAD1	'3556.484189	'3557.987607	3.006836	0.22712	0.08291399	
BLNK	'2337.970759	'2339.470303	2.999088	0	0.083311402	
ALOX15	'3886.131873	'3887.630785	2.997824	0.23825	0.08337643	
AGPAT2	'1422.215419	'1423.704369	2.9779	0.05842	0.084408725	
PTPRCAP	'1095.086818	'1096.570117	2.966598	0	0.085000434	
LAMC2	'5963.197504	'5964.661339	2.92767	0.26295	0.087073075	
ZNF652	'2779.909825	'2781.37172	2.92379	0	0.087282636	
ADAM29	'4768.630747	'4770.06861	2.875726	0	0.089924413	
FANCG	'3679.075463	'3680.506114	2.861302	64.17295	0.090734029	
IL10RA	'3125.740658	'3127.169121	2.856926	0	0.090981215	
MRPL43	'1378.43526	'1379.856535	2.84255	0	0.091798427	
MSL2	'2520.996753	'2522.387422	2.781338	0	0.095368465	
MFSD6L	'3309.70469	'3311.082865	2.75635	999	0.096869018	
RHOB	'856.584233	'857.937926	2.707386	0	0.099884542	
NXT1	'642.059909	'643.410321	2.700824	0	0.100296398	
TMEM43	'2109.690069	'2111.036892	2.693646	0	0.100749043	
UNC13C	'10555.39521	'10556.73477	2.67912	0.16444	0.101671898	
TMEM106B	'1217.34541	'1218.654183	2.617546	0	0.105687775	
ATP10D	'7192.292223	'7193.595163	2.60588	0.0991	0.106468044	
YTHDC1	'3081.148524	'3082.426216	2.555384	0	0.109919104	
WSB2	'1866.427345	'1867.689585	2.52448	0	0.112091726	
POLR2F	'562.601985	'563.854256	2.504542	0	0.113518483	
ZFP64	'3248.343421	'3249.587598	2.488354	0	0.114691618	
LRRTM3	'2556.565005	'2557.807239	2.484468	0	0.11497522	
TOP3A	'5199.623112	'5200.861978	2.477732	0.39434	0.115468651	
JAM2	'1441.091987	'1442.312927	2.44188	0	0.118134566	
EPB49	'1818.089368	'1819.305021	2.431306	0.09143	0.118933774	
EXD1	'2906.136374	'2907.337534	2.40232	0.23754	0.121155453	
SFRP1	'1508.657222	'1509.855272	2.3961	0	0.121638162	
MAP4K3	'4021.195999	'4022.388812	2.385626	0	0.12245583	
KLHDC4	'2858.059321	'2859.246077	2.373512	0.08567	0.123409138	
SDC2	'947.343999	'948.520249	2.3525	0	0.125082268	
CLK4	'2165.822964	'2166.972518	2.299108	0	0.12944832	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
ALDH1A3	'2496.471096	'2497.6187	2.295208	0	0.129773825	
MOAP1	'1705.273252	'1706.416425	2.286346	0	0.13051687	
ANKRD52	'5052.69928	'5053.841837	2.285114	0	0.130620544	
SMPD3	'3077.580815	'3078.722138	2.282646	0	0.130828504	
RPS12	'640.061453	'641.19555	2.268194	0	0.132053708	
GEMIN7	'641.326779	'642.450314	2.24707	0	0.133867661	
RPL23A	'868.768654	'869.877515	2.217722	0	0.136434237	
MRGPRE	'1602.902089	'1604.008367	2.212556	0.20297	0.136891697	
PLCB1	'5510.43087	'5511.534979	2.208218	0.18447	0.137277163	
C7orf60	'1791.652705	'1792.753992	2.202574	0	0.1377805	
PLCH2	'7498.501558	'7499.595882	2.188648	0.07643	0.139031306	
METTL6	'1402.082974	'1403.174998	2.184048	0	0.139447264	
TMC8	'3632.139994	'3633.230983	2.181978	0.09925	0.1396349	
HNRPLL	'2492.543885	'2493.633088	2.178406	0	0.139959353	
PNPT1	'3659.111042	'3660.19476	2.167436	0	0.140961087	
PSMD4	'1696.869015	'1697.940246	2.142462	0	0.143271798	
GALNT12	'3049.986876	'3051.057702	2.141652	0	0.143347453	
PFDN6	'550.711318	'551.781627	2.140618	0	0.143444095	
SLC35C1	'1829.013005	'1830.081458	2.136906	0	0.14379164	
VPS13D	'20747.91371	'20748.98202	2.136626	0.24918	0.143817894	
ATAD5	'9296.074037	'9297.139039	2.130004	0.45339	0.144440379	
PNMA1	'1586.634667	'1587.679366	2.089398	0	0.148324508	
TTC29	'2306.440372	'2307.480176	2.079608	0.26066	0.149278508	
NR1D2	'2651.018227	'2652.053427	2.0704	0	0.150182128	
AHSA1	'1500.734365	'1501.768204	2.067678	0	0.150450432	
MOCS3	'2330.30798	'2331.340434	2.064908	999	0.150724025	
C8orf40	'467.375966	'468.400389	2.048846	0	0.152321608	
STX2	'1322.110596	'1323.116704	2.012216	0.18191	0.156037255	
CCRL1	'1662.00451	'1663.005994	2.002968	0	0.15699154	
IL19	'1202.648611	'1203.640994	1.984766	0	0.158889218	
PSMD9	'1065.550326	'1066.539932	1.979212	0.14915	0.159473446	
ATG16L1	'2891.754625	'2892.738586	1.967922	0	0.160668603	
MBTPS2	'2424.006126	'2424.985216	1.95818	0	0.161708098	
GPR89A	'1485.51403	'1486.481371	1.934682	0	0.16424712	
ME2	'2646.362749	'2647.325726	1.925954	0	0.165201778	
PAFAH1B1	'1902.580745	'1903.536548	1.911606	0	0.166784971	
C1orf27	'2080.574106	'2081.520585	1.892958	0	0.168868666	
NUP88	'3817.006419	'3817.949096	1.885354	0.23653	0.169726876	
TNS3	'7655.654267	'7656.570793	1.833052	0.08837	0.175767483	
CWC22	'4319.348749	'4320.260558	1.823618	0.24384	0.176883219	
ITGB8	'3617.623606	'3618.529087	1.810962	0.19417	0.178392872	
DNAI2	'3180.89052	'3181.794673	1.808306	0.29491	0.178711575	
CASP8	'2452.305364	'2453.198888	1.787048	999	0.181286249	
GLYAT	'1576.763793	'1577.652602	1.777618	999	0.182442095	
VSIG1	'2093.026636	'2093.91053	1.767788	0	0.183656069	
KCNB1	'3940.893112	'3941.770789	1.755354	0	0.185205073	
TRIM39	'2366.996942	'2367.873509	1.753134	0.19406	0.18548323	
SCG3	'2152.168136	'2153.041794	1.747316	0.16882	0.186214505	
GCK	'2425.550404	'2426.418419	1.73603	0.18481	0.187642639	
EIF2C2	'4034.40605	'4035.269279	1.726458	0	0.188863876	
NCKAP1L	'5393.563547	'5394.420276	1.713458	223.54827	0.190537327	
CEP78	'3500.776449	'3501.632696	1.712494	0.18302	0.190662106	
FCRL2	'3055.863519	'3056.715555	1.704072	0.27336	0.191756308	
TMEM194A	'2096.066125	'2096.908713	1.685176	0	0.194238101	
CPT1B	'3719.953779	'3720.789215	1.670872	0.13284	0.196141778	
ELF4	'3310.369554	'3311.183923	1.628738	0	0.20187769	
DHRS7	'1625.961809	'1626.768318	1.613018	0	0.204068083	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
GOLGA5	'3484.577311	'3485.379682	1.604742	0.28938	0.205232493	
LETM2	'2521.852498	'2522.651831	1.598666	999	0.20609236	
FOLR2	'1278.089474	'1278.86525	1.551552	0	0.21290647	
CPA5	'2349.00998	'2349.770752	1.521544	0.25207	0.217385989	
LGALS7	'626.064415	'626.821435	1.51404	0.1542	0.218523652	
ZNF192	'2771.793598	'2772.540093	1.49299	999	0.221753123	
IL17RB	'2644.798083	'2645.539702	1.483238	0	0.223268594	
CMBL	'1194.682626	'1195.394836	1.42442	999	0.232677261	
PMFBP1	'5169.899451	'5170.610716	1.42253	0.15214	0.232987426	
SLC24A4	'2704.386551	'2705.090559	1.408016	0.18908	0.235386028	
UPF2	'5623.482225	'5624.184043	1.403636	0.1917	0.236115733	
ATAD2	'6456.401914	'6457.102406	1.400984	999	0.236558886	
GAL3ST4	'2423.955902	'2424.655077	1.39835	999	0.23700003	
HM13	'1874.02498	'1874.72132	1.39268	0	0.237953033	
RALGDS	'4387.302	'4387.994484	1.384968	0.17276	0.239256725	
AGAP10	'4366.158345	'4366.849842	1.382994	999	0.239591818	
HSD17B3	'1583.614138	'1584.305456	1.382636	0.23308	0.239652651	
THY1	'745.783696	'746.472078	1.376764	0	0.240653126	
PCDHA1	'5052.302579	'5052.986702	1.368246	0	0.242113474	
C19orf47	'2054.367518	'2055.048826	1.362616	0	0.24308462	
USP18	'2026.232912	'2026.890368	1.314912	999	0.251507233	
CHST4	'1995.992898	'1996.648641	1.311486	0.17849	0.252125783	
PADI1	'3540.739725	'3541.36778	1.25611	0.29349	0.262388701	
LIPH	'2243.204681	'2243.827984	1.246606	999	0.264201704	
PRRC1	'2120.255252	'2120.874888	1.239272	0	0.265611403	
C1orf101	'5590.179626	'5590.798643	1.238034	0.47854	0.265850287	
DCAF5	'4504.197216	'4504.812647	1.230862	0.21036	0.267239465	
LTK	'4352.243313	'4352.845494	1.204362	0.40173	0.272451595	
MTIF3	'1538.859533	'1539.455723	1.19238	999	0.274850007	
CORO1C	'2136.269354	'2136.856475	1.174242	0	0.278531335	
ZNF540	'3153.625649	'3154.21116	1.171022	0	0.279191347	
TSPAN8	'1578.49152	'1579.071235	1.15943	3.05102	0.281583785	
INTS6	'4110.290396	'4110.863803	1.146814	0	0.284217085	
CCDC82	'2745.65851	'2746.219826	1.122632	0.11558	0.289352421	
CENPT	'3154.255509	'3154.812694	1.11437	0.23757	0.291133976	
PM20D2	'2162.676127	'2163.218536	1.084818	999	0.297622231	
IRX6	'2444.250586	'2444.789654	1.078136	0.31672	0.29911492	
VPREB1	'804.869619	'805.368643	0.998048	999	0.317783296	
PLEKHB2	'1115.904617	'1116.376716	0.944198	0	0.331200557	
PTTG2	'1129.869265	'1130.340543	0.942556	0.42901	0.33162137	
TMEM121	'1355.1797	'1355.621615	0.88383	0	0.347154815	
C14orf180	'1003.488817	'1003.926941	0.876248	999	0.349231385	
LAPTM4B	'2137.076964	'2137.507756	0.861584	0	0.3532958	
MSRB2	'999.225301	'999.647305	0.844008	0	0.358252991	
GCGR	'2923.684159	'2924.104025	0.839732	0.40949	0.35947343	
CCL24	'712.146747	'712.558175	0.822856	999	0.36434646	
FMO6P	'712.116478	'712.527778	0.8226	999	0.364421082	
TACR2	'1976.965101	'1977.351107	0.772012	999	0.379595343	
TBCB	'1153.112118	'1153.495698	0.76716	0	0.381097065	
SLC22A17	'2376.611478	'2376.993525	0.764094	0	0.382050345	
ZNF561	'3224.418581	'3224.796934	0.756706	0.15601	0.384361341	
APOBEC1	'1256.979388	'1257.346386	0.733996	0.28481	0.391590988	
PCDHA3	'4896.389442	'4896.74613	0.713376	0	0.398325335	
CAPN7	'3743.155384	'3743.508949	0.70713	0.34233	0.400398232	
ABHD4	'1660.85629	'1661.207506	0.702432	0	0.401967712	
ITGB3BP	'887.226493	'887.577019	0.701052	0.27023	0.402430433	
ABCB11	'6822.215651	'6822.563878	0.696454	0.52137	0.403977773	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
TMEM61	'1208.925089	'1209.267768	0.685358	999	0.407747799	
WDR74	'1903.682049	'1904.02461	0.685122	999	0.407828542	
SDSL	'1770.02526	'1770.36455	0.67858	0.17796	0.410076125	
ZBP1	'2567.133305	'2567.467728	0.668846	0.43788	0.413454233	
CCDC68	'1603.138857	'1603.471976	0.666238	999	0.414366294	
TMEM232	'3271.504092	'3271.828446	0.648708	999	0.420574982	
PINX1	'1711.389349	'1711.712507	0.646316	999	0.421432893	
ZNF20	'2603.165437	'2603.488594	0.646314	0.34923	0.421433612	
C1orf43	'1159.684909	'1160.006122	0.642426	13.66894	0.42283367	
CISH	'1389.174593	'1389.492609	0.636032	999	0.425151331	
DDB2	'2011.582547	'2011.899186	0.633278	0	0.426155465	
HAUS2	'1108.952017	'1109.266222	0.62841	188.64626	0.427939137	
MTG1	'1717.875265	'1718.189193	0.627856	0.40336	0.428142839	
C4orf31	'2782.711384	'2783.024786	0.626804	999	0.428530057	
TFEC	'1628.197261	'1628.504783	0.615044	999	0.432894951	
SULF2	'4179.558198	'4179.863063	0.60973	0	0.434889488	
C4orf7	'518.665652	'518.965588	0.599872	999	0.438626868	
MBD6	'4426.046513	'4426.345309	0.597592	0	0.439498265	
KMO	'2494.904817	'2495.202426	0.595218	153.83975	0.440408414	
PIGA	'2362.636073	'2362.93067	0.589194	0.4397	0.442730963	
MS4A7	'1299.98196	'1300.273217	0.582514	999	0.445328597	
GUCY2F	'5371.428237	'5371.716734	0.576994	999	0.447492995	
AGGF1	'3402.359564	'3402.637109	0.55509	373.24246	0.456245349	
ADAM9	'3865.388462	'3865.664643	0.552362	999	0.457354185	
MAGEB17	'1973.919317	'1974.194743	0.550852	2.37785	0.457969776	
TMCC3	'2203.782516	'2204.054791	0.54455	0.31231	0.460553152	
CXCR5	'1773.304065	'1773.575551	0.542972	0.33252	0.461203637	
TSSK4	'1833.7892	'1834.056594	0.534788	0.47104	0.464600811	
CCDC36	'3126.376435	'3126.643456	0.534042	999	0.464912458	
GPR176	'2455.710324	'2455.971066	0.521484	999	0.470209335	
C12orf5	'1454.222571	'1454.478868	0.512594	999	0.474018084	
NPY5R	'1989.808585	'1990.064879	0.512588	0.33983	0.474020672	
EFS	'2802.097949	'2802.353254	0.51061	0	0.474874911	
SIPA1	'4986.772256	'4987.026523	0.508534	999	0.475774166	
ZFP57	'2766.379139	'2766.630014	0.50175	80.49616	0.478732195	
MAGEB3	'1942.204132	'1942.454261	0.500258	999	0.479386781	
RGS18	'1078.169038	'1078.41639	0.494704	999	0.481836428	
CNTFR	'1737.135498	'1737.382779	0.494562	28.90954	0.481899328	
C9orf9	'840.414529	'840.656687	0.484316	0.21679	0.486473823	
FAM55B	'2830.753192	'2830.994719	0.483054	0.51067	0.487042227	
HEYL	'1751.629788	'1751.869368	0.47916	0.43143	0.488803049	
GPT2	'2464.144341	'2464.367285	0.445888	0	0.504294174	
DNAJC24	'684.223707	'684.445937	0.44446	999	0.504977621	
DEF8	'2630.671745	'2630.889964	0.436438	38.73116	0.508846711	
H2AFB3	'625.769214	'625.983581	0.428734	999	0.51261081	
PAX9	'1572.315118	'1572.528142	0.426048	999	0.513934534	
OR10G3	'1723.978989	'1724.185126	0.412274	999	0.520817564	
USP26	'5057.832404	'5058.037624	0.41044	0.62746	0.521746263	
C4orf33	'1021.592956	'1021.797959	0.410006	0.35439	0.52196646	
USP1	'3480.606726	'3480.809011	0.40457	0.33811	0.524738506	
COQ3	'1950.902599	'1951.102957	0.400716	0.53562	0.526719716	
IRF8	'2086.719212	'2086.919246	0.400068	0	0.527054141	
GCDH	'2327.451119	'2327.646705	0.391172	999	0.531683991	
KLRG2	'2203.569861	'2203.762959	0.386196	2.69469	0.534305754	
MRPL55	'877.665762	'877.855259	0.378994	999	0.538142123	
GPR179	'14282.67412	'14282.8632	0.378166	0.5135	0.5385864	
IL17REL	'1708.366699	'1708.549248	0.365098	999	0.545688479	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
SUSD3	'1285.377875	'1285.554687	0.353624	999	0.552068806	
OR6M1	'1728.833098	'1729.006875	0.347554	999	0.555501028	
CLEC4E	'1201.727993	'1201.895365	0.334744	999	0.562878912	
CEACAM6	'2795.139867	'2795.290262	0.30079	0.54566	0.583387585	
ZNF117	'3441.994382	'3442.140896	0.293028	0.54976	0.588286619	
RD3	'981.889969	'982.03411	0.288282	999	0.591323574	
S1PR3	'1732.335071	'1732.476252	0.282362	0	0.595157241	
CNTN6	'5057.310872	'5057.448682	0.27562	0.57277	0.599586501	
ZNF275	'2173.64185	'2173.777182	0.270664	0	0.602886703	
FAM103A1	'520.744181	'520.87713	0.265898	0	0.606096797	
CEBPZ	'5166.991786	'5167.124437	0.265302	999	0.606500785	
DNAJC30	'1248.116322	'1248.247065	0.261486	0.3349	0.609101086	
RCN2	'1491.296319	'1491.426102	0.259566	0.51373	0.610418475	
COX5B	'679.25987	'679.384847	0.249954	0.47196	0.617107469	
ABHD10	'1500.848214	'1500.970801	0.245174	0.43535	0.620493901	
TMED4	'1062.344757	'1062.466293	0.243072	999	0.621996106	
ISYNA1	'2711.729069	'2711.842251	0.226364	0.231	0.634233073	
HIST1H2AL	'744.31161	'744.417999	0.212778	0	0.644598695	
OVOL2	'1301.030814	'1301.134101	0.206574	28.67774	0.649466023	
RTN4RL2	'1990.360683	'1990.455307	0.189248	999	0.663543239	
MRGPRD	'1879.322675	'1879.41671	0.18807	185.81133	0.664527817	
TNIP3	'2039.700399	'2039.794051	0.187304	0.58593	0.665170012	
KCNJ9	'1728.482785	'1728.576078	0.186586	33.39415	0.665773381	
TMEM38B	'1445.915498	'1446.000282	0.169568	0.58445	0.680496025	
PNLIPRP3	'2314.436194	'2314.518569	0.16475	0.58762	0.684820432	
POGK	'2868.663829	'2868.744538	0.161418	999	0.68785434	
DMGDH	'4203.583001	'4203.661866	0.15773	0.56811	0.691255108	
SMR3B	'486.771851	'486.840298	0.136894	0	0.711388532	
MPHOSPH9	'4893.435126	'4893.501402	0.132552	0.35353	0.715800575	
SMC5	'5110.801645	'5110.867893	0.132496	2.02828	0.715858009	
KANK3	'4442.227461	'4442.286026	0.11713	0	0.732168326	
EPSTI1	'2232.528198	'2232.583529	0.110662	0.64145	0.739391713	
GP1BA	'4200.859031	'4200.913705	0.109348	1.16577	0.740887653	
SH3D21	'4135.321452	'4135.373315	0.103726	0.55375	0.747403293	
SOAT2	'2725.367354	'2725.417688	0.100668	2.10542	0.751029476	
SLC6A4	'3062.258893	'3062.30843	0.099074	0	0.752943713	
LHX2	'1796.568774	'1796.6118	0.086052	0	0.769257534	
C11orf20	'1250.557578	'1250.59839	0.081624	0	0.775108562	
PRKCD	'3134.617382	'3134.649381	0.063998	0.58235	0.800285013	
DDHD2	'3298.057418	'3298.086678	0.05852	1.33913	0.808850619	
NPFFR1	'2089.880752	'2089.905892	0.05028	999	0.822576767	
ARHGAP4	'5883.903523	'5883.927986	0.048926	2.00633	0.824942764	
DNAJC5G	'1132.581273	'1132.604785	0.047024	1.31331	0.828325105	
SV2B	'3191.150927	'3191.173939	0.046024	0	0.830132177	
EXPH5	'10701.00498	'10701.0248	0.039638	1.24566	0.842190041	
SYNPO2L	'4887.128117	'4887.144501	0.032768	3.50012	0.856352399	
HELB	'5542.203898	'5542.218648	0.0295	1.15529	0.863629641	
GPR39	'2379.909495	'2379.92106	0.02313	1.24656	0.879119499	
ZC3H13	'7602.064378	'7602.075711	0.022666	0	0.880328878	
CCDC157	'3833.879137	'3833.888795	0.019316	0.81391	0.889464362	
RAB17	'1171.129436	'1171.138555	0.018238	0.8149	0.892573813	
DLEC1	'9085.756135	'9085.764404	0.016538	1.40218	0.897674043	
C19orf68	'3319.919125	'3319.926784	0.015318	999	0.901500626	
LRPPRC	'7708.098349	'7708.103219	0.00974	0.95049	0.921383267	
TTF1	'5078.404723	'5078.408307	0.007168	1.09052	0.932528484	
PPIG	'3511.160684	'3511.163126	0.004884	0.91773	0.944284698	
PLAU	'2338.287027	'2338.289422	0.00479	1.07606	0.944822602	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
CYP3A5	'2730.707074	'2730.709251	0.004354	0.95175	0.94738989	
CHL1	'6211.812707	'6211.814819	0.004224	0.88153	0.948180125	
ERCC3	'3776.690577	'3776.692657	0.00416	0	0.94857365	
CHRDL2	'2445.551465	'2445.552464	0.001998	0	0.964347236	
GFOD2	'1869.464095	'1869.465064	0.001938	0	0.964886292	
COPS4	'1959.403746	'1959.404639	0.001786	1.06262	0.966290561	
FKRP	'2437.646072	'2437.646937	0.00173	0	0.966822939	
GNAO1	'2115.472659	'2115.473421	0.001524	0	0.968859739	
PIAS1	'2899.37697	'2899.377705	0.00147	0	0.969416137	
EBI3	'1154.109118	'1154.109664	0.001092	0.94395	0.973638365	
OAS1	'2334.418475	'2334.418997	0.001044	1.02988	0.974224046	
FBXL12	'1532.75429	'1532.754792	0.001004	0	0.974722492	
DCAF12L2	'2618.319768	'2618.320234	0.000932	0	0.975645425	
IDO2	'2230.192375	'2230.192836	0.000922	0	0.975776394	
ILKAP	'1841.498495	'1841.498938	0.000886	0	0.976253872	
CD69	'1045.196033	'1045.196475	0.000884	0	0.976280681	
FAAH2	'2753.813241	'2753.813673	0.000864	0.96247	0.976550456	
L3MBTL1	'3976.056969	'3976.0574	0.000862	0	0.976577605	
SLC16A8	'2346.492548	'2346.492971	0.000846	0	0.976795938	
RNF11	'655.292812	'655.293204	0.000784	0	0.977662151	
KPTN	'2402.788645	'2402.789032	0.000774	0	0.977805032	
MAP3K7	'2660.905164	'2660.905532	0.000736	0	0.978356589	
SCN1B	'1019.185074	'1019.18544	0.000732	0	0.978415469	
GPRASP2	'4102.306255	'4102.306578	0.000646	1.0259	0.979722726	
TUBB	'2154.245482	'2154.245797	0.00063	0	0.979975359	
ANGEL2	'2366.578917	'2366.57923	0.000626	0	0.980039017	
FLT3	'4938.71545	'4938.715762	0.000624	1.04733	0.980070923	
CYTH1	'1782.949148	'1782.94942	0.000544	0	0.981391981	
ZC3H12D	'2708.412194	'2708.412464	0.00054	0	0.981460507	
LHFPL2	'1093.406444	'1093.406709	0.00053	0	0.98163294	
NDUFA6	'805.108162	'805.108405	0.000486	0	0.982411734	
TNFAIP8L3	'1465.138179	'1465.138396	0.000434	0	0.983379139	
ASPH	'3783.701989	'3783.702183	0.000388	0	0.984284513	
KRT36	'2449.920834	'2449.921018	0.000368	0	0.984694859	
SUV39H1	'1814.111869	'1814.112027	0.000316	0	0.985817241	
LSM7	'453.512187	'453.512323	0.000272	0	0.986841547	
CDC23	'2708.19025	'2708.19038	0.00026	0	0.987135056	
EIF2C4	'3719.55317	'3719.5533	0.00026	0	0.987135056	
NDP	'595.335328	'595.335453	0.00025	0	0.987384863	
PRSS55	'2132.264034	'2132.264154	0.00024	0	0.98763972	
DNAJC17	'1458.535889	'1458.536003	0.000228	0	0.987952665	
RAD21L1	'2719.831063	'2719.831171	0.000216	0	0.988273962	
GSC	'1065.45745	'1065.457555	0.00021	0	0.988437959	
DCAF4L1	'1947.941783	'1947.941885	0.000204	0	0.988604316	
RPL26	'712.945063	'712.945165	0.000204	0	0.988604316	
HIST1H2AJ	'620.351488	'620.351588	0.0002	0	0.988716584	
MPV17L	'1181.753186	'1181.753275	0.000178	0	0.989355208	
BROX	'1818.441608	'1818.441691	0.000166	0	0.989720261	
CA10	'1497.611748	'1497.611829	0.000162	0	0.989844862	
FOSB	'1438.019202	'1438.019282	0.00016	0	0.989907739	
ICT1	'1155.089174	'1155.089253	0.000158	0	0.989971011	
ZNF575	'1660.839157	'1660.839234	0.000154	0	0.990098767	
DERL1	'1106.312854	'1106.312928	0.000148	0	0.990293555	
DCAF7	'1558.923107	'1558.92318	0.000146	0	0.990359359	
ZNF157	'2379.434433	'2379.434505	0.000144	0	0.990425615	
MED7	'980.949476	'980.949547	0.000142	0	0.990492333	
LYG1	'1103.421785	'1103.421856	0.000142	0	0.990492333	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
PPM1E	'3396.768172	'3396.768243	0.000142	0	0.990492333	
FBXO22	'1930.720791	'1930.720859	0.000136	0	0.990695358	
C20orf160	'2427.307989	'2427.308052	0.000126	0	0.991043956	
CHMP5	'937.877506	'937.877569	0.000126	0	0.991043956	
CHST2	'2516.659279	'2516.659342	0.000126	0	0.991043956	
RBBP7	'2093.814624	'2093.814685	0.000122	0	0.991187256	
PIP4K2C	'1757.574984	'1757.575044	0.00012	0	0.991259787	
DLX6	'1107.777672	'1107.777729	0.000114	0	0.991481086	
DIRC2	'2215.782114	'2215.782171	0.000114	0	0.991481086	
CDC20	'2290.255237	'2290.255293	0.000112	0	0.991556141	
MPZL2	'1008.251831	'1008.251887	0.000112	0	0.991556141	
PLK2	'3091.218566	'3091.21862	0.000108	0	0.99170829	
HIST1H3G	'641.629555	'641.629609	0.000108	0	0.99170829	
WDFY2	'1824.215567	'1824.21562	0.000106	0	0.991785421	
IFI27L1	'554.40056	'554.40061	1E'04	0	0.992021287	
TAGLN	'885.16576	'885.165809	9.8E'05	0	0.992101475	
CD2AP	'3055.097339	'3055.097386	9.4E'05	0	0.992264343	
MED19	'1132.968568	'1132.968614	9.2E'05	0	0.992347077	
HLF	'1269.765222	'1269.765267	9E'05	0	0.992430716	
NPY1R	'1730.458239	'1730.458283	8.8E'05	0	0.992515289	
WFDC11	'494.399765	'494.399805	8E'05	0	0.992863599	
TMEM92	'872.502025	'872.502063	7.6E'05	0	0.993044292	
DCTN6	'847.906568	'847.906604	7.2E'05	0	0.993229806	
METAP1D	'1550.472563	'1550.472599	7.2E'05	0	0.993229806	
OR13J1	'1779.142836	'1779.142872	7.2E'05	0	0.993229806	
GIMAP2	'1824.156761	'1824.156796	7E'05	0	0.993324497	
LSM10	'586.604886	'586.604921	7E'05	0	0.993324497	
TMEM208	'764.313312	'764.313347	7E'05	0	0.993324497	
GADD45A	'733.845811	'733.845843	6.4E'05	0	0.993616992	
CAV1	'809.615718	'809.615746	5.6E'05	0	0.994029234	
PGAM1	'1123.194258	'1123.194286	5.6E'05	0	0.994029234	
CCDC115	'881.708084	'881.70811	5.2E'05	0	0.994246422	
C9orf142	'1044.044003	'1044.044028	5E'05	0	0.994358151	
FXYD3	'495.779143	'495.779166	4.6E'05	0	0.994588525	
FAM64A	'1282.482638	'1282.482658	4E'05	0	0.994953769	
MBNL2	'1567.260762	'1567.260779	3.4E'05	0	0.9953476	
GPHA2	'627.576985	'627.577001	3.2E'05	0	0.995486507	
NPFF	'606.916141	'606.916156	3E'05	0	0.995629828	
ZNRD1	'572.059201	'572.059216	3E'05	0	0.995629828	
CCDC69	'1442.396546	'1442.39656	2.8E'05	0	0.995778011	
ENOPH1	'1178.249985	'1178.249997	2.4E'05	0	0.996091196	
TMEM139	'1120.623334	'1120.623345	2.2E'05	0	0.996257603	
RABGGTA	'2637.846194	'2637.846205	2.2E'05	0	0.996257603	
SNRPA1	'1117.342356	'1117.342366	2E'05	0	0.996431764	
CNPY1	'413.535203	'413.535211	1.6E'05	0	0.99680847	
RBP7	'647.188536	'647.188544	1.6E'05	0	0.99680847	
ADAT2	'896.743828	'896.743835	1.4E'05	0	0.997014596	
ARV1	'1317.52056	'1317.520565	1E'05	0	0.997476872	
BET1	'508.096101	'508.096106	1E'05	0	0.997476872	
DEFB110	'340.49901	'340.499014	8E'06	0	0.997743245	
FAM165B	'284.955599	'284.955603	8E'06	0	0.997743245	
IFNA2	'1006.051638	'1006.051642	8E'06	0	0.997743245	
PRRG1	'979.429862	'979.429866	8E'06	0	0.997743245	
DEFB103A	'336.132905	'336.132908	6E'06	0	0.998045592	
GNG5P2	'353.079637	'353.07964	6E'06	0	0.998045592	
MRPL21	'1129.843978	'1129.843981	6E'06	0	0.998045592	
RPS23	'645.084014	'645.084016	4E'06	0	0.998404232	

Gene	lnL&free	lnL&fixed	2ΔlnL	branch_w	pvalue	k
HNRNPD	'1491.679054	'1491.679055	2E'06	0	0.998871621	
TBRG1	'1916.754361	'1916.754361	0	0	1	
ARL6IP1	'940.042088	'940.041513	'0.00115	0	#NUM!	
ATP5H	'762.138911	'762.138322	'0.001178	0	#NUM!	
C10orf11	'975.762981	'975.762944	'7.4E'05	0	#NUM!	
C8orf39	'460.718432	'460.662941	'0.110982	0	#NUM!	
CCDC132	'4370.455322	'4370.45505	'0.000544	0	#NUM!	
CCNB1	'1927.613143	'1927.067892	'1.090502	4.88494	#NUM!	
CDT1	'2995.291441	'2995.291344	'0.000194	0	#NUM!	
COL5A2	'6701.802802	'6697.666027	'8.27355	50.19781	#NUM!	
DBX1	'2071.865235	'2071.865102	'0.000266	0	#NUM!	
FAM126B	'2587.999078	'2587.998749	'0.000658	0	#NUM!	
GCOM1	'2849.396212	'2849.395886	'0.000652	0	#NUM!	
GMNN	'1050.005305	'1035.103295	'29.80402	0	#NUM!	
KIAA0562	'4760.826301	'4760.466418	'0.719766	22.3534	#NUM!	
LRRC2	'1794.284508	'1794.28448	'5.6E'05	0	#NUM!	
MAP4K4	'6266.87664	'6066.485725	'400.78183	0	#NUM!	
MBLAC2	'1292.951492	'1292.951466	'5.2E'05	0	#NUM!	
NSUN3	'1619.488938	'1619.488932	'1.2E'05	0	#NUM!	
OAZ2	'820.725354	'820.725343	'2.2E'05	0	#NUM!	
PLB1	'7881.849975	'7857.54055	'48.61885	999	#NUM!	
PLP1	'1162.283124	'1162.283109	'3E'05	0	#NUM!	
POU2F2	'2166.487983	'2166.485041	'0.005884	0	#NUM!	
PPM1K	'1668.005841	'1668.005837	'8E'06	0	#NUM!	
PPP1R12A	'4527.3883	'4527.387714	'0.001172	0	#NUM!	
PRMT6	'1672.066826	'1672.066785	'8.2E'05	0	#NUM!	
RAP1GAP2	'3635.355246	'3634.940065	'0.830362	17.94914	#NUM!	
RBBP6	'8242.341213	'8240.754346	'3.173734	17.05038	#NUM!	
RNF34	'1774.831438	'1774.831422	'3.2E'05	0	#NUM!	
ROBO4	'5274.092492	'5269.221154	'9.742676	131.6388	#NUM!	
S100A4	'429.462564	'429.462562	'4E'06	0	#NUM!	
SEMA6B	'4181.896831	'4181.827038	'0.139586	25.45196	#NUM!	
SLC31A1	'859.479808	'859.479761	'9.4E'05	0	#NUM!	
TBXA2R	'1671.25683	'1671.256805	'5E'05	0	#NUM!	
TIAF1	'617.587775	'617.587692	'0.000166	0	#NUM!	
TRAIP	'2359.984013	'2304.927098	'110.11383	0	#NUM!	
WDR5B	'1588.90202	'1588.90201	'2E'05	0	#NUM!	
WDR63	'4329.81815	'4325.555269	'8.525762	68.97497	#NUM!	
ZC4H2	'923.282245	'923.282232	'2.6E'05	0	#NUM!	
ZFP37	'3102.52558	'3100.967788	'3.115584	154.23522	#NUM!	

Seminal Tau Estimates

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4*ω*	Uniform*'Kα*	Uniform4*Ks*
ǀA1BG	0.986517989	0.3239	0.25302	0.22093	0.33426	0.0682	0.204
ǀA4GALT	0.509892371	0.2318	0	0.25532	0.09809	0.031	0.3155
ǀABP1	0.982225799	0.1464	0.16249	0.059	0.17234	0.0388	0.2249
ǀACAT2	0.8810401	0.5148	0.20988	999	0.50645	0.0513	0.1013
ǀACE	0.626527252	0.2448	0.10081	0.25098	0.10981	0.0333	0.3037
ǀACE2	0.960818221	0.4483	0.31145	0.79755	0.66947	0.096	0.1434
ǀACLY	0.93173551	0.1509	0.07015	0.20104	0.06161	0.0089	0.1443
ǀACO1	0.918213974	0.0345	0	0.14859	0.13829	0.0144	0.1039
ǀACP5	0.974619229	0.2053	0.50447	0.17393	0.11253	0.0221	0.1961
ǀACPP	0.986627448	0.4027	0	1.55687	0.73724	0.0522	0.0708
ǀACR	0.726102454	0.3695	0.51625	0.4463	0.40141	0.0769	0.1916
ǀACRBP		0.2206	0.18156	0.72929	0.41611	0.0717	0.1724
ǀACRV1	0.944208332	1.0706	0.91888	999	0.42613	0.0873	0.205
ǀACTN1	0.928330678	0	0	0	0.0318	0.0077	0.2425
ǀACTN4	0.937518567	0	0	0	0.00599	0.0026	0.4381
ǀACTR1A	0.657011092	0	0	0	0	0	0.1522
ǀACYP1	0.806234685	0	0	0	0.3842	0.0372	0.0967
ǀADAM10	0.844470356	0	0	0	0.07671	0.006	0.0777
ǀADAM7	0.967263277	0.4806	2.05232	0.44915	0.51589	0.0608	0.1179
ǀADAMTS1	0.910386364	0.0341	0	0.08843	0.08923	0.0153	0.1711
ǀADAMTSL1	0.131651053	0.2254	0.25075	0.23449	0.15136	0.0177	0.1167
ǀAGA	0.714249307	0.1262	0.17525	0.11645	0.47452	0.0478	0.1008
ǀAGR2	0.959137219	=1	999	0	0.23294	0.0144	0.0617
ǀAGRN	0.695480499	0.2105	0.12711	0.18264	0.13581	0.0436	0.3213
ǀAGT	0.952422834	0.1102	0.05588	0.28914	0.23471	0.0582	0.2481
ǀAHCY	0.893903555	0	0	0	0.20319	0.058	0.2856
ǀAKR1A1	0.891417289	0.1081	0	9.00822	0.11113	0.0105	0.0941
ǀAKR1B1	0.935673745	0.8814	15.36762	0.6451	0.11948	0.0172	0.1436
ǀAKR7A2	0.837908576	0.3306	0.14674	0.20186	0.1908	0.057	0.299
ǀALAD	0.947169166	0.1477	0.43863	0.08637	0.24398	0.0329	0.1346
ǀALB	0.96711393	0.4767	0.53772	0.60557	0.38549	0.052	0.1349
ǀALCAM	0.838792606	0.0268	0.08925	0	0.08863	0.0089	0.1
ǀALDH1A1	0.886798256	0	0	0	0.09454	0.0114	0.1209
ǀALDH7A1	0.742355283	0.1595	0.17772	0.24165	0.16655	0.0213	0.1278
ǀALDH9A1	0.782573657	0.1606	0.10673	276.10715	0.18802	0.0236	0.1253
ǀALDOA	0.837688917	0	0	0	0.02534	0.0054	0.2137
ǀALDOC	0.892544222	0.3387	0	999	0.09505	0.0094	0.0989
ǀAMBP	0.747611234	0.2353	0.20814	0.2808	0.16497	0.0292	0.1773
ǀANG	0.984225297	0.3211	0	999	1.26483	0.1571	0.1242
ǀANPEP	0.949496316	0.2683	0.19946	0.21283	0.21071	0.0443	0.2102
ǀANTXR2		0.1962	0.12156	0.62507	0.15789	0.0172	0.1087
ǀANXA1	0.941400227	0	0	0	0.07163	0.0073	0.1019
ǀANXA11	0.832586205	0	0	0	0.61009	0.3073	0.5037
ǀANXA2	0.903276137	0	0	0	0.00787	0.0013	0.1647
ǀANXA3	0.968432692	0.1841	0.28474	0.21678	0.21532	0.0291	0.1354
ǀANXA4	0.891151157	0.1035	93.17268	0	0.16539	0.014	0.0848
ǀANXA5	0.802320918	0	0	0	0.15992	0.009	0.0563
ǀANXA6	0.819084717	0.2587	0.36517	0.18691	0.20573	0.0425	0.2067
ǀANXA7	0.67634399	0.9834	999	0.41839	0.21453	0.0171	0.0799
ǀAPCS	0.984497916	0.6304	0.82071	0.81126	0.66684	0.0833	0.125
ǀAPEH	0.911997485	0.1625	999	0	0.08984	0.0084	0.0932
ǀAPLP2	0.872336265	0.1907	0.08186	1.1892	0.13033	0.0176	0.135
ǀapoa1BP		0.3404	0.1769	999	0.25795	0.0291	0.1128
ǀAPOA2	0.69717964	1.2973	0	999	0.50302	0.0777	0.1545
ǀAPOB	0.980764928	0.4805	0.79527	0.69561	0.50294	0.051	0.1015
ǀAPOD	0.905266193	0.4595	0.84798	0.42371	1.85478	0.1371	0.0739
ǀAPOE	0.789355457	0.8281	0.325	0.40181	0.21988	0.0833	0.3789
ǀAPOH	0.97358555	0.1502	0.36502	0.12241	0.28839	0.0395	0.137
ǀAPP	0.710562208	0.0488	0.12154	0	0.17444	0.0246	0.141
ǀARF1	0.752109437	0	0	0	0	0	0.2302
ǀARF6	0.848733605	0	0	0	0	0	0.0569
ǀARHGDIA	0.761823503	0.2147	0.17681	0.23852	0.26962	0.0308	0.1144

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform4Ka	Uniform4Ks
!ARSA	0.730702727	0.5192	0.06558	0.98003	0.22162	0.0422	0.1905
!ASAH1	0.757848688	0.4523	1.68469	0.16382	0.41078	0.0536	0.1306
!ASRGL1	0.936297677	0.8384	0.41063	1.64008	0.28671	0.0419	0.1463
!ATRN	0.618783094	0.5897	0.06379	0.87493	0.26264	0.0411	0.1566
!AZGP1	0.937757419	0.0586	0	0.02571	0.42468	0.0812	0.1912
!B2M	0.688262033	=1	0	999	0.51482	0.0596	0.1157
!B4GALT1	0.644216289	0.4457	0.1937	0.9607	0.2536	0.0488	0.1924
!B4GALT4	0.514133744	=1	999	999	0.33034	0.0375	0.1135
!BAIAP2	0.746361808	0.0552	0.08856	0	0.0372	0.013	0.3496
!BASP1	0.848334417	0.1069	0.20527	0	0.19262	0.0193	0.1002
!BCAN	0.589515728	0.1044	0.27577	0.05843	0.19515	0.0266	0.1364
!BGN	0.909669363	0.0448	0.04839	0	0.02656	0.0089	0.3337
!BPIL1	0.982735518	0.2811	999	0.16722	0.2419	0.0416	0.172
!BPNT1	0.423310409	0	0	0	0.18307	0.0189	0.1032
!BTD	0.763217657	0.1945	0.31258	0.20868	0.36377	0.0397	0.1091
!C19orf10	0.835291324	0	0	0	0.03204	0.0086	0.2677
!C1RL	0.75333861	0.3118	0.17337	0.87262	0.28272	0.057	0.2016
!C3	0.966136663	0.2919	0.16778	0.44555	0.22609	0.044	0.1944
!C9	0.881669444	0.6772	1.16237	0.58742	0.4675	0.0739	0.1581
!CA2	0.969548589	=1	999	4.48114	0.27904	0.0316	0.1131
!CA4	0.970441331	1.2871	999	0.90917	0.61962	0.1208	0.195
!CA6	0.986621426	0.2643	0.68256	0.06997	0.24573	0.0592	0.241
!CAB39	0.856419277	0	0	0	0.03366	0.0015	0.0443
!CAB39L	0.451048377	0	0	0	0.0312	0.003	0.0974
!CACNA2D1	0.27766876	0.0965	0.6622	0	0.06728	0.007	0.1038
!CACYBP	0.747489545	0	0	0	0.16147	0.0134	0.0827
!CALR	0.90635438	0	0	0	0.02978	0.0044	0.148
!CAMP	0.982501308	0.161	0	0.15276	1.17322	0.1246	0.1062
!CANT1	0.912214624	0.2743	0.08189	0.40663	0.10605	0.0456	0.43
!CAP1	0.864639568	0.9465	1.21671	0	0.19238	0.019	0.0989
!CAPG	0.938955595	0.0795	0.32622	0	0.07453	0.0117	0.1569
!CAPN1	0.689425376	0.0474	0.05596	0	0.02918	0.0087	0.2996
!CAPNS1		0.2708	0.14107	0.89818	0.06818	0.0161	0.2364
!CAPZA1	0.866317547	0	0	0	0.08727	0.005	0.0574
!CAPZA2	0.839002551	0.1839	0	0.7462	0.05711	0.0033	0.0572
!CAPZB	0.652147858	0.0594	0.13617	0	0.46787	0.1497	0.32
!CAT	0.822142683	0.1468	0.12154	0.47147	0.25119	0.0319	0.1271
!CCT2	0.851548058	0	0	0	0.00897	0.0009	0.0949
!CCT3	0.828050623	0.0774	0	0.16461	0.24102	0.0495	0.2056
!CCT4	0.826405823	0	0	0	0.041	0.0035	0.0841
!CCT5	0.843017748	0	0	0	0.0113	0.0016	0.1381
!CCT7	0.794382082	0	0	0	0.05102	0.0063	0.1237
!CCT8	0.801290293	0.4664	0	1.0878	0.07093	0.0068	0.0953
!CD109	0.354357003	0.2838	0.18862	0.54133	0.36155	0.0448	0.1238
!CD14	0.946861584	0.5301	0.806	0.50295	0.43576	0.0473	0.1086
!CD151	0.857741559	0	0	0	0.08282	0.0231	0.2786
!CD38	0.957387924	0.2863	0.38486	0.38497	0.84752	0.0681	0.0803
!CD44	0.850667522	0.3659	1.0852	0.35501	0.45853	0.0504	0.1099
!CD47	0.670315312	0.4818	0.3981	0.77145	0.1187	0.0105	0.0883
!CD59	0.556346293	=1	0	999	2.49128	0.2234	0.0897
!CD63	0.701662811	=1	0	5.77044	0.08642	0.0079	0.0916
!CD81	0.806437414	0	0	0	0.01699	0.0072	0.4263
!CD9	0.907115864	0.1451	0	0.1549	0.08598	0.0126	0.1467
!CDC42	0.908392241	0	0	0	0.09607	0.0022	0.0225
!CDH1	0.759775966	0.056	0	0.15391	0.19729	0.0339	0.1721
!CFB	0.792644222	0.4057	0.20558	0.77887	0.3508	0.0488	0.1392
!CFL1	0.526835667	0	0	0	0.00954	0.0025	0.2668
!CKB	0.863002666	0	0	0	0.02772	0.0062	0.2252
!CLIC1	0.833541818	0	0	0	0.2248	0.0218	0.0971
!CLN5	0.890102598	0.4799	0.53756	0.72974	0.46382	0.0546	0.1178
!CLSTN1	0.827806571	0.0747	0.08677	0.07965	0.05783	0.0134	0.2326
!CLTC	0.567841832	0	0	0	0.01865	0.0011	0.0613

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4*ω*	Uniform'*Kα*	Uniform4*Ks*
!CLU	0.828648974	0.3355	0.22678	0.46319	0.2118	0.041	0.1936
!CNDP2	0.726227738	0.1692	0.3241	0.0885	0.10332	0.8795	2.2665
!CNP	0.895945052	0	0	0	0.09662	0.0142	0.1466
!CNTN3	0.255762756	0.0518	0.12177	0	0.13329	0.018	0.1353
!CNTNAP2	0.527180192	0.0645	0.04948	0.09814	0.13809	0.0314	0.2272
!col12A1	0.879210822	0.0718	0.05979	0.13388	0.1314	0.0143	0.1085
!COL18A1	0.911416916	0.2064	0.28816	0.16815	0.28163	0.0619	0.2197
!COL6A1	0.59501635	0.1694	0.0839	0.17141	0.15215	0.0632	0.4154
!COL6A2	0.550010044	0.0339	0.03886	0.0123	0.17475	0.0808	0.4625
!COL9A1	0.802672474	0.5901	0.75531	0.83335	0.31564	0.0324	0.1028
!COLEC12	0.880497455	0.0691	0.17617	0.04288	0.06913	0.0109	0.1573
!COMP	0.973950283	0.5379	252.68745	0.3199	0.12853	0.0343	0.2666
!COPB2	0.778845762	0.1752	999	0.15304	0.09465	0.0068	0.0721
!CP	0.856297937	0.1556	0.30693	0.17011	0.28965	0.0273	0.0943
!CPAMD8		0.1896	0.26805	0.12627	0.18279	0.0396	0.2169
!CPD	0.896274373	0.2694	0.13941	0.65493	0.28376	0.0172	0.0606
!CPE	0.889485919	0.043	0	0	0.1066	0.0113	0.1056
!CPM	0.790332514	0.3865	415.88677	0.38313	0.23619	0.0255	0.1078
!CPO		1.5005	0.32023	67.11266	0.44663	0.0914	0.2046
!CPVL	0.961911019	0.7789	0.9999	1.60321	0.47714	0.0516	0.1082
!CPZ		0.1832	0.06131	0.19147	0.0753	0.0158	0.2097
!CREG1	0.862998345	0.0881	0.08775	0	0.14957	0.0252	0.1684
!CRISP1	0.679879477	0.4099	0	0.46738	0.60043	0.105	0.1749
!Crisp2	0.964513586	0.2789	0.29113	0	0.49591	0.0598	0.1206
!CRISP3	0.969209915	0.2776	0.69841	0.17259	0.43931	0.059	0.1343
!CRTAC1	0.864212517	0.1132	0.08946	0.15027	0.08009	0.0112	0.1395
!CRYZ	0.934223798	0.0727	0.12861	0	0.33434	0.0496	0.1485
!CST1	0.986360373	0.5387	0.25793	1.01633	0.4454	0.2108	0.4732
!CST3	0.79371137					0.0173	0.2337
!CST6	0.946462404	=1	0	999	0.14608	0.0298	0.2043
!CTBS	0.943752699	0.2366	999	0.19442	0.33236	0.0414	0.1245
!CTSB	0.89325358	0.0482	0.0517	0.0379	0.09991	0.0272	0.2722
!CTSD	0.534869984	0.1517	0.06837	0.09173	0.07036	0.0346	0.4914
!CTSF	0.821464245	0.3264	0.116	0.65887	0.26689	0.0489	0.1831
!CTSH	0.93595512	0.0562	0.06574	0	0.17724	0.0306	0.1725
!CTSO	0.905782999	0.075	0.37468	0	0.42717	0.0358	0.0839
!CTSZ	0.640052419	0	0	0	0.23084	0.0578	0.2505
!CUL3	0.63955807	0	0	0	0.03312	0.0023	0.0705
!CYB561	0.734390788	0.2866	0.21025	0.28276	0.34622	0.1505	0.4346
!CYB5R2	0.939534405	0.4224	0.46677	0.57112	0.2849	0.0444	0.1559
!DAG1	0.720528121	0.4179	2.05784	0.10224	0.21846	0.023	0.1053
!DBI	0.831957851	0.1542	0.32804	0.0001	0.3187	0.046	0.1442
!DCD	0.985846548	0.3666	0	999	0.78102	0.0812	0.104
!DCXR	0.980259388	0.8536	0.98686	0	0.23412	0.0535	0.2285
!DDAH1	0.869252649	0.3177	0	0.39011	0.07909	0.0087	0.1095
!DDB1	0.802476151	0	0	0	0.023	0.0025	0.1089
!DDR1	0.833007439	0	0	0	0.04061	0.0054	0.1336
!DDT	0.930729706	0	0	0	0.14877	0.0333	0.224
!DEFB129	0.833796607	0	0	0	0.69522	0.0536	0.0772
!DNAJB9	0.836322376	0.2592	0	0.34002	0.41566	0.0352	0.0846
!DNAJC3	0.635911841	0.0697	0.18444	0	0.05636	0.0065	0.1147
!DNASE1	0.644537037	0.4299	999	0.20643	0.18122	0.0452	0.2495
!DNASE2	0.597122867	0.2526	999	0.11715	0.33377	0.0548	0.1641
!DPEP3	0.920753146	0.179	0.28248	0	0.38552	0.0551	0.143
!DPP4	0.907597832	0.142	0.07655	0.77512	0.27757	0.0179	0.0645
!DPP7	0.612380636	0.1951	0.10363	0.12925	0.11549	0.0412	0.3565
!DSC2	0.86538844	0.3668	0.43987	0.48533	0.36703	0.0424	0.1154
!DSC3	0.936356006	0.2295	0.25246	0.31797	0.25095	0.0303	0.1205
!ECM1	0.958739584	0.5333	999	0.40398	0.54571	0.0491	0.09
!EDIL3	0.509641154	0.0582	0.16359	0	0.09572	0.0088	0.092
!EEF1A1	0.548987301	0	0	0	0	0	0.092
!EEF1G	0.62763694	0.1004	0.36637	0	0.17534	0.0207	0.118

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform'Ka	Uniform4Ks
!EEF2	0.736337371	0.0171	0	0.01681	0.00178	0.001	0.5629
!EFEMP1	0.947203248	0	0	0	0.11517	0.0068	0.0592
!EFHD2	0.914363302	=1	0	999	0.04856	0.0307	0.6323
!EGF	0.948436722	0.3627	0.63945	0.34077	0.5994	0.053	0.0884
!ELSPBP1	0.968622471	0.2401	0.22429	0.66002	0.14843	0.026	0.1751
!ENO1	0.905274675	0	0	0	0.01082	0.0021	0.1969
!ENPP3		0.283	0.34352	0.42578	0.29381	0.0341	0.116
!ENPP5		0.1678	0	0.42004	0.33018	0.026	0.0787
!EPHA5	0.455485135	0.1022	0.1353	0.13559	0.15929	0.0133	0.0837
!ESD	0.660130326	0.0566	0	999	0.12855	0.012	0.0931
!EXTL2	0.907046225	=1	5.79159	999	0.22022	0.0142	0.0647
!F11R	0.701080943	=1	8.26353	0	0.35622	0.0318	0.0892
!FAM12A	0.602912241	=1	999	999	0.89891	0.1	0.1112
!FAM12B	0.928680988	0.4838	0.30178	999	0.56441	0.0395	0.07
!fam3B	0.407389744	0.3055	0.18914	999	0.72136	0.0687	0.0952
!FAM3C	0.83091062	0.2964	0	0.35888	0.0976	0.0061	0.0625
!FASN	0.755314507	0.163	0.10855	0.08686	0.1235	0.0517	0.4186
!FBLN2	0.969957718	0.192	0.15615	0.1989	0.12755	0.019	0.1492
!FBP1	0.967827591	0.2391	0.69396	0.12038	0.07692	0.0169	0.2201
!FCGBP	0.959101272	0.2442	0.2529	0.19957	0.19151	0.0318	0.166
!FDPS	0.702614765	0	0	0	0.24122	0.0288	0.1195
!FH	0.733066002	0.1593	0.33587	0.15323	0.10285	0.0128	0.1244
!FKBP4	0.848252425	0.4141	0.19166	999	0.23325	0.0277	0.1188
!FLNB	0.745497075	0.0665	0.09018	0.08318	0.05836	0.0089	0.1524
!FMOD	0.745140693	0	0	0	0.04614	0.0091	0.1975
!FN1	0.925553223	0.0822	0.12835	0.08359	0.1145	0.0135	0.1176
!FOLH1	0.765437285	0.2986	0.50067	0.2256	0.3166	0.0327	0.1034
!FSTL1	0.926465521	0.0692	0	0.18429	0.03158	0.003	0.0965
!FTH1	0.779994947	0	0	0	0.06923	0.0078	0.1122
!FUCA1	0.841025641	0.3468	0.76634	0.38102	0.25481	0.0374	0.1466
!FUCA2	0.79125558	0	0	0	0.22975	0.0214	0.0933
!FUT3	0.369083661	0.1961	0.13256	0.12806	0.16557	0.0927	0.5599
!GAA	0.903281824	0.2145	0.13423	0.15923	0.12394	0.0376	0.303
!GALC	0.852287902	0.0379	0.07638	0	0.23822	0.0237	0.0993
!GALNS	0.832453416	0.2381	0.41783	0.10532	0.12852	0.0441	0.3429
!GALNT6	0.933240197	0.184	0	0.48501	0.11878	0.0147	0.1237
!GALNT7	0.909517926	0.1069	0.30632	0.11681	0.14096	0.0081	0.0578
!GANAB	0.708724388	0.1849	0	0.35118	0.21498	0.0177	0.0825
!GAPDH	0.739653959	0	0	0	0.0398	0.008	0.2013
!GAPDHS	0.954986077	0.3344	0.1367	1.263	0.21675	0.0375	0.1731
!GAS6	0.939221701	0.2063	0.103	0.20246	0.11006	0.0398	0.3616
!GBA		0.2585	1.00182	0.08356	0.57864	0.1306	0.2256
!GC	0.97046162	0.1215	0.38423	0.10117	0.37888	0.0399	0.1054
!GCHFR	0.969471664	0	0	0	0.18092	0.0218	0.1206
!GDF15	0.809835595	0.4725	0.40562	0.36285	0.39784	0.0713	0.1792
!GDI2	0.746294976	0.0408	0	0.34707	0.06813	0.0087	0.128
!GFRA2	0.32871932	0.0619	0	0.21926	0.03267	0.0071	0.218
!GGH	0.908304913	0.0974	0.37758	0	0.46332	0.054	0.1165
!GGT1	0.944878625	0.1465	0.24345	0.0274	0.11826	0.0386	0.3265
!GLA	0.876028079	=1	0	999	0.32047	0.0248	0.0775
!GLB1	0.864732054	0.4506	132.78404	0.31954	0.44713	0.0538	0.1204
!GLB1L	0.400946074	0.2823	0.41061	0.37288	0.47739	0.0342	0.0716
!GLG1	0.692780483	0.048	0	0.1537	0.04455	0.0055	0.1232
!GLO1	0.813028485	0.069	0.10837	0	0.14205	0.0196	0.138
!GM2A	0.800967402	0.3282	0.73685	0	0.4432	0.0593	0.1339
!GMPPA	0.802999915	=1	0	999	0.09519	0.0105	0.1101
!GNAI3	0.808819311	0	0	0	0	0	0.0751
!GNB1	0.761268601	0.1029	0	29.0653	0.01164	0.0014	0.121
!GNB2	0.774064104	0	0	0	0.03504	0.0063	0.1787
!GNB2L1	0.80176233	0	0	0	0	0	0.1383
!GNG12	0.90290303	0	0	0	0.13522	0.013	0.0961
!GNMT	0.980769405	0	0	0	0.06685	0.0153	0.2294

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform'Ka	Uniform4Ks
!GNPDA1	0.737080471	0	0	0	0.04066	0.0048	0.1187
!GNPTG	0.783939563	0.3246	0.2594	0.51461	0.12664	0.0497	0.3926
!GNS	0.914335844	0.1231	0.13506	0.20331	0.13572	0.0147	0.108
!GOT1	0.846983966	0	0	0	0.10364	0.0154	0.1482
!GP2	0.969853013	0.1977	0.14204	0.31688	0.42542	0.0612	0.1439
!GPC1	0.898392456	0.0726	0.0742	0.03225	0.05502	0.0239	0.4342
!GPC4	0.812135283	0	0	0	0.17128	0.0127	0.0744
!GPD1L	0.85549224					0.0153	0.1594
!GPI	0.852565841	0.4195	0.58895	0.36035	0.09336	0.0184	0.1976
!GPR115	0.353513986	0.3448	0.42955	0.43246	0.40563	0.0623	0.1536
!GPR56	0.926474371	0.4858	0.3688	0.33484	0.19109	0.0378	0.1979
!GPR64	0.983215854	0.4288	0.30943	999	0.39159	0.0227	0.0579
!GPRC5C	0.751967611	0.2121	0.20961	0.12302	0.09742	0.0281	0.2885
!GPX3	0.930606603	0	0	0	0.17703	0.0267	0.1508
!GRHPR	0.95560047	0.2062	0.12014	0.36417	0.22933	0.0377	0.1643
!GRN	0.901604818	0.4073	0.97642	0.16174	0.37234	0.0506	0.1358
!GSN	0.822157902	0.0824	0.06337	0.09073	0.10021	0.0193	0.1921
!GSR	0.901859995	0.1471	0.12238	0.22571	0.22362	0.0491	0.2194
!GSS	0.754921628	0.1692	0.43862	0.1456	0.23469	0.0189	0.0806
!GSTM3	0.92897353	0.1362	3.23394	0	0.10633	0.0158	0.1486
!GSTO1	0.869318217	0.2894	0.15836	999	0.27514	0.026	0.0944
!GSTP1	0.822431704	0.3446	0.26269	0	0.11791	0.0287	0.2433
!GSTT1	0.86185942	0	0	0	0.25068	0.0307	0.1224
!GSTZ1	0.926386026	1.327	999	999	0.33622	0.0393	0.1168
!GUSB	0.853353671	0.2359	0.43925	0	0.27561	0.0727	0.2638
!HDHD2	0.554386074	0.6538	0.95928	0	0.25007	0.0196	0.0783
!HEBP2	0.868136656	0.5764	9.65516	0.45765	0.17335	0.022	0.1269
!HEXA	0.767148063	0.1255	0.36677	0	0.20408	0.0213	0.1043
!HEXB	0.905201968	0.701	0.60543	1.78109	0.4545	0.0504	0.1109
!HINT1	0.742776657	0	0	0	0.09701	0.0117	0.1207
!HIST2H2BE	0.93470052	0	0	0	0	0	0.297
!HPRT1	0.839267784	0	0	0	0.29012	0.035	0.1207
!HPX	0.985293256	0.105	0.36198	0	0.67457	0.1034	0.1532
!HRSP12	0.875091605	0.3349	0.4322	0	0.22527	0.0256	0.1137
!HSPA1L	0.936231123	0.2084	0.22237	0.37233	0.03881	0.0472	1.2174
!HSPA2	0.842812768	0	0	0.0001	0.00735	1.0543	
!HSPA4	0.880619857	0.283	2.73528	0.17898	0.06868	0.006	0.0877
!HSPA5	0.79464099	0	0	0	0.0487	0.0055	0.1139
!HSPA8	0.679663162	0	0	0	0	0	0.1623
!HSPB1	0.860393244	0.3502	0	0.1803	0.05552	0.0176	0.3162
!HSPG2	0.889377496	0.1996	0.12357	0.16128	0.4074	0.276	0.6775
!Hyou1	0.706535615	0.3611	0.42983	0.53707	0.12987	0.0148	0.1143
!IDE	0.829995196	0.057	0	0.30895	0.0866	0.0078	0.0897
!IDH1	0.876145163	0.0694	0.16124	0.05341	0.265	0.0411	0.1551
!IDI1	0.850195074	0.2877	0.91068	0.15478	0.28544	0.0504	0.1764
!IDS	0.77436319	0.9508	0.42364	2.12116	0.29901	0.0275	0.092
!IDUA	0.458659613	0.9879	0.20641	1.24348	0.28007	0.0663	0.2369
!IGF2R	0.902826056	0.1427	0.08515	0.34904	0.22362	0.033	0.1475
!IGFBP2	0.934205904	0	0	0	0.027	0.0052	0.1918
!IGFBP5	0.754510376	0.4672	0.19398	0.37035	0.06919	0.0089	0.1284
!IGHG2		0.4938	0.4243	0.15711	0.28039	0.097	0.3458
!IGHG4		0.3959	0.30085	0.09472	0.19341	0.0716	0.3703
!IGJ	0.96180607	0.6208	0.40954	999	1.05716	0.0642	0.0607
!IGKC	0.68058715	=1	999	0	2.36478	0.2409	0.1019
!IGLV1=40	0.786868401	0.5135	0.42633	999	0.56706	0.1145	0.202
!IL1R1	0.831045511	0.5714	999	0.38306	0.35872	0.0359	0.1
!IL1RAP	0.662017149	0	0	0	0.06479	0.0078	0.1201
!IL1RL1	0.826758728	0.3302	0.42727	0.31722	0.55601	0.1906	0.3428
!IL6ST	0.83815782	0.245	0.36962	0.23244	0.19931	0.0172	0.0861
!IMPA1	0.761417384	0.3086	0.31828	0.32034	0.34041	0.0314	0.0924
!INHBB	0.914852598	0.4449	0.25346	0.37155	0.04703	0.0078	0.1666
!IQGAP1	0.925812499	0.0244	0.04864	0	0.05349	0.0049	0.0924

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4*ω*	Uniform*'Ka*	Uniform4*Ks*
!IQGAP2	0.881169981	0.1448	0.2524	0.19846	0.18891	0.0131	0.0692
!ITIH5	0.975923021	0.2291	0.26992	0.23182	0.21116	0.0463	0.2193
!KAL1	0.489592908	0.0458	0	0.2313	0.20081	0.0221	0.1102
!KIF5B	0.602587963	0.0925	0.12976	0	0.11556	0.0156	0.1354
!KLK11	0.925823791	0.7639	1.29504	0.27502	0.27337	0.055	0.201
!KLK2	0.97863358	1.2942	999	0.38829	0.41834	0.0498	0.119
!KLK3	0.986714011	0.3932	0.51369	0.37947	0.39957	0.1085	0.2716
!KPNB1	0.753354878	0	0	0	0.02703	0.0027	0.0997
!KRT1	0.985791198	0.0935	0.06962	0.12825	0.11737	0.0166	0.1414
!KRT10	0.971305806	0.3332	0.54365	0.35063	0.20231	0.0349	0.1724
!KRT5	0.965456143	0.0704	0.08145	0.06406	0.06082	0.0153	0.2516
!KRT8	0.738466698	0.4399	0.09428	0.49118	0.19706	0.0667	0.3385
!KRT9	0.286931348	0.1063	0	0.56867	0.4345	0.056	0.129
!LAMA5	0.956903327	0.1846	0.135	0.14525	0.13514	0.0445	0.329
!LAMB2	0.914779439	0.3009	0.41074	0.38118	0.28588	0.0375	0.1312
!LAMC1	0.938147934	0.1534	0.39034	0.13084	0.09255	0.0133	0.1433
!LAMP1	0.750869167	0.2908	0.22379	0.28986	0.15986	0.0366	0.2288
!LAMP2	0.846233023	0.6386	1.13829	0.38233	0.46213	0.0262	0.0567
!LAP3	0.863859859	0	0	0	0.38199	0.0922	0.2415
!LCN1	0.379778904	0.4871	999	0.26345	0.32753	0.106	0.3238
!LCN2	0.963814129	0.3074	0	0.63813	0.41134	0.0734	0.1784
!LCP1	0.96837838	0.0365	0.10293	0	0.02083	0.0023	0.1102
!LDHA	0.841817617	0.2021	0.20924	0.41912	0.09163	0.008	0.0877
!LDHB	0.76023985	0	0	0	0	0	0.1125
!LDHC	0.959758111	0	0	0	0.18715	0.0196	0.1049
!LDLR	0.640672358	0.0983	0.0763	0.0706	0.13874	0.0368	0.2653
!LEFTY2	0.755005599	0	0	0	0.06355	0.039	0.6142
!LGALS3	0.906475681	0.8616	0.46211	1.85749	0.59968	0.0608	0.1015
!LGALS3BP	0.860831897	0.3261	0.25155	0.17342	0.17687	0.0567	0.3208
!LGMN	0.865146299	0.1083	0.16531	0	0.17889	0.0421	0.2353
!LIFR	0.441056481	0.2927	0.27437	0.39903	0.21051	0.0228	0.1083
!LIPA	0.847820624	0.4662	0.95995	0.43466	0.52468	0.0674	0.1285
!LIPG	0.960237864	0.0418	999	0	0.21196	0.0365	0.1722
!LIPI	0.322751827	0.2394	0.36399	0.18501	0.66784	0.0765	0.1146
!LMAN2	0.590038204	0.1043	0	0.11347	0.03762	0.0059	0.156
!LNPEP	0.825113027	0.1682	0.10188	0.40974	0.34041	0.0295	0.0867
!LPL	0.965452299	0.037	0.09781	0	0.08979	0.0153	0.1702
!LRG1	0.95016863	0.2694	0.24939	0.3781	0.28021	0.0586	0.2092
!LSAMP	0.724462596	0	0	0	0.04607	0.0029	0.062
!LTA4H	0.903088181	0	0	0	0.19132	0.0121	0.0634
!LTF	0.972177316	0.5939	0.80108	0.63017	0.54832	0.1212	0.221
!LYZ	0.916041846	0	0	0	0.77421	0.0803	0.1037
!LZTFL1	0.901849684	0.569	0.54807	999	0.31176	0.0139	0.0446
!MAMDC2		0.0985	0.22232	0	0.11294	0.0115	0.1015
!MAN2A1	0.826620395	0.0645	0.07672	0.07106	0.21517	0.0201	0.0932
!MAN2B1	0.950123519	0.2585	0.59972	0.13572	0.14342	0.0256	0.1787
!MAN2B2	0.824635661	0.1843	0.20409	0.1369	0.25926	0.0813	0.3134
!MANBA	0.941127525	0.1553	0.29347	0.19262	0.2677	0.0294	0.1098
!MARCKS	0.867260481	0.3525	0.31344	0.59828	0.13143	0.0191	0.1457
!MATN2	0.951754575	0.1446	0.24428	0.14611	0.19117	0.0219	0.1147
!MDH1	0.757780001	0.1562	0.19345	0	0.12758	0.0107	0.0841
!MDH2	0.848789504	0.087	0	0.18733	0.08792	0.0153	0.1743
!MFAP4	0.965625783					0.0066	0.1951
!MGAM	0.971835738	0.1544	0.21455	0.17008	0.21447	0.0341	0.1588
!MINPP1	0.959300497	0.2703	0.22343	0.49178	0.30424	0.0392	0.129
!MLPH	0.963131897	0.4226	0.62194	0.29186	0.52134	0.1408	0.2701
!MME	0.968697633	0.0796	0.15016	0	0.07672	0.0094	0.1225
!MMP14	0.829708449	=1	999	999	0.08387	0.0086	0.1021
!MMP2	0.942063166	0.0292	0.0358	0	0.05326	0.0115	0.2156
!MMP7	0.961176527	0.2073	0.18996	0.28602	0.295	0.043	0.1457
!MPI	0.895879501	0.1597	0	7.54864	0.17907	0.017	0.0948
!MPST	0.921739209	0.1936	0.10754	0.09183	0.13639	0.0532	0.3903

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform4Ka	Uniform4Ks
!MSLN	0.945971386	0.7036	1.37847	0.3705	0.41431	0.1216	0.2934
!MSMB	0.982691946	0.5441	999	0	1.45178	0.1655	0.114
!MUC5B	0.969038196	0.4838	0.49053	0.33699	0.37182	0.1075	0.2891
!MUC6	0.268476193	0.4692	0.47946	0.35637	0.33656	0.0705	0.2094
!MYH9	0.834804108	0.036	0.0001	0.04022	0.01165	0.0035	0.304
!MYO1C	0.636425078	0.3035	0.17035	0.28979	0.06255	0.0199	0.3189
!NAGA	0.942796372	0.3005	0.27601	0	0.15037	0.0265	0.1765
!NAGLU	0.608065347	0.0578	0.0579	0	0.08384	0.0175	0.209
!NAPA	0.843048779	0	0	0.0001	0.0001	0	0.141
!NBL1	0.940834077					0.014	0.1666
!NCSTN	0.748267214	0.0922	0	0.76311	0.21163	0.0258	0.1217
!NELL1	0.887047705	0.3253	0.63516	0.41033	0.22725	0.0243	0.1068
!NEO1	0.705307285	0.0994	0.17332	0.10834	0.14864	0.0134	0.0903
!NEU1	0.830729463	0	0	0	0.14015	0.0206	0.147
!NIF3L1	0.900637491	0.1648	0.15503	0.36048	0.37359	0.0393	0.1052
!NME3	0.781640723	0	0	0	0.02462	0.0072	0.2912
!NP		0.1547	0.21285	0.21667	0.37191	0.0365	0.0982
!NPC2	0.856705214	0	0	0	0.07267	0.0097	0.1337
!NPEPPS	0.697640443	0	0	0	0.11108	0.0052	0.0466
!NRCAM	0.693718601	0.0277	0.06746	0	0.1105	0.0107	0.0971
!NRP1	0.747605929	0.0838	0.13274	0.10251	0.1187	0.0124	0.1048
!NUCB1	0.824660828	0.1566	0	0.32321	0.12083	0.0256	0.2122
!NUCB2	0.92219826	0.122	0.23605	0	0.49462	0.0611	0.1235
!NUTF2	0.855863616	0	0	0	0.24164	0.0541	0.2238
!ODZ2	0.443933681	0.0211	0.05218	0	0.02107	0.0028	0.1351
!OLFM1	0.803796391	0.0328	0	0.29854	0.02472	0.0068	0.2765
!OLFM4	0.979879529	0.0434	0	0.13058	0.36665	0.0537	0.1466
!ORM1	0.985026773	0.1947	0.31442	0.11577	0.34271	0.0888	0.2591
!ORM2		0.3987	0.628	0.1137	0.39559	0.1099	0.2779
!OS9	0.782687025	0.2073	0	0.82103	0.12269	0.0139	0.1133
!P4HB	0.84091794	0.0643	0	0.10391	0.08835	0.0178	0.2018
!PACSIN2	0.83747926	0.2184	0.06935	0.31402	0.13757	0.0579	0.4212
!PAEP	0.98402504	0.4005	0.41339	0.22631	0.61304	0.1131	0.1845
!PAICS	0.79082366	0.375	0.34949	0.7046	0.27061	0.0265	0.0979
!PAM	0.773811424	0.1516	0.15185	0.38173	0.28683	0.0204	0.0711
!Park7	0.648197272	0.1123	0	18.52626	0.1005	0.0078	0.0775
!PCMT1	0.777027233	=1	10.71224	0	0.12522	0.0088	0.0699
!PDCD6	0.581191994	0.4132	0.27657	0.38589	0.14806	0.0352	0.238
!PDCD6IP	0.793768723	0.0308	0.04782	0	0.03412	0.0027	0.0802
!PDGFA	0.712105709	0.5085	0.47821	0.61584	0.28039	0.0647	0.2308
!PDIA3	0.837401555	0	0	0	0.14971	0.0173	0.1158
!PEBP4		0.1922	0.11581	0.28485	0.38835	0.0702	0.1809
!PFAS	0.933147464	0.1728	0.22023	0.19512	0.20845	0.0304	0.1459
!PFKP	0.802369364	0.0331	0.01941	0.03818	0.06371	0.0216	0.3383
!PFN1	0.818980867	1.3715	0	999	0.29469	0.0249	0.0846
!PFN2	0.838744017	0	0	0	0.31537	0.0048	0.0151
!PGAM2	0.977197892	0	0	0	0.02754	0.0064	0.2325
!PGC	0.964948651	1.2432	0.2563	999	0.15509	0.0358	0.2307
!PGCP	0.950071275	0.5268	0.41384	999	0.37912	0.0256	0.0676
!PGD	0.888926459	0.091	0	0.25013	0.13151	0.0253	0.1924
!PGK1	0.857075921	0	0	0	0.20731	0.0158	0.0763
!PGK2	0.953840563	0.1021	0	0.3636	0.20829	0.0201	0.0963
!PGLS	0.859997248	0.0742	0.35207	0	0.09575	0.0188	0.1968
!PGM1	0.898278854	0.1755	0.38308	0.20561	0.10201	0.012	0.1172
!PGM2	0.788276467	0.085	0.03651	0.22513	0.3495	0.1098	0.3143
!PHGDH	0.932250389	0.0693	0	0.18427	0.08515	0.0123	0.1441
!PI15	0.332133115	0	0	0	0.10346	0.011	0.1063
!PIGR	0.966983477	0.7749	0.82879	0.67717	0.47638	0.0876	0.1838
!PIP	0.976413619	0.7754	0.45832	1.60428	2.33674	0.253	0.1083
!PITPNA	0.876961427	0	0	0	0.08676	0.0093	0.1077
!PKM2	0.780358204	0.3257	0.99525	0	0.16829	0.0229	0.1362
!PLA1A	0.96723372	0.0524	0.1332	0	0.40009	0.0618	0.1545

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform'$K\alpha$	Uniform4K_S
!pla2g2A	0.950832112	0.2822	999	0	0.41423	0.087	0.21
!PLA2G7	0.894553653	0.8617	0.34979	999	0.36576	0.038	0.1038
!PLOD2	0.973828113	0.1424	255.56801	0.08307	0.12028	0.013	0.1077
!PLOD3	0.785462706	0.1402	0	1.28407	0.10437	0.0262	0.2514
!PLXNB2	0.719376599	0.1442	0.04453	0.11466	0.06133	0.0294	0.4799
!PODXL2	0.824159673	0.082	0.26049	0	0.27153	0.0275	0.1012
!PPAP2A	0.953263319	0.3177	0	999	0.25775	0.0136	0.0528
!PPIA	0.699357756	0	0	0	0.04806	0.0056	0.1155
!PPIB	0.817742458	=1	0	13.47723	0.034	0.0044	0.1295
!PPIC	0.870079184	0.6534	999	0	0.22018	0.0332	0.1508
!PPP1CC	0.737601991	0	0	0	0	0	0.0586
!PPP1R7	0.651029782	0.0716	0	0.18364	0.05014	0.0051	0.102
!PPP2CA	0.759456185	0.9079	0	0.98228	0.04184	0.0044	0.1042
!PPP2R4	0.640453662	0.2494	0.28489	0.50635	0.34304	0.0694	0.2023
!PPP5C	0.697010073	0.0262	0.03804	0	0.03747	0.0076	0.2039
!PPT1	0.843728115	0.2017	999	0	0.12499	0.0163	0.1302
!PRCP	0.716860703	0.9196	0.64706	999	0.4072	0.0515	0.1265
!PRDX1	0.7963966	0	0	0	0.1014	0.0078	0.0768
!PRDX2	0.746492271	0	0	0	0.12405	0.025	0.2013
!PRDX4	0.855954248	0.6153	0	0.71585	0.33071	0.0215	0.0651
!PRDX5	0.805623891	0.7327	0.91331	0	0.3221	0.0321	0.0997
!PRDX6	0.797081474	0	0	0	0.08072	0.0089	0.1099
!PRKACA	0.6717426	1.3297	0	108.97906	0.21771	0.0496	0.2278
!PRKAR1A	0.785409635	0	0	0	0.02182	0.0025	0.1154
!PRKAR2A	0.598087754	0.3066	0	0.32196	0.26782	0.0336	0.1255
!PRKCSH	0.710117435	0.0719	0.03943	0.13117	0.11368	0.0286	0.252
!PROM2	0.37986549	0.2666	0.41648	0.11239	0.25088	0.0684	0.2725
!PROS1	0.845341141	0.3928	999	0.34265	0.36304	0.0366	0.1009
!PRSS22	0.472806474	0.4728	0.43331	0.28842	0.25859	0.0496	0.1919
!PRSS8	0.934291005	0.1712	0	0.30715	0.28973	0.0625	0.2157
!PSAP	0.808600327	0.0995	0.16537	0	0.11398	0.0149	0.1309
!PSAT1	0.955546379	0.3069	0	0.63182	0.14332	0.0171	0.1195
!PSCA	0.945875175	0.1712	0	999	0.12498	0.047	0.3758
!PSMA1	0.830046783	0	0	0	0.05462	0.0081	0.1479
!PSMA2	0.773173276	0	0	0	0.19882	0.0182	0.0914
!PSMA3	0.899708047	0	0	0	0.22828	0.0448	0.1963
!PSMA4	0.814739747	0	0	0	0.02917	0.0035	0.1187
!PSMA5	0.868156312	0	0	0	0	0	0.0624
!PSMA6	0.827058782	0	0	0	0.15024	0.0136	0.0908
!PSMA7	0.761283442	0.1049	0.40545	0	0.06726	0.0096	0.1434
!PSMB1	0.692966403	0	0	0	0.12317	0.0144	0.1173
!PSMB2	0.74969859	0	0	0	0.16208	0.0225	0.1386
!PSMB4	0.690763991	0.3333	0	0.42206	0.08328	0.0092	0.1105
!PSMB5	0.754466056					0.0073	0.1047
!PSMB6	0.716413187	0.0865	0.15358	0	0.08442	0.0105	0.1242
!PSMB7	0.7244121	0.1094	86.93101	0	0.07857	0.0106	0.1346
!PSMB8	0.924306947	0.1611	0.14993	0.21505	0.40269	0.0413	0.1025
!PSMD14	0.909577126	0	0	0	0	0	0.0315
!PSMD2	0.7439238	0	0	0	0.05075	0.0049	0.0969
!PSME4	0.813634852	0.1712	0.12557	0.33059	0.09526	0.0084	0.0887
!PTGDS	0.813891805	0.0904	0.04011	0.07089	0.12775	0.0365	0.2857
!PTN	0.721752451	0	0	0	0.05059	0.0057	0.1126
!PTPRD	0.784780512	0.0281	0.06159	0	0.0833	0.0093	0.1114
!PTPRF	0.760748656	0.0342	0.05915	0.01179	0.04714	0.0097	0.2053
!PTPRJ	0.331004799	0.2612	0.74921	0.24513	0.43859	0.0706	0.161
!PTPRS	0.795808065	0.1126	0.0243	0.15704	0.05222	0.0167	0.3191
!PURA	0.674641064	0	0	0	0.06875	0.0036	0.0526
!PYGB	0.845025108	0	0	0	0.11028	0.051	0.4623
!QPCT	0.937881824	0.1856	0	0.64822	0.24935	0.0286	0.1145
!QSCN6	0.88930987	0.7992	0.755	1.11002	0.28271	0.0402	0.1422
!RAB10	0.669101485	0	0	0	0	0	0.0283
!RAB11B	0.76423549	0	0	0	0	0	0.392

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4ω	Uniform'$K\alpha$	Uniform4Ks
!RAB13	0.854471619	0	0	0	0	0	0.1558
!RAB14	0.645322553	0	0	0	0	0	0.064
!Rab18		0	0	0	0.0552	0.004	0.0733
!RAB1A	0.71066118	0	0	0	0.07614	0.0047	0.0612
!RAB1B	0.650698163	0.3149	0	0.27326	0.07787	0.0182	0.2342
!RAB27A	0.917424293	0.8677	0.88091	13.78288	0.15118	0.0156	0.1029
!RAB27B	0.66420111	=1	0	999	0.21051	0.0152	0.0722
!RAB2A	0.76838231	=1	0	0	0.0001	0	0.0221
!RAB3B	0.94543152	0.1484	0.18368	0	0.02735	0.0043	0.1554
!RAB3D	0.43901001	0.059	0.08161	0	0.04423	0.0098	0.2222
!RAB5B	0.862212182	0	0	0	0.25884	0.0331	0.1279
!RAB5C	0.855410023	0.3197	912.90738	0.438	0.09729	0.0099	0.1014
!RAC1	0.682407483	0	0	0	0.12088	0.007	0.0577
!RAD23B	0.684710371	0.1948	0	0.30837	0.13207	0.0142	0.1078
!RALA	0.942044417	0	0	0	0.33887	0.0592	0.1746
!RALB	0.8305974	0	0	0	0.08639	0.008	0.0932
!RAP1B	0.900401642	0	0	0	0	0	0.0788
!RBP4	0.851907312	0	0	0.0001	0.02341	0.0042	0.1804
!RDX	0.663712817	0	0	0	0.1668	0.0238	0.1426
!RELN	0.929411415	0.1508	0.06098	0.31401	0.09263	0.0113	0.1218
!RHOA	0.714124355	0	0	0	0	0	0.0419
!RNASE1	0.581677333	0.3054	0.27992	0.27774	0.3914	0.0684	0.1747
!RNASE4	0.89342991	=1	999	0	0.23967	0.0365	0.1524
!RNASET2	0.60054953	0.5832	999	0.35359	0.23948	0.0577	0.2411
!RPLP0	0.707625706	0	0	0	0.04414	0.003	0.0669
!RRBP1	0.807676684	0.1635	0.1557	0.20111	0.13849	0.0288	0.208
!RTN4RL1	0.299037195	0.3377	0	1.00639	0.07028	0.0339	0.4826
!RUVBL1	0.861830363	0	0	0	0	0	0.101
!RUVBL2	0.918740399	0	0	0	0.00916	0.0027	0.2947
!s100A11	0.88706195	0	0	0	0.09238	0.0141	0.1531
!SCGB2A1	0.965959797	=1	0	999	0.50319	0.1086	0.2158
!SCPEP1	0.913646606	0.3675	0	1.22281	0.28463	0.0314	0.1102
!SDC1	0.967561796	0.1358	1.42824	0	0.42477	0.0612	0.1441
!SDCBP	0.873451351	0	0	0	0.14582	0.0153	0.105
!SDCBP2		0.4464	999	0.17091	0.17189	0.0378	0.2201
!SDK2	0.34016962	0.0696	0.05912	0.03316	0.04119	0.0094	0.2271
!SELENBP1	0.970201379	0.2707	999	0.19634	0.11919	0.0232	0.1949
!SEMA3C	0.82906797	0.0419	0	0.09591	0.1026	0.0098	0.0955
!SEMA3F	0.593188048	0.388	0.32034	0.42871	0.09798	0.0173	0.1768
!SEMA7A	0.276871277	0.4677	0.1369	0.49306	0.11662	0.0236	0.2021
!SEMG1	0.985521315	0.9024	0.94668	0.92915	0.90477	0.1874	0.2071
!SEMG2	0.96754494	0.714	0.55491	1.63109	1.07914	0.15	0.139
!SEPP1	0.831632483	0.5868	1.1796	0.57964	0.71077	0.0633	0.0891
!SERPINA1	0.738906257	0.1502	0.12628	0.23738	0.4603	0.0723	0.157
!SERPINA3	0.963011739	0.416	0.29712	0.76868	0.69942	0.1373	0.1963
!SERPINA4	0.982616527	0.1859	95.81563	0	0.31022	0.0472	0.1523
!SERPINA5	0.961235209	0.3831	0.15801	0.43314	0.21902	0.0582	0.2657
!SERPINA6	0.977081775	0.7122	7.47813	0.43999	0.35446	0.053	0.1495
!SERPINB5	0.982397361	0.1134	0.19102	0	0.15915	0.0152	0.0957
!SERPINB6	0.845433886	0.3691	0	0.39352	0.14886	0.0469	0.3149
!SERPINC1	0.98244169	0.1002	0	0.33628	0.37296	0.0615	0.165
!SERPINF1	0.912971756	0.1432	0.18517	0.07661	0.13839	0.0433	0.3127
!SERPING1	0.951728062	0.486	0.48326	999	0.35049	0.0537	0.1533
!SERPINI1	0.883312768	0.2784	0.41226	0.41431	0.24428	0.0226	0.0923
!sez6L2	0.96112958	0.2102	105.9891	0.21333	0.11038	0.0148	0.1342
!SFN	0.963100811	0	0	0	0.01088	0.0032	0.2915
!SH3BGRL2	0.890436747	0	0	0	0.05585	0.0042	0.076
!SI	0.984415019	0.1244	0.10295	0.18361	0.27066	0.0349	0.1289
!SIL1	0.866371628	0.1838	0.23532	0.16554	0.22735	0.0475	0.2089
!SLC15A2	0.594541936	0.1322	0.29201	0.10877	0.29309	0.0223	0.076
!SLC1A1	0.579188031	0.3252	0.10075	1.62434	0.09929	0.0154	0.1552
!SLC35F2	0.922001646	0.1069	0	0.44879	0.18336	0.0242	0.132

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4*ω*	Uniform*'Ka*	Uniform4*Ks*
!SLC44A4	0.943541505	0.2206	0.15814	0.13059	0.17158	0.0289	0.1684
!SLIT2	0.924615553	0.0508	0	0.1409	0.09964	0.0136	0.136
!SLPI	0.977003331	0.2933	0	0.38756	0.55658	0.1019	0.1831
!SMOC2	0.959932254	0.0812	0.10544	0.07629	0.08184	0.012	0.1471
!SMPD1	0.589343978	0.1705	0.12727	0.27823	0.23664	0.0315	0.133
!smpdl3A	0.906084728	1.7518	0.86229	999	0.34902	0.0391	0.1121
!SMPDL3B	0.329254079	0.1551	0.371	0.14698	0.43209	0.077	0.1783
!SMS	0.848603406	0.1466	0	999	0.23779	0.0367	0.1542
!SOD1	0.771542471	0	0	0	0.59912	0.0769	0.1284
!SOD3	0.962750568	0	0	0	0.07039	0.0315	0.4473
!SORD	0.950735954	0.5105	0.49046	0.81743	0.28128	0.0529	0.188
!SORL1	0.8930763	0.1018	0.19729	0.06386	0.10077	0.015	0.1492
!SORT1	0.759281004	0.1564	0.40232	0.13838	0.14231	0.014	0.0982
!SPACA3	0.338565891	0.9784	0	1.06423	0.65389	0.0892	0.1364
!SPINK2	0.94464532	=1	999	999	1.33875	0.1708	0.1276
!SPINT1	0.935000569	0	0	0	0.27985	0.0477	0.1704
!SPINT3	0.978716611	=1	999	999	1.11091	0.106	0.0954
!SPOCK3	0.547521842	0.1586	0	0.30725	0.11295	0.0129	0.1145
!SPON2	0.965110577	0.2592	0.18166	0	0.11153	0.0256	0.2292
!ST14	0.662773879	0.106	0.03884	0.10004	0.09418	0.0307	0.3263
!STEAP2	0.482322616	0.2026	0.26459	0.27043	0.11769	0.0105	0.089
!STXBP2	0.919716277	0.0989	0.07939	0.07773	0.06415	0.0183	0.2852
!SYT1	0.908815088	0	0	0	0.02594	0.0024	0.0907
!SYT7		0.6459	0	1.05382	0.06	0.0118	0.1967
!TAGLN2	0.88315778	0	0	0	0.05075	0.007	0.1381
!TALDO1	0.871058291	0.1555	0	0.2268	0.12716	0.0172	0.1351
!TCP1	0.83880433	0	0	0	0.03	0.0032	0.107
!TEX101	0.922243175	1.033	999	0.90322	0.75291	0.0806	0.107
!TF	0.766058719	0.1866	0.19	0.26901	0.54147	0.0872	0.161
!TFPI2	0.968659201	0.0967	0.12425	0	0.55887	0.0526	0.094
!TFRC	0.932596083	0.608	0	0.83744	0.21664	0.0434	0.2002
!TGFB1	0.76526679	0	0	0	0.01709	0.0035	0.2025
!TGFB3	0.620946597	0	0	0	0.01365	0.0011	0.0792
!TGFBR3	0.925857162	0.1423	0.0548	0.44064	0.18951	0.0197	0.104
!TGM4	0.854186748	1.5045	1.15225	999	0.38754	0.0541	0.1395
!THBS1	0.945701652	0.1072	0.0711	0.21665	0.04402	0.0066	0.1496
!THBS2	0.963833342	0.0652	0	0.1337	0.06881	0.0198	0.2874
!THBS4	0.960505412	0.2277	0.14747	0.36907	0.13337	0.0179	0.1341
!TIMP1	0.872423166	0.5615	0.51888	1.14032	0.81715	0.0557	0.0682
!TIMP2	0.976169847	0.1945	0	0.19753	0.03019	0.008	0.2647
!TIMP3	0.96086978	0	0	0	0.02181	0.0039	0.1773
!TKT	0.891038329	0.0561	0.05593	0.04662	0.03005	0.0069	0.2312
!TMC5	0.920199288	0.4369	0.87688	0.502	0.40918	0.0556	0.1359
!TMEFF2	0.960655793	0	0	0	0.08682	0.0054	0.0617
!TMEM8	0.831230679	0.1579	0.137	0.05254	0.11682	0.0417	0.3571
!tmpRSS2	0.841889929	1.3496	2.16049	1.2577	0.50285	0.1037	0.2063
!TNFSF10	0.943770436	0.2006	0.13919	0.83718	0.3777	0.0384	0.1017
!TOLLIP	0.70829404	0.1659	0	0.10302	0.02961	0.0126	0.4244
!tor1B	0.749524138	0.1037	0	0.34982	0.08296	0.0095	0.115
!TP53I3	0.856189185	0.2264	0.21603	0.4282	0.22876	0.0268	0.1171
!TPI1	0.50598943	0	0	0	0.08996	0.0132	0.1471
!TPP2	0.880123131	0.0867	0	0.14274	0.12797	0.0184	0.1441
!TPT1	0.497400063	0	0	0	0.31717	0.0197	0.0621
!TSG101	0.772681923	0	0	0	0.0311	0.0024	0.076
!TSN	0.743092622	0	0	0	0	0	0.0646
!TSNAX	0.844084164	0.2808	0	0.35194	0.09848	0.0095	0.0966
!TSTA3	0.791635322	0.3816	0.08791	1.04752	0.1166	0.0242	0.2078
!TTR	0.947287292	0.344	0.87706	0.29078	0.59375	0.0644	0.1085
!TUBB1	0.782471627	0.1469	0.3361	0	0.07015	0.0131	0.1874
!TWSG1	0.833028032	=1	4.12342	0	0.02561	0.002	0.0792
!TXN	0.913545177	0	0	0	0.34466	0.02	0.0581
!UBE2L3	0.857563441	0	0	0	0.1222	0.0126	0.1028

Gene	Tau	Hcpairwise	Human	Chimp	Uniform4*ω*	Uniform*'Kα*	Uniform4*Ks*
!UBE2N	0.818361186	=1	0	0	0.0001	0	0.0376
!UGCGL1	0.697196004	0.1814	0.23767	0.29013	0.1394	0.0145	0.1039
!UGDH	0.925270433	0	0	0	0.04163	0.0037	0.09
!USP14	0.850627662	0	0	0	0.09211	0.0058	0.0629
!VAMP2	0.902307671	0	0	0	0	0	0.0848
!VAMP8	0.89206583	0	0	0	0	0	0.1315
!VAT1	0.793476519	1.2271	1.28489	0.96145	0.16604	0.0311	0.1875
!VCL	0.839738119	0	0	0	0.07167	0.0055	0.0774
!VCP	0.809963388	0	0	0	0.02398	0.0023	0.0973
!VPS28	0.669693297	0.0627	0	260.8564	0.05097	0.0282	0.553
!VTN	0.98390818	0.1517	0.24196	0	0.46352	0.0724	0.1561
!VWF	0.956636972	0.1941	0.15127	0.24267	0.16405	0.0249	0.1518
!WFDC2	0.977251134	0	0	0	0.20458	0.0487	0.2382
!WFDC8	0.301050751	0.3159	0.36656	0.48714	0.63099	0.1005	0.1593
!WFDC9		=1	999	0	1.00331	0.0995	0.0991
!XPNPEP1	0.772654174	0.038	0.08782	0	0.02849	0.0031	0.1074
!YWHAB	0.777105221	0	0	0	0	0	0.1029
!YWHAE	0.79593326	0	0	0	0.09136	0.0037	0.0409
!YWHAG	0.051671795	0	0	0	0	0	0.2309
!YWHAQ	0.715910527	0	0	0	0.33806	0.0224	0.0663
!YWHAZ	0.698954133	0	0	0	0	0	0.0222
!ZPBP	0.961110915	0.4698	0.33782	0.92544	0.34036	0.0435	0.1279

Control Tau Estimates

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
ABCB11	0.455605972	0.2331	0.38869	0.22053	0.28618	0.0377	0.1318
ABCD3	0.77734788	0	0	0	0.13009	0.0188	0.1445
ABHD10	0.840084815	0	0	0	0.2221	0.023	0.1035
ABHD4	0.804971471	0	0	0	0.06569	0.0103	0.1563
ACCN1	0.779133525	0	0	0	0.24264	0.0504	0.2079
ACOT12	0.034226884	0.1666	0.16105	0.24626	0.2554	0.0366	0.1433
ACSM1	0.440796369					0.0717	0.1332
ADAM29	0.815814337	0.2552	0.18449	0.28075	0.44471	0.0826	0.1856
ADAM9	0.934585243	0.1495	0	0.7285	0.16305	0.016	0.0981
ADAMTS8	0.775783717	0.2222	0.27034	0.13234	0.10182	0.0136	0.1333
ADAT2	0.380053832	0.1496	7.89283	0	0.22183	0.0181	0.0815
ADH1A	0.964084721	0.3941	0.09841	999	0.40953	0.1178	0.2878
ADNP2	0.592038007	0.0721	0	0.13749	0.1646	0.0206	0.125
ADRA1B	0.285400641	0.459	0.19774	0.24015	0.09743	0.023	0.2357
AGAP10		0.7679	0.7089	1.31184	0.87447	0.1641	0.1877
AGGF1	0.487288555	0.852	999	0.48452	0.31754	0.0276	0.0868
AGPAT2	0.917701548	0.2455	0.08927	0.15003	0.07626	0.0358	0.469
AHSA1	0.807416107	0.3011	0	999	0.13916	0.0076	0.0545
ALDH1A3	0.956041748	0.0531	0.21908	0	0.11748	0.0175	0.1488
ALKBH3	0.606359111	0	0	0	0.11509	0.0101	0.0881
ALOX15	0.528522468	0.0732	0.10672	0	0.28034	0.0717	0.2558
AMBN	0.920938467	0.3201	0.45873	0	1.29269	0.0816	0.0631
ANGEL2	0.663483048	0	0	0	0.14992	0.0102	0.0684
ANKRD52	0.19656035	0.2563	0.06566	0.96985	0.16149	0.0147	0.0909
ANO1	0.983211356	0.1104	0.11798	0.05024	0.05996	0.0174	0.2899
APC2	0.578547754	0.1858	0.1021	0.11836	0.08569	0.033	0.3854
APOBEC1	0.822154404	1.1436	999	0.39106	0.35525	0.0483	0.1361
ARCN1	0.739258536	0	0	0	0.05611	0.0046	0.0826
ARHGAP19	0.893484816	0.0428	0.46567	0	0.16643	0.0172	0.1032
ARHGAP4	0.914875411	0.038	0.0595	0	0.24802	0.1016	0.4097
ARHGEF25	0.750512517	0.083	0.13501	0	0.32586	0.0209	0.0641
ARL6IP1	0.868606826	0	0	0	0.11307	0.0098	0.0864
ARV1	0.833873915	0.1442	0	0.41918	0.31252	0.0276	0.0885
ASB1	0.64479671	0	0	0	0.02141	0.0042	0.1981
ASCC3	0.923249448	0.2453	0.21136	0.34432	0.11789	0.0096	0.0811
ASH2L	0.847687722	0.2013	0.26543	0	0.07034	0.0069	0.0974
ASPH	0.709810562	0.3598	0.28167	0.68067	0.31762	0.0332	0.1046
ATAD2	0.893987944	0.2936	0.48214	0.20194	0.23109	0.0195	0.0843
ATAD5	0.535051181	0.6879	0.4476	1.14855	0.5056	0.0522	0.1032
ATG16L1	0.395411409	0.0779	0.20817	0	0.10018	0.0111	0.1107
ATP10D	0.363480339	0.1622	0.52583	0.04817	0.31096	0.033	0.1062
ATP5H	0.613597256	0	0	0	0.35319	0.0327	0.0925
B4GALT5	0.842636466	0.0596	0	4.4978	0.0594	0.0048	0.08
BCCIP	0.878158776	-1	999	999	0.7671	0.0518	0.0675
BCL9L		0.1867	0.13991	0.19108	0.10357	0.0145	0.1399
BET1	0.852890865	0	0	0	0.30585	0.0118	0.0385
BLNK	0.957071098	0.2329	0.38282	0.19175	0.25319	0.0353	0.1395
BROX	0.369755954	0.1482	0.11446	0.34768	0.11335	0.0089	0.0781
C10orf11	0.237639828	0.0777	0.23786	0	0.39057	0.0356	0.0913
C11orf20	0.951863085	0.6138	0	63.01992	0.34281	0.1315	0.3837
C11orf40		1.7451	999	1.60398	1.55366	0.2002	0.1288
C11orf80	0.303049613	0.3452	0.52138	0.21019	0.60189	0.0702	0.1166
C11orf84		0.1116	0.1745	0	0.37879	0.2302	0.6076
C12orf5	0.908507064	0.9026	0	0.97227	0.53333	0.0675	0.1265
C14orf180		0.5344	56.22955	0.27727	0.61768	0.158	0.2558
C14orf181		-1	999	0	0.97191	0.0388	0.0399
C17orf51		0.1729	999	0	0.82216	0.0949	0.1154
C19orf47	0.02429406	0.3422	0	1.04863	0.12431	0.0199	0.1597
C19orf68		0.7794	0.06482	0.62644	0.16196	0.0517	0.3193
C1orf101		1.4059	0.73172	2.44149	0.73027	0.1062	0.1454
C1orf187		0.3401	0.36526	0.36161	0.22563	0.0352	0.1562
C1orf27	0.8984711	-1	999	999	0.33672	0.0222	0.0659

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
C1orf43		0.6454	0	0.88067	0.09663	0.0078	0.0803
C1QTNF7	0.036790668	0	0	0	0.14347	0.0138	0.096
C20orf160	0.823848126	0	0	0	0.33617	0.0864	0.2569
C21orf59	0.787209646	0.1282	0.09869	0.17071	0.05525	0.0095	0.1727
C22orf41		0.2537	0.37014	0	0.07235	0.0105	0.1456
C4orf31	0.945755209	0.0245	0	0.07167	0.12253	0.0155	0.1262
C4orf33		0.6954	999	0.34595	0.46533	0.0501	0.1077
C4orf7		0.3249	0	999	1.64355	0.1593	0.0969
C7orf60	0.833216895	-1	4.5764	4.43677	0.04471	0.0035	0.0784
C8orf39	0.2816749	-1	999	0	999	0.0413	0
C8orf40		0	0	0	0.0001	0	0.0799
C9orf142	0.942281422	0.755	999	0.45351	0.34087	0.0429	0.1258
C9orf46	0.906221597	0	0	0	0.05665	0.0077	0.1357
C9orf9	0.923636096	0.3741	0.06096	0.27709	0.1529	0.045	0.2942
CA10	0.529252251	0	0	0	0.01332	0.0015	0.1132
CA5A	0.419143176	1.0845	999	1.0715	0.4998	0.0295	0.059
CACNG6	0.215468961	0.255	999	0	0.33835	0.0533	0.1575
CAPN11	0.731120995	0.922	999	0.70719	0.3139	0.0634	0.202
CAPN7	0.804378074	0.1168	0.17702	0	0.10233	0.01	0.0975
CAPS2	0.397678109	0.4384	0.25592	0.47753	0.3361	0.0562	0.1673
CARD11	0.746528055	0.0304	0.01561	0.03029	0.07595	0.0263	0.346
CASP8	0.570716056	0.1374	0	0.38531	0.42606	0.0482	0.1131
CAV1	0.920123611	0	0	0	0.03265	0.005	0.1529
CCDC115	0.910970766	0	0	0	0.21616	0.0331	0.1533
CCDC132	0.602391242	0.3258	0.1847	0.41607	0.07944	0.0084	0.1058
CCDC157		1.907	1.39981	2.83119	0.37409	0.0539	0.1441
CCDC36		0.3769	0.68146	0.4071	0.75733	0.0585	0.0772
CCDC68	0.85197971	-1	999	0	0.65398	0.0419	0.064
CCDC69	0.917852305	0.2005	0.20776	0.41667	0.40889	0.0371	0.0908
CCDC73		0.3634	0.28658	0.71922	0.73278	0.0655	0.0893
CCDC82	0.274536279	0.1986	1.08258	0	0.62107	0.0624	0.1004
CCL24	0.296759747	0.4166	0.23441	0.47309	0.35182	0.0967	0.2748
CCNB1	0.939688766	-1	5.80552	0	0.25128	0.0132	0.0527
CCRL1	0.443392195	0.293	0.44063	0.4415	0.39503	0.0284	0.0718
CD2AP	0.942511958	0.1738	0.2562	0	0.24962	0.0267	0.1071
CD300C	0.901741194	0.4477	0.55178	0.33872	0.7195	0.1239	0.1723
CD69	0.945117212	0.2715	0.35336	0	0.44299	0.0612	0.1382
CDC20	0.95373324	0.6483	0	999	0.06302	0.0057	0.0904
CDC23	0.880666015	0.0605	0.15011	0	0.09586	0.0074	0.0776
CDC37	0.759928218	0.0363	0	0.07249	0.00621	0.0023	0.3689
CDCA2	0.093627674	0.3911	0.75561	0.27625	0.46008	0.0596	0.1294
CDCA3	0.940822601	-1	0	999	0.40356	0.024	0.0594
CDK13	0.518708749	0.1231	0.14957	0.17953	0.10513	0.006	0.0568
CDK9	0.830401421	0	0	0	0.01091	0.0023	0.2129
CDT1	0.941130374	0.225	0.39148	0.11822	0.15736	0.0618	0.3925
CEACAM6	0.947246701	0.1107	0.17964	0	0.7904	0.3141	0.3975
CEBPZ	0.840451467	0.628	0.54003	1.03201	0.38003	0.0374	0.0984
CENPT	0.760930216	1.1706	999	0.96016	0.77714	0.0842	0.1083
CEP78	0.663880533	0.2176	0.41487	0.1679	0.3478	0.0335	0.0962
CES5A	0.244597465	0.2283	0.38381	0.24916	0.48386	0.0723	0.1494
CHL1	0.938801113	0.1197	0.19033	0.10072	0.19809	0.0293	0.1479
CHM	0.321519585	0.4359	999	0.1709	0.2921	0.0212	0.0726
CHMP5	0.765115262	0	0	0	0.0001	0	0.1039
CHRDL2	0.919418577	0.045	0.06956	0	0.1641	0.0388	0.2362
CHST2	0.934675784	0	0	0	0.07547	0.0134	0.1775
CHST4	0.561178216	0.3059	0.693	0.17148	0.28245	0.0437	0.1549
CISH	0.930809887	0.3503	0	0.43632	0.3206	0.0376	0.1172
CLCN4	0.601614085					0.0105	0.1902
CLEC4E	0.848815973	-1	999	999	0.58328	0.0752	0.1289
CLK4	0.881446381	0	0	0	0.13393	0.0099	0.0742
CMBL		0	0	0	0.31914	0.0318	0.0997
CNPY1		0.5242	999	0.5075	0.62828	0.0273	0.0435

Gene	Tau	H-C pairwise	Human	Chimp	Uniform *ω*	Uniform *Ka*	Uniform *Ks*
CNTFR	0.583005367					0.0127	0.1374
CNTN6	0.581755637	0.1954	0.15	0.3022	0.19901	0.0229	0.1148
COL20A1	0.15921871	0.3697	0.16805	0.59872	0.22552	0.0387	0.1714
COL5A2	0.960687645	0.0538	0	0.17421	0.08985	0.0081	0.0907
COPS4	0.785715591	0.0583	0.11861	0	0.09887	0.0075	0.0757
COQ3	0.683348461	-1	999	999	0.63308	0.0576	0.0909
CORO1C	0.902878975	0.0404	0.41613	0	0.04779	0.0042	0.0887
COX5B	0.880043395	-1	999	999	0.74972	0.0715	0.0953
CPA5		0.2018	0.12519	0.34588	0.16552	0.0363	0.2194
CPB2	0.973364648	0.591	1.14706	0.38346	0.51219	0.0576	0.1125
CPT1B		0.6152	0.3049	999	0.13443	0.0214	0.1589
CWC22	0.190865197	0.1525	0.30302	0.0744	0.22459	0.0224	0.0998
CXCR5	0.785878183	0.3424	0.21796	0.22237	0.08145	0.0178	0.2183
CYLC1	0.58699662	0.5365	0.3744	61.56125	0.94067	0.0894	0.0951
CYP3A5	0.936410295	0.4577	0.85451	0.42477	0.54142	0.0671	0.124
CYP4F11	0.966667788	0.1268	0.13362	0.13652	0.23863	0.0621	0.2604
CYTH1	0.725168538	0	0	0	0.00665	0.0011	0.1707
DACT2		0.3874	0.31498	0.26524	0.27172	0.0587	0.2159
DARC	0.913998906	0.371	0.97585	0.24279	0.60104	0.0737	0.1225
DBX1	0.082338638	0.4519	0.13993	0.7461	0.194	0.0496	0.2557
DCAF12L2		0.1143	0.08971	0	0.1266	0.0583	0.4604
DCAF4L1		0.2425	0	0.27089	0.17259	0.0222	0.1289
DCAF5	0.677878682	0.0901	0	0.20844	0.12757	0.0136	0.1069
DCAF7	0.718469775	0	0	0	0.01161	0.0013	0.1144
DCTN6	0.735629323	0	0	0	0.02566	0.0026	0.1006
DDB2	0.953889964	0	0	0	0.10933	0.0122	0.1118
DDHD2	0.783351899	0	0	0	0.31257	0.0191	0.0611
DDTL		0	0	0	0.62793	0.1328	0.2114
DEF8	0.861265432	0.5098	0.17761	0.58453	0.08634	0.0263	0.3044
DEFB103A	0.085616122	0.3331	0	0.56403	0.08913	0.0157	0.1764
DEFB110		-1	999	999	1.19831	0.0644	0.0537
DENND4B	0.837862985	0.1831	0.13943	0.33826	0.17505	0.0187	0.1069
DERL1	0.811123113	0	0	0	0.0566	0.0037	0.0646
DGAT1	0.957115725	0	0	0	0.25792	0.0604	0.2343
DHRS7	0.513790563	0.1077	0	0.14012	0.33835	0.0259	0.0765
DHTKD1	0.883996066	0.2876	0.78831	0.1599	0.21395	0.0341	0.1596
DIRC2	0.849581787	0.2358	0.16411	6.57373	0.10554	0.0085	0.0808
DLEC1	0.598748749	0.3155	0.34088	0.3661	0.32377	0.0434	0.1342
DLX6	0.320742932	0	0	0	0.27729	0.0082	0.0295
DMGDH	0.230040179	0.1574	0.30431	0.10168	0.20438	0.021	0.1026
DNAI2	0.82088379	0.0763	0.0798	0.04981	0.15138	0.0407	0.2686
DNAJC17	0.673748406	0.3112	0	999	0.12622	0.02	0.1584
DNAJC24	0.831043167	0	0	0	0.16564	0.0237	0.143
DNAJC30	0.590754197	0.3603	999	0	0.37881	0.0708	0.1868
DNAJC5G	0.339531136	1.1338	999	0.73407	0.90695	0.1114	0.1229
DRAP1	0.728090112	0.0764	0	0.06648	0.12032	0.0211	0.1752
DSCR3	0.679864051	0.0444	0.07415	0	0.07754	0.0174	0.2243
DUSP1	0.899096511	0	0	0	0.0001	0	0.1662
EBI3	0.984041974	0.3506	0	0.57739	0.23925	0.0538	0.2247
ECEL1	0.959318593	0.1518	0.11465	0.07971	0.0406	0.0132	0.3245
EFS	0.858993899	0.1428	0.36648	0.11025	0.29914	0.0346	0.1157
EIF2C2	0.788386279	0.0511	0	0	0.02379	0.0042	0.1783
EIF2C4	0.428411255	0	0	0	0.0001	0	0.0505
ELF4	0.832137336	0.2674	0.14983	0.28889	0.23113	0.0287	0.124
ENOPH1	0.784280396	0	0	0	0.10166	0.0079	0.0773
EPB41L1	0.731008675	0.0389	0.0554	0	0.07384	0.0104	0.1411
EPB49	0.894123913	0	0	0	0.01706	0.0023	0.1374
EPHB3	0.435110759	0.0438	0	0.08187	0.02051	0.0032	0.1547
EPSTI1	0.861190834	0.5845	1.94606	0.23665	0.57515	0.0656	0.114
EPT1		0	0	0	0.15899	0.0117	0.0737
ERC1	0.514931377	0.2021	0.47092	0.27057	0.04897	0.006	0.1226
ERCC3	0.787293601	0.3636	999	0.31795	0.05756	0.0094	0.1641

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
EXD1		1.8178	999	1.25372	0.55544	0.0468	0.0843
EXPH5	0.757298929	0.5259	0.44524	0.87018	0.57323	0.0657	0.1146
FAAH2		0.4242	0	1.14011	0.37276	0.0413	0.1109
FAM103A1	0.37101956	0.2609	0.27898	0	0.03079	0.0037	0.1209
FAM111A	0.862606358	2.4305	3.0891	3.59806	1.28121	0.0892	0.0696
FAM120A	0.653763199	0	0	0	0.23679	0.0249	0.1052
FAM126B	0.044290721	0	0	0	0.21272	0.0249	0.117
FAM131A	0.894631167	0	0	0	0.09811	0.0132	0.1343
FAM165B		0	0	0	0.28081	0.0389	0.1386
FAM167A	0.030615823	0.1626	0.17595	0	0.12596	0.022	0.1749
FAM55B		0.9046	1.62279	1.25921	0.44134	0.0423	0.0958
FAM64A	0.902355845	1.3765	999	0.88731	0.63812	0.076	0.1191
FANCG	0.914501643	0.2824	0.57525	0.23911	0.71818	0.1148	0.1599
FBL	0.8379227	0	0	0	0.1293	0.0204	0.1574
FBXL12	0.883243522	0	0	0	0.02168	0.0055	0.2542
FBXO22	0.30245149	0.634	4.60099	0.41468	0.22695	0.0191	0.0842
FCRL2	0.974370808	0.78	1.26087	0.81053	0.71925	0.1065	0.148
FGF2	0.963947731	0.5757	0	1.35994	0.27381	0.019	0.0694
FGGY	0.579303153	0.2111	0.9069	0	0.17813	0.0176	0.099
FKRP	0.306036745	0.2526	0	0.23832	0.05172	0.0183	0.3543
FLT3	0.939049385	1.4551	1.49832	999	0.28362	0.0293	0.1033
FMO6P	0.456387087	0.4166	0.23431	0.47291	0.35202	0.0967	0.2748
FOLR2	0.791311821	0.1612	0.44759	0	0.11806	0.0247	0.2096
FOSB	0.977199942	0	0	0	0.02275	0.0014	0.0611
FTSJ2	0.855366025	0.672	0.6453	6.7416	0.27228	0.0439	0.1614
FXYD3	0.902632348	-1	0	999	0.58545	0.0891	0.1521
FZR1	0.734341851	0.1351	0	0.40031	0.01962	0.007	0.3588
G6PC	0.963346739	0.2095	0.17985	0.36118	0.21468	0.0244	0.1138
GADD45A	0.871841339	0	0	0	0.01978	0.0027	0.1374
GAL3ST4	0.458246415	0.7101	0.43124	999	0.39561	0.0378	0.0955
GALNT12	0.959041557	0.098	999	0	0.19299	0.0407	0.211
GCDH	0.935935884	0.4669	0.2603	0.3677	0.1696	0.0408	0.2403
GCGR	0.681262327	0.1528	0.04538	0.22253	0.24368	0.064	0.2625
GCK	0.447383569	0.0768	0	0.18518	0.12391	0.0419	0.3385
GCOM1	0.302241979	0.1432	0.09153	999	0.2764	0.0459	0.1661
GEMIN7	0.299167791	0.1801	0	0.23244	0.3048	0.0307	0.1007
GFOD2	0.377956067	0.0832	0	0.17625	0.02629	0.007	0.2651
GFRAL		0.3582	999	0.11339	0.70157	0.0581	0.0828
GIMAP2	0.884283655	0.1864	0.25615	0.25611	0.68287	0.0665	0.0974
GJA4	0.516068839	0.1371	0.09806	0.14531	0.05652	0.0133	0.2346
GLYAT	0.949948856	0.0926	0.12015	0	0.51996	0.0606	0.1166
GMNN	0.934206506	0.2891	0.24619	0	0.21798	0.0342	0.157
GNAO1	0.702240903	0	0	0	0.07131	0.0639	0.8966
GNAT2	0.819602503	0	0	0	0.05255	0.0053	0.1015
GNG5P2		0	0	0	0.7149	0.0593	0.0829
GNPAT	0.803196117	0.1848	0.21426	0.3177	0.23519	0.0236	0.1003
GOLGA5	0.787967775	0.1454	0.53303	0	0.27329	0.0233	0.0852
GOLGA6C		0.5956	0.2843	1.79584	0.66482	0.2213	0.3328
GP1BA	0.581831362	0.2297	0.14378	0.42561	0.71596	0.1404	0.1961
GPHA2		0	0	0	0.27905	0.0343	0.1229
GPR176	0.808947979	0.2903	0.11128	0.3875	0.10446	0.0142	0.1355
GPR179		0.4263	0.29731	0.67831	0.64299	0.1138	0.177
GPR39	0.280435897	0.32	0.15392	0.46451	0.22396	0.0485	0.2164
GPR89A		0	0	0	0.0382	0.0029	0.0765
GPRASP2		2.0782	2.43135	999	0.37416	0.032	0.0856
GPT2		0.2683	0	0.43692	0.04079	0.0082	0.2012
GRIK3	0.304810256	0.0557	0.02606	0.05978	0.0197	0.0047	0.2393
GSC	0.040902891	0.1727	0.06466	0	0.03351	0.0059	0.1759
GUCA1B	0.307215512	0	0	0	0.0001	0	0.1916
GUCY2F	0.30415724	0.4082	0.59318	0.37834	0.24456	0.0213	0.0869
H2AFB3		1.1638	0.28522	999	0.32992	0.0727	0.2205
HAUS2	0.524567498	0	0	0	0.33325	0.0288	0.0864

Gene	Tau	H-C pairwise	Human	Chimp	Uniform *ω*	Uniform *Ka*	Uniform *Ks*
HELB	0.199157509	0.1571	0.20363	0.17904	0.44281	0.043	0.0971
HES5		0	0	0	0.02211	0.0068	0.3088
HEYL	0.381547619	0.4914	1.18385	0.19302	0.29903	0.0499	0.1668
HIST1H2AJ	0.426590693	0	0	0	0.0001	0	0.3734
HIST1H2AL	0.480942648	0	0	0	0.00265	0.0033	1.2256
HIST1H3F	0.317250365	0	0	0	0.0001	0.0001	1.3929
HIST1H3G	0.508857809	0	0	0	0.0001	0	0.2363
HLF	0.780031085	0	0	0	0.02597	0.0016	0.0628
HM13	0.946491625	0	0	0	0.0199	0.0021	0.1075
HMGCR	0.901478455	0.1034	0.17525	0.08775	0.24855	0.0282	0.1136
HNRNPD	0.734744282	0	0	0	0.16507	0.0054	0.0327
HNRPLL	0.74921878	0.0386	0	0	0.03584	0.0041	0.1155
HRH3	0.584824274	0.4931	0.09579	0.266	0.08087	0.027	0.3342
HSD17B3	0.942858121	1.3096	0.96259	999	0.28111	0.0345	0.1227
HSPB2	0.957965787					0.0128	0.0769
HSPBP1	0.703406136					0.0013	0.1326
ICT1	0.874284653	0.3036	0.64166	0	0.38557	0.0709	0.1839
IDO2		0.665	0.66306	0.98275	0.53352	0.0614	0.1151
IFI27L1	0.90337797	-1	999	0	0.73215	0.1036	0.1415
IFI44	0.798314639	0.4293	0.34383	0.7523	0.83808	0.0696	0.0831
IFNA2	0.322267628	-1	999	999	0.79254	0.074	0.0933
IL10RA	0.929372691	0.2585	0.22783	0.33258	0.44695	0.0621	0.139
IL17RB	0.873979538	0.4891	0.81571	0.60821	0.43	0.0478	0.1112
IL17REL						0.0475	0.2233
IL19	0.28983424	0.4666	0.84576	0.59796	0.68451	0.0812	0.1186
ILKAP	0.881659315	0	0	0	0.06408	0.0073	0.1146
INTS6	0.787155845	0.557	999	0.52193	0.26447	0.0218	0.0826
IRF8	0.973605865	0.0381	0.30332	0	0.09154	0.016	0.1753
IRX6		0.2917	1.68518	0.09147	0.34715	0.0528	0.1522
ISYNA1	0.960094279	0.2302	0.1426	0	0.04974	0.0165	0.3311
ITGB3BP	0.942485761	0.5388	999	0.2768	0.68178	0.0571	0.0838
ITGB8	0.349221271	0.0851	0	0.21537	0.14252	0.0134	0.0938
JAG2	0.801202849	0.3614	0.01214	0.36304	0.0704	0.0312	0.4426
JAM2	0.852356608	0.3214	884.46638	0.37811	0.19363	0.0201	0.1038
KANK3	0.746342641	0.2863	0.18053	0.2285	0.26894	0.0658	0.2446
KCNB1	0.93964274	0	0	0	0.02316	0.0032	0.1395
KCNG2	0.298111264	0.3016	0.03221	0.13187	0.04569	0.0091	0.1988
KCNJ9	0.667414768	0.5164	0	0.15919	0.03396	0.0088	0.2582
KDM5D	0.909679487	0.4915	0.38478	1.26854	0.2689	0.0498	0.1852
KIAA0562	0.650067281	0.1386	0.24548	0.13201	0.26197	0.0323	0.1233
KIAA0947	0.797077774	0.4057	0.33253	0.63097	0.39879	0.0565	0.1416
KIDINS220	0.754277578	0.1019	0	0.18538	0.08429	0.0095	0.1126
KLHDC4	0.907387314	0.3827	0.25953	0.74056	0.19851	0.0476	0.2397
KLRG2		0.2201	0.14897	0.29331	0.32378	0.0674	0.2083
KMO	0.79101845	0.4007	999	0.4092	0.45969	0.0457	0.0994
KPTN	0.405666747	0.4507	0.30948	0.47562	0.28064	0.0642	0.2286
KRT36	0.291393755	0.5851	0.52022	0.37067	0.21687	0.0459	0.2115
KRTAP4-7	0.572749181	0.8621	999	0	0.23364	0.2103	0.9003
L3MBTL1	0.570314721	0.1565	0.26231	0.10016	0.27676	0.025	0.0902
LAIR1	0.94494438	0.4549	0.21334	1.17361	0.98035	0.1433	0.1462
LAMA4	0.555891434	0.2976	0.16257	0.65699	0.1886	0.0171	0.0904
LAMC2	0.962315465	0.4537	0.75821	0.62255	0.44835	0.0371	0.0827
LAPTM4B	0.913605089	0.2045	0.17499	0.23338	0.46177	0.1591	0.3445
LDB3	0.851436786	0.708	0	0.71836	0.15996	0.0429	0.2683
LEPREL4	0.838532128	0.2136	0.30391	0.09822	0.06629	0.0152	0.2286
LETM2	0.223951735	0.9438	999	0.53396	0.57597	0.0879	0.1526
LGALS7						0.015	0.2544
LHFPL2	0.818046356	0	0	0	0.11937	0.0166	0.1389
LHFPL5	0.031348222	0.157	0	0.21741	0.01008		0.1948
LHX2	0.816919871	0	0	0	0.02486	0.005	0.2007
LIPH	0.091962525	0.2224	0.43894	0.28841	0.40303	0.0377	0.0935
LPAR3	0.326244344	0.1509	0.23529	0	0.15342	0.0278	0.181

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
LRPPRC	0.879353105	0.1481	0	0.54466	0.76638	0.0844	0.1101
LRRC2	0.915898605	0.8378	1.42259	0	0.41602	0.0324	0.0778
LRRC27		1.0017	0.75358	2.3798	0.78222	0.0825	0.1055
LRRTM3	0.491276157	0	0	0	0.04283	0.0024	0.057
LSM10	0.818309295	0	0	0	0.11765		0.1544
LSM7	0.881850546	0	0	0	0.01271	0.0039	0.3065
LTK	0.75027319	0.2559	0.17888	0.28336	0.24546	0.0367	0.1496
LYG1		0.2091	0.21699	0.30281	0.79833	0.09	0.1127
MAGEA8	0.927220409	0.4726	0	999	0.31908	0.0268	0.0841
MAGEB17		0.3425	0.64831	0.28549	0.49983	0.0841	0.1683
MAGEB3	0.455108173	-1	999	999	0.75453	0.0865	0.1146
MAP2	0.325542077	0.3075	0.32376	0.50226	0.30916	0.0261	0.0843
MAP3K7	0.663669357	0	0	0	0.02344	0.0015	0.065
MAP4K3	0.744131592	0.3646	0.47708	0.36402	0.09243	0.0075	0.0808
MAP4K4	0.874368758	0.1017	0	0.15498	0.0812	0.0075	0.0926
MAP4K5	0.706807981	0.0841	0	0.17747	0.51013	0.1254	0.2458
MARK2	0.432557534					0.0074	0.0813
MARVELD3	0.208421194	0.3452	0.38538	0.361	0.39837	0.0397	0.0997
MAT2A	0.869123453	0	0	0	0.05471	0.0058	0.1057
MBD6	0.780715879	0.0808	0.20654	0	0.29706	0.0147	0.0493
MBLAC2		0.2207	0.26616	0	0.06274	0.0068	0.1089
MBNL2	0.611084312	0	0	0	0.08903	0.003	0.0341
MBTPS2	0.29617357	0.0406	0	0.17272	0.05409	0.0058	0.1077
MDM4	0.72522529	0.1134	0.12877	0.20269	0.13548	0.0067	0.0498
ME2	0.894399664	0.1024	0.11246	0.1124	0.05195	0.0056	0.1069
MED19	0.646321398	0.1555	0	7.85595	0.03658	0.004	0.1103
MED7	0.670919533	0	0	0	0.0001	0	0.0727
MEGF10	0.929699759	0.1155	0.14714	0.18045	0.07245	0.0105	0.1454
METAP1D	0.181130372	0.0759	0.11273	0	0.31651	0.0177	0.0558
METTL6	0.03361249	0.2783	0.3378	0.33705	0.40283	0.037	0.0918
MFSD6L		0.6967	0.80235	0.68543	0.45263	0.0751	0.1659
MIER1	0.548404581	0	0	0	0.03199	0.0031	0.0962
MLLT6	0.032698083	0.8958	0.39307	286.52238	0.07658	0.006	0.0777
MLXIPL	0.698164191	0.174	0.12876	0.22392	0.21341	0.01	0.0468
MOAP1	0.841638713	0.2323	999	0.09594	0.2101	0.0216	0.1026
MOCS3	0.506119095	0.1858	0	0.43906	0.29627	0.0353	0.1193
MPHOSPH9	0.803944251	1.04	0.36635	2.18326	0.35669	0.0295	0.0826
MPV17L	0.340006868	0.5735	0.84203	0.16514	0.49477	0.1092	0.2206
MPZL2	0.667949826	0.1067	0	0.15029	0.15926	0.0139	0.0873
MRGPRD		1.8661	0.5417	999	0.40455	0.1095	0.2706
MRGPRE	0.133040233	0.1064	0	0.40202	0.08977	0.0368	0.4098
MRPL20	0.536725847	0	0	0	0.26008		0.3901
MRPL21		0.5295	999	0.22886	0.29047	0.0544	0.1872
MRPL43		0.4396	0	0.40031	0.36544	0.1014	0.2276
MRPL55		-1	0.59356	999	0.45772	0.0876	0.1915
MS4A7		0.3328	999	0.32495	0.49329	0.0609	0.1234
MSL2	0.848056469	0	0	0	0.04331	0.0026	0.0591
MSRB2	0.76149645	0.505	0	0.70021	0.2631	0.0529	0.2012
MTG1	0.79796415	0.6705	0.97589	0.31174	0.29918	0.0481	0.1608
MTIF3	0.665849435	-1	288.11553	0	0.84182	0.0981	0.1165
MYL6B	0.904348112	0.1569	0.27916	0	0.11479	0.0631	0.5498
NCKAP1L	0.935287283	0.0763	0.11546	0.07275	0.14652	0.0158	0.1076
NCOR2	0.478007792	0.0917	0.05217	0.07968	0.06662	0.0198	0.2969
NDP	0.803172988	0.1049	0	0.39567	0.03482	0.0035	0.1019
NDUFA6	0.734575243	0	0	0	0.2592	0.0434	0.1674
NLGN3	0.528560655	0.1657	999	0	0.02587	0.0017	0.0666
NPFF	0.276225008	-1	999	0	1.32221	0.0939	0.071
NPFFR1	0.372016632	0.4182	0.27753	0.11886	0.11288	0.0289	0.2558
NPY1R	0.961025582	0.0469	0.14601	0	0.0435	0.0038	0.0883
NPY5R	0.760676393	0	0	0	0.06886	0.0061	0.0893
NR1D2	0.901632746	0.1551	0.19879	0.14829	0.0573	0.0061	0.1057
NR1I3	0.941770749	0	0	0	0.23094	0.0222	0.0963

Gene	Tau	H-C pairwise	Human	Chimp	Uniform *ω*	Uniform *Ka*	Uniform *Ks*
NR2C2	0.613414112	0.0519	0	0.09776	0.03019		0.1048
NSUN3	0.644010855	0.3065	0.28696	999	0.32474	0.0228	0.0702
NT5M	0.616672053	0.6613	0.22969	999	0.16816	0.0146	0.087
NUDCD1	0.440099236	0.1908	0.33262	0.16669	0.24199	0.0191	0.0791
NUP88	0.730328493	0.2188	0.15118	0.56964	0.31658	0.0383	0.121
NXT1	0.854478762	0	0	0	0.0001	0	0.1557
OAS1	0.94299627	-1	999	999	1.0655	0.1074	0.1008
OAZ2	0.828072309	0	0	0	0.05829	0.0027	0.0458
OLA1	0.788972961	0	0	0	0.10932	0.0048	0.0441
OR10G3	0.038120567	0.4639	0.63016	0.44001	0.462	0.0675	0.1461
OR13J1	0.112298196	1.0662	38.1917	0.65747	0.38906	0.1156	0.2972
OR14A2		0.4365	0.43476	0.71448	0.79819	0.058	0.0727
OR1A2	0.458766619	0.61	0.21946	2.66947	0.87692	0.0588	0.0671
OR1N1	0.27461461	1.2786	999	0.83047	0.71648	0.0298	0.0415
OR1N2	0.282874713	0.2729	0.42938	0.2097	0.57511	0.0401	0.0698
OR2J3	0.316194332	0.6621	1.9063	0.48574	0.45275	0.0657	0.1452
OR51F2	0.032163462	1.4389	999	0.29138	0.74253	0.0291	0.0392
OR5AS1	0.222059758	0.3073	0	2.19927	0.41454	0.0486	0.1173
OR5H6		0.445	0.4801	0.74825	0.53688	0.0775	0.1443
OR6M1	0.025641026	0.3286	0.90572	0.30245	0.50467	0.0706	0.1398
OR6X1	0.030769231	0.6008	3.32697	0.21588	0.52466	0.0627	0.1195
ORC2	0.835693204	0.4722	0.19683	999	0.15016	0.0124	0.0828
OVOL2	0.715192742	0.129	0	0.15304	0.04459	0.0129	0.2889
PADI1	0.274082952	0.3606	0.27422	0.67733	0.20957	0.0453	0.2164
PAFAH1B1	0.836360014	0.4414	0.39615	0.79176	0.19401	0.0153	0.0788
PAX9	0.310157791	0.1156	0	0.08416	0.03506	0.0064	0.1817
PCDH7	0.601005338					0.0046	0.1106
PCDHA1		0.5691	0.33679	0.79144	0.29576	0.0518	0.1752
PCDHA3	0.306594794	0.1703	0.12937	0.20511	0.17195	0.031	0.18
PCDHB5		0.2369	0.13652	0.41743	0.27942	0.0611	0.2188
PDK3	0.555588494	0	0	0	0.04152		0.0594
PDZD7	0.293684105	0.1314	0	0.12946	0.13174	0.036	0.2733
PER3	0.632093976	0.3615	0.36338	0.7828	0.51372	0.0674	0.1312
PFDN6	0.612822297	0	0	0	0.05592	0.004	0.0707
PGAM1	0.699497166	0	0	0	0.03469	0.0035	0.1015
PIAS1	0.813402242	0	0	0	0.00964	0.0007	0.0765
PIGA	0.743247102	0.158	999	0	0.58822	0.0376	0.0639
PINX1		0.2817	0.4139	0.42657	0.41847	0.0548	0.1309
PIP4K2C	0.783025418	0.1519	0.13231	0.40004	0.14508	0.0155	0.1067
PITPNM1	0.635615646	0.2128	0.0996	0.26387	0.08239	0.0196	0.2373
PLAU	0.964202916	0.3016	0.59594	0.28628	0.35402	0.056	0.1581
PLB1	0.355299145	0.1801	0.17849	0.27603	0.31859	0.0503	0.1579
PLCB1	0.546917438	0.0189	0	0.08391	0.09634	0.0075	0.0779
PLCH2	0.918336546	0.1829	0.14157	0.12343	0.11674	0.0376	0.3217
PLEKHA5	0.918267643	0.3636	1.30863	0.10785	0.20914	0.0086	0.0411
PLEKHB2	0.795058917	0.1034	0	0.45786	0.16318	0.0228	0.1396
PLK2	0.948042036	0.0483	0	0.18948	0.09085	0.0068	0.0748
PLP1	0.88009603	0	0	0	0.07234	0.0018	0.0244
PLS3	0.901657328	0.1122	0	0.20172	0.03425	0.0023	0.0665
PLXDC2	0.946358231	0.1528	0.62486	0	0.13644	0.0193	0.1415
PM20D2	0.190245262	0.0823	0.2263	0	0.24738	0.0284	0.1148
PMFBP1	0.577445953	0.3142	0.38756	0.8683	0.53977	0.0563	0.1043
PNKP	0.809136681	0.2609	0.03532	0.40001	0.13825	0.0409	0.2962
PNLIPRP3	0.548597991	0.3625	1.50106	0.12216	0.61214	0.0437	0.0714
PNMA1	0.82503235	0	0	0	0.13351	0.0104	0.0778
PNPLA7	0.093076394	0.5128	0.26618	0.41258	0.24036	0.0497	0.2067
PNPT1	0.642426761	0.0917	0.15576	0	0.19903	0.0201	0.101
POFUT2	0.503957784	0.312	0.35839	0.34709	0.08607	0.0164	0.1909
POGK	0.728177204	0.0489	0.18508	0	0.07697	0.0099	0.1286
POLR2F	0.714172099	0	0	0	0.07162	0.0075	0.1044
POU2F2	0.65402268	0	0	0	0.09881	0.0121	0.1223
PPIG	0.80533061	0.0858	0	0.29844	0.32185		0.0995

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform $K\alpha$	Uniform Ks
PPM1E	0.819337745	0.0997	0	0.1938	0.28141	0.0148	0.0525
PPM1K	0.634600532	0	0	0	0.12621	0.032	0.0631
PPP1R12A	0.832080106	1.0501	0.15326	2.02744	0.11377	0.0086	0.0756
PPP2R2C	0.868797457	-1	0	23.10117	0.01826	0.0047	0.2557
PRKCD	0.947421104	0.1065	0.08401	0.10032	0.02783	0.0058	0.2085
PRKRIP1	0.592035487	0.5908	0	999	0.13991	0.0227	0.162
PRMT6		0	0	0	0.02662	0.0046	0.1722
PRPF4B	0.674134538	0.0571	0.0725	0	0.06779	0.0081	0.1199
PRRC1	0.690559981	0.2163	0.11583	0.53258	0.24139	0.023	0.0954
PRRG1	0.867322304	0.1635	0.20929	0.22288	0.11671	0.0072	0.062
PRSS55	0.25120006	0.3556	0.18115	0.95142	0.40917	0.0904	0.2209
PSMD4	0.680962994	0	0	0	0.02592	0.0025	0.0976
PSMD9	0.872157006	-1	999	999	0.13632	0.024	0.1762
PTPRCAP	0.932466601	0.1281	0.20133	0	0.22203	0.0442	0.199
PTTG2	0.541471067	0.321	0.13389	1.17915	0.8162	0.1055	0.1292
PYGO2	0.065033238	0.1741	0.27061	0	0.14517	0.0082	0.0564
RAB17	0.926693085	0.2365	0.22186	0	0.31202		0.2394
RABEP1	0.687758382	0.1048	0.17385	0.14548	0.09904	0.0112	0.1135
RABGGTA	0.801751124	0.0982	0.28147	0	0.18157	0.0747	0.0905
RAD21L1	0.698843749	0.8197	0.5143	999	0.66225	0.042	0.0633
RAE1	0.710153415	0.0347	0	0.0908	0.03208	0.0052	0.161
RALGDS	0.806275584	0.0542	0	0.08805	0.10056	0.0234	0.2331
RAP1GAP2	0.876629827	0.0765	0.04711	0.07278	0.07865	0.0185	0.2353
RBBP6	0.767237183	0.0848	0.02778	0.16274	0.14204	0.0142	0.1001
RBBP7	0.769191541	0.4963	0	0.87899	0.16826	0.01	0.0597
RBCK1	0.722866593	0.0788	0	0.1128	0.04825	0.0058	0.1194
RBM7	0.83866515	0.1413	0.30268	0	0.1533	0.0198	0.1293
RBP7	0.955229289	0	0	0	0.54877	0.0474	0.0864
RC3H1	0.218132791	0.0539	0.1115	0	0.13467	0.0087	0.0646
RCN2	0.809107391	0.1734	0	0.20213	0.12665	0.0124	0.098
RD3	0.162923077	0.0933	0.0446	0.07484	0.10484	0.0302	0.2883
RESP18		3.4947	999	1.8818	1.03761	0.0902	0.0869
RFX7	0.541448902	0.1111	0.23113	0.064	0.15548	0.0121	0.078
RGS18	0.895005115	0.2683	0	0.57262	0.37106	0.024	0.0648
RGS8	0.152051433	0.1471	0.15214	0	0.08965	0.0067	0.0742
RHOB	0.754929954	0	0	0	0.00865		0.4671
RNF11	0.867698109	0	0	0	0.0001	0	0.0447
RNF208	0.892739722	0	0	0	0.02538	0.004	0.2011
RNF216	0.803871493	0.0701	0	0.37708	0.16529	0.0167	0.1013
RNF34	0.788345638	0.6038	0	16.39712	0.15787	0.0149	0.0944
ROBO4	0.220348282	0.394	0.45938	0.74994	0.32214	0.0437	0.1358
ROR2	0.45344222	0.1048	0.12934	0.0363	0.04994	0.0129	0.2588
RPL23A	0.581130196	0	0	0	0.34186	0.0865	0.2531
RPL26	0.760005102	0	0	0	0.19832	0.0273	0.1375
RPS12	0.697421532	0	0	0	0.144	0.0215	0.149
RPS23	0.650120099	0	0	0	0.0001	0	0.1298
RTN4RL2		0.7241	0.18632	0.3266	0.10758	0.0316	0.2933
S100A4	0.920349451	0	0	0	0.0001	0	0.1474
S1PR3		0.1599	0.20194	0	0.07308	0.0155	0.2114
SCG3	0.924696745	0.09	0	0.30963	0.1282		0.1186
SCN1B	0.846294324	0	0	0	0.04253	0.0113	0.2662
SCT	0.95690936	0.4046	999	0	0.2481	0.0152	0.0585
SDAD1	0.511092755	0	0	0	0.34749	0.0485	0.1394
SDC2	0.953885805	0.6525	3.80162	0	0.1843	0.0145	0.0926
SDHA	0.720599663	0.1589	0	0.24925	0.22614	0.0439	0.1941
SDSL	0.543844915	0.2107	1.01101	0	0.19743	0.0471	0.2385
SEC13	0.747967633	0.3997	0.38693	0.6985	0.11993	0.0152	0.1271
SEC14L5	0.891713983	0.1998	0.15072	0.14716	0.07534	0.021	0.2785
SECTM1	0.965180812	0.4542	0.37069	0.7297	0.50986	0.0658	0.129
SEMA4B	0.975122847	0.2638	0.20101	0.21798	0.13293	0.0196	0.1472
SEMA6B	0.591911765	0.2274	0.09551	0.18602	0.04865	0.0126	0.2597
SERINC5	0.315536081						

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
SFRP1	0.895500476	0.0707	0.06314	0	0.0472	0.0169	0.3584
SH3D21	0.3869606	0.5622	0.43642	999	0.54033	0.0724	0.134
SHMT2	0.925419386	0.2584	0.39588	0.26377	0.14247	0.0141	0.0992
SHPRH	0.105238881	0.1355	0.16987	0.16675	0.15954	0.0185	0.1159
SIPA1	0.905739847	0	0	0	0.06162	0.0127	0.2065
SIX6	0.917079226	0	0	0	0.0515	0.0071	0.1373
SLC16A8	0.906453064	0.2625	0.22593	0.1181	0.08908	0.0209	0.2348
SLC22A17	0.557977645	0.0937	7.11878	0	0.02267	0.0026	0.1126
SLC24A4	0.298040614	0.1047	0.05226	0.35598	0.07227	0.0117	0.1622
SLC25A23	0.690419033	0.0959	0	0.14894	0.0302	0.0048	0.1598
SLC31A1	0.87598865	0	0	0	0.27658	0.0154	0.0556
SLC35C1	0.335888889	0.1747	0.06431	0.13076	0.0749	0.0247	0.3303
SLC45A2	0.479579816	0.3254	0.39235	278.55217	0.27837	0.0352	0.1265
SLC4A4	0.799855613	0.0332	0	0.08127	0.11363		0.0666
SLC5A3	0.825250579	0.1038	0.28388	0	0.10763	0.0065	0.0607
SLC6A4	0.882311699	0.1268	0.18463	0.09221	0.07005	0.0121	0.1723
SLC7A14	0.033594282	0.1227	0.25427	0.07648	0.05471	0.008	0.1456
SLIT1	0.731720553	0.0668	0.02807	0.08537	0.06266	0.0137	0.2191
SMC2	0.91858028	0.0936	0	0.19067	0.09617	0.0101	0.1055
SMC5	0.752837169	0.3324	0.74257	0.24664	0.24785	0.0209	0.0845
SMPD3	0.873552632	0.0659	0.14589	0.03447	0.03518	0.0085	0.2426
SMR3B	0.985298039	2.8286	0	999	0.71114	0.1409	0.1981
SNRPA1	0.815332807	0	0	0	0.0001	0	0.0739
SOAT2	0.735219326	0.1917	0.17779	0.21247	0.21479	0.0384	0.179
SOCS4	0.394252573	0.1386	0.15558	0	0.08137	0.0081	0.0996
SPIB	0.981639991	0.085	0.14698	0	0.06607	0.005	0.0757
SPTB	0.955820248	0.1392	0.08104	0.19836	0.09327	0.02	0.2148
SQSTM1	0.582786985	0.0316	0.03643	0	0.14793	0.0419	0.2831
SREK1	0.825308031	0.2015	0.26091	0.34506	0.09477	0.0058	0.0607
STAT5B	0.837950097	0.0373	0.12765	0	0.03661	0.0055	0.1515
STH		0.4922	999	0.22154	0.95266	0.0982	0.103
STUB1	0.638258179	0	0	0	0.0001	0	0.3835
STX2	0.770641669	0.1404	0	999	0.13497	0.0136	0.101
SULF2	0.084078923	0.1611	0.09981	0.18504	0.06703	0.0154	0.2305
SUMF1	0.569642361	0.1622	0.06966	0.61838	0.29505	0.0334	0.1133
SUSD3	0.98062921	0.1362	0.12717	0.08503	0.24717	0.046	0.186
SUV39H1	0.719960437	0	0	0	0.0001	0	0.1129
SV2B	0.872973258	0.1435	0.08816	0.35683	0.02962	0.0041	0.1368
SYNJ2BP	0.693968233	0.3266	0	0.48711	0.34558	0.0177	0.0512
SYNPO2L	0.974302522	0.0945	0	0.27147	0.38996	0.0421	0.108
TAC4		1.3689	999	1.23552	0.86078	0.0889	0.1033
TACR2	0.606346382	0.3212	0.24053	0.23609	0.1945	0.0335	0.1721
TAGLN	0.934354239	0	0	0	0.01342	0.0021	0.1576
TBC1D17	0.765390937	0.1185	0.11111	0.07331	0.05219	0.0125	0.2402
TBC1D9	0.876649337	0	0	0	0.0128	0.0015	0.119
TBCB	0.734629475	0	0	0	0.04941	0.0109	0.2216
TBR1	0.606103546	0	0	0	0.00823	0.0007	0.0838
TBRG1	0.336069322	0.4769	0.82814	0.41275	0.33208	0.0199	0.0598
TBXA2R	0.702316702	0.0557	0.04187	0	0.06219	0.0245	0.394
TEKT5	0.042398342	0.2523	0.19198	0.18865	0.14052	0.0494	0.3514
TFEC	0.965412944	0.3005	0	0.76882	0.38492	0.0253	0.0658
TGM1	0.965095282	0.1414	0.10978	0.32806	0.07911		0.2036
THY1	0.895114811	0	0	0	0.03844	0.0079	0.2053
TIAF1		-1	999	0	1.56927	0.097	0.0618
TJP2	0.927957107	0.1648	0.33056	0.16573	0.1903	0.0257	0.1349
TMC8	0.889431438	0.5722	0.42575	0.30686	0.16858	0.0359	0.2129
TMCC3		0.0426	0.07474	0	0.06746	0.0084	0.1252
TMED4		0.317	0	999	0.06661	0.012	0.1798
TMEM105		0.7536	999	0	1.0875	0.0828	0.0762
TMEM106B	0.789802459	0	0	0	0.09353	0.0081	0.0867
TMEM121	0.473685897					0.0048	0.325
TMEM139	0.798474411	1.0562	0.62617	999	1.34675	0.0721	0.0536

Gene	Tau	H-C pairwise	Human	Chimp	Uniform ω	Uniform *Ka*	Uniform *Ks*
TMEM178	0.944523765					0.0198	0.1139
TMEM179	0.039073427	-1	0	455.03689	0.1174	0.0289	0.2463
TMEM18	0.29947256	0	0	0	0.16057	0.0184	0.1147
TMEM194A	0.690090948	0.6207	999	0.44807	0.36685	0.0234	0.0639
TMEM208	0.764067429	0	0	0	0.06763	0.0055	0.0812
TMEM232		0.587	1.41466	0.57597	0.40741	0.044	0.1079
TMEM38B	0.933546003	-1	0	999	0.20856	0.0256	0.1227
TMEM42		0	0	0	0.07808	0.0058	0.0739
TMEM43	0.833827405	0.1649	0.11869	0.2366	0.10472	0.0253	0.2414
TMEM61	0.034639348	0.2725	0	0.38494	0.35218	0.077	0.2187
TMEM92		0.5508	0.18823	1.00321	0.56742	0.0726	0.128
TNFAIP8L3	0.263141794	0.1519	0	0.36598	0.18326	0.0301	0.1645
TNFSF9	0.927735924					0.0385	0.1433
TNIP3	0.558029173	0.1301	0.3731	0	0.55937	0.085	0.1519
TNS3	0.322598751	0.0907	0.07818	0.10024	0.16329	0.0351	0.2147
TOP3A	0.562445508	0.2319	2.89737	0.03616	0.2615	0.0363	0.1389
TRAIP	0.332398754	0.4092	0.47644	0	0.38503	0.035	0.0909
TRIM39	0.233740334	0.3218	0.40642	0	0.1087	0.0084	0.0769
TSPAN15	0.751983904	0	0	0	0.064	0.0122	0.191
TSPAN8	0.973990833	0.4452	0.15012	1.02842	1.69742	0.1882	0.1109
TSSK2	0.633716196	-1	17.83598	16.0685	0.10263	0.0223	0.2177
TSSK4	0.791626781	0.3013	0.10784	0.74746	0.5521	0.0701	0.127
TTC29	0.939623691	0.2802	0.40549	0.40457	0.57975	0.0362	0.0624
TTF1	0.714708726	0.1652	0.37088	0.16315	0.5884	0.0796	0.1353
TTLL9	0.195855438	0.1642	0.15323	0.08778	0.20965	0.0491	0.234
TTYH1	0.893112805	0.2071	0.31179	0.07737	0.0886	0.0162	0.1829
TUBB	0.845656789	0	0	0	0.16238	0.026	0.1599
TXNDC11	0.662823519	0.6043	0.74432	0.87643	0.31256	0.034	0.1087
UBLCP1	0.741387871	0	0	0	0.02682	0.0027	0.1007
UGT1A3		0.2506	0.39161	0.30136	0.39584	0.0477	0.1206
UNC13C	0.893169456	0.1825	0.35949	0.14371	0.14659	0.0174	0.1184
UPF2	0.815731818	0.0671	0.1559	0.06185	0.07336	0.0059	0.0801
USP1	0.880626736	0.1654	0.43511	0	0.21049	0.0144	0.0684
USP18	0.867548939	0.1593	0.30149	0.17399	0.39733	0.0685	0.1723
USP26	0.033963307	0.9795	0.69315	1.86038	0.90656	0.0873	0.0963
USP7	0.745253657	0.0379	0.11529	0	0.01015	0.0008	0.0822
VCX2	0.74255519	1.6507	2.40479	1.80532	0.63864	0.205	0.321
VPREB1	0.963234958	0.3105	0.65786	0.16529	0.47646	0.0698	0.1466
VPS13D	0.604562639	0.1183	0.24218	0.11025	0.12546	0.0124	0.0986
VPS52	0.501520251	0	0	0	0.07923	0.0077	0.0973
VSIG1	0.041509972	1.272	999	0.90899	0.59697	0.0414	0.0694
WDFY2	0.377618779	0.2948	0.43477	0	0.09537	0.0074	0.0772
WDR33	0.366442308	0.0527	6.84237	0	0.06752	0.0048	0.0718
WDR5B	0.622449536	0.3037	0	0.36974	0.20814	0.0227	0.1089
WDR63	0.14654152	0.211	0.14465	0.72349	0.39106	0.0318	0.0814
WDR74	0.603337935	2.0648	999	1.15279	0.26369	0.0282	0.107
WFDC11		0.4825	331.38799	0	0.61073	0.1043	0.1708
WFDC6	0.693660557	0.5723	999	0.48772	1.10794	0.0743	0.0671
WISP3	0.725602999	0.1228	0.18157	0.22734	0.2632	0.0224	0.0853
WSB2	0.881073889	0	0	0	0.09507		0.0855
YLPM1	0.683389804	0.1206	0.25342	0.10541	0.13547	0.0089	0.0657
YTHDC1	0.510313421	0.097	0.92987	4.36211	0.03828	0.0081	0.0622
ZBP1	0.477530785	0.4775	0.32938	2.06832	0.81373	0.1181	0.1452
ZBTB38	0.465903788	0.1645	0.12572	0.3321	0.17502	0.0173	0.0989
ZC3H12D		0.3472	0.15892	0.35785	0.19087	0.043	0.2254
ZC3H13	0.75454987	0.0592	0.16738	0	0.13398	0.013	0.0967
ZC4H2	0.347137746	0	0	0	0.0001	0	0.0608
ZCCHC17	0.69068278	0	0	0	0.02179	0.002	0.0916
ZFP37	0.525942384	2.9411	193.36647	0.91022	0.87814	0.0479	0.0545
ZFP57	0.035977564	2.0257	999	0.74642	0.41787	0.0458	0.1095
ZFP64	0.489962766	0.1714	0.33145	0	0.05215	0.0103	0.1967
ZFYVE20	0.185914305	0.3022	0.57403	0.28577	0.20531	0.0197	0.0959

Gene	Tau	H(C*pairwise	Human	Chimp	Uniform*ω	Uniform'Ka	Uniform*Ks
ZMYND17	0.034532289	0.2766	0.17875	1.44738	0.43223	0.0393	0.0909
ZNF117	0.627155258	1.0698	999	1.01278	0.60373		0.3579
ZNF157	0.427561443	0.2769	0.12206	0.00422	0.34854	0.0248	0.0712
ZNF192	0.283393807	1.7782	1.71142	0.838	0.46068	0.216	0.0616
ZNF20		A1	999	48.6143	0.46875	0.0413	0.088
ZNF235	0.550878709	0.1632	0.14871	0.27111	0.32765	0.0342	0.1045
ZNF275	0.035720601	0.1468	0.10577	0.28249	0.07994	0.0195	0.2444
ZNF30	0.198028563	0.5017	0.53032	0.71913	0.47462	0.0661	0.1393
ZNF302	0.455167801	0.4487	0.624	1.4514	0.49188	0.0888	0.1805
ZNF324B	0.611505504	0.2451	0.10175	0.30654	0.19381	0.0594	0.3063
ZNF335	0.461777669	0.1731	0.17329	0.22537	0.13374	0.0192	0.1434
ZNF528	0.829931699	0.1592	0.26026	0.12966	0.35099	0.0464	0.1322
ZNF540	0.880894131	0.9239	1.3702	0.5098	0.44193	0.0359	0.0811
ZNF561		0.5107	0.37007	1.50363	0.65825	~~0.1985~~	0.3015
ZNF569	0.289256502	0	0	0	0.14679	0.0141	0.0961
ZNF570		0	0	0	0.08974	0.0071	0.0792
ZNF574	0.620877904	0.2633	0.14184	0.63593	0.05399	0.0063	0.1162
ZNF575	0.039736973	1.7849	0.6042	999	0.26699		0.1432
ZNF592	0.571652384	0.0621	0.1418	0.06068	0.12998	0.013	0.1
ZNF625						0.0179	0.0948
ZNF652	0.834561377	0.1839	0.15636	0.31129	0.21862	0.0154	0.0703
ZNRD1		0	0	0	0.20302	0.0148	0.0729

Tissue of expression

Bulbourethral Diverticulum – maximum expression

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
87991	ALB	Alb	0.38549	0.052	0.0023	0.0033	
87994	ALDOA	Aldoa	0.02534	0.0054	0	0	
88255	ANXA6	Anxa6	0.20573	0.0425	0.0019	0.0019	
88227	C3	C3	0.22609	0.044	0.0022	0.0046	
88269	CA2	Car2	0.27904	0.0316	0.0018	0.0037	
104652	CAPZB	Capzb	0.46787	0.1497	0.0014	0	
88476	CP	Cp	0.28965	0.0273	0.001	0.0012	
94865	DBI	Dbi	0.3187	0.046	0.0035	0	
95669	GC	Gc	0.37888	0.0399	0.001	0.001	
95742	GLO1	Glo1	0.14205	0.0196	0.0025	0	
95791	GOT1	Got1	0.10364	0.0154	0	0	
95797	GPI	Gpi1	0.09336	0.0184	0.0015	0.0045	
95865	GSTP1	Gstp2	0.11791	0.0287	0.002	0	
105112	HPX	Hpx	0.67457	0.1034	0.001	0	
96240	HSPB1	Hspb1	0.05552	0.0176	0	0.0039	
96759	LDHA	Ldha	0.09163	0.008	0.0013	0.0013	
96836	LTA4H	Lta4h	0.19132	0.0121	0	0	
97051	MDH1	Mdh1	0.12758	0.0107	0	0	
1933118	PGAM2	Pgam2	0.02754	0.0064	0	0	
97555	PGK1	Pgk1	0.20731	0.0158	0	0	
97565	PGM1	Pgm2	0.10201	0.012	0.0026	0.0009	
109486	PRDX2	Prdx2	0.12405	0.025	0	0	
97828	PYGB	Pygb	0.11028	0.051	0	0	
891968	SERPINA1	Serpina1e	0.4603	0.0723	0.0011	0.0023	
103123	SERPINB6	Serpinb6a	0.14886	0.0469	0	0.0103	
98821	TF	Trf	0.54147	0.0872	0.0013	0.002	
98797	TPI1	Tpi1	0.08996	0.0132	0	0	
108109	YWHAG	Ywhag	0	0	0	0	
87947	ADSSL1	Adssl1			0.0068	0.0019	

Bulbourethral Diverticulum

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*
103251	ACLY	Acly	0.06161	0.0089	0.0004	0.0033
1929955	AKR1A1	Akr1a1	0.11113	0.0105	0	0.0015
1353494	AKR1B1	Akr1b3	0.11948	0.0172	0.0014	0.0029
87991	ALB	Alb	0.38549	0.052	0.0023	0.0033
87994	ALDOA	Aldoa	0.02534	0.0054	0	0
96819	ANXA1	Anxa1	0.07163	0.0073	0	0
108481	ANXA11	Anxa11	0.61009	0.3073	0	0
88246	ANXA2	Anxa2	0.00787	0.0013	0	0
1201378	ANXA3	Anxa3	0.21532	0.0291	0.0029	0.0044
88030	ANXA4	Anxa4	0.16539	0.014	0.0014	0
106008	ANXA5	Anxa5	0.15992	0.009	0	0
88255	ANXA6	Anxa6	0.20573	0.0425	0.0019	0.0019
2178103	ARHGDIA	Arhgdia	0.26962	0.0308	0.0013	0.0027
88227	C3	C3	0.22609	0.044	0.0022	0.0046
88269	CA2	Car2	0.27904	0.0316	0.0018	0.0037
104652	CAPZB	Capzb	0.46787	0.1497	0.0014	0
88407	CKB	Ckb	0.02772	0.0062	0	0
2388633	CLTC	Cltc	0.01865	0.0011	0	0
1913304	CNDP2	Cndp2	0.38803	0.8795	0.0033	0.0011
88476	CP	Cp	0.28965	0.0273	0.001	0.0012
101932	CPE	Cpe	0.1066	0.0113	0	0.001
94865	DBI	Dbi	0.3187	0.046	0.0035	0
95288	EEF2	Eef2	0.00178	0.001	0	0.0006
95485	FASN	Fasn	0.1235	0.0517	0.002	0.0022
2444336	FCGBP	Fcgbp	0.19151	0.0318	0.0049	0.0048
95669	GC	Gc	0.37888	0.0399	0.001	0.001
99845	GDI2	Gdi2	0.06813	0.0087	0	0.0011
95742	GLO1	Glo1	0.14205	0.0196	0.0025	0
101849	GNB2L1	Gnb2l1	0	0	0	0
95791	GOT1	Got1	0.10364	0.0154	0	0
95797	GPI	Gpi1	0.09336	0.0184	0.0015	0.0045
95851	GSN	Gsn	0.10021	0.0193	0.0006	0.0006
95865	GSTP1	Gstp2	0.11791	0.0287	0.002	0
1321133	HINT1	Hint1	0.09701	0.0117	0	0
105112	HPX	Hpx	0.67457	0.1034	0.001	0
95835	HSPA5	Hspa5	0.0487	0.0055	0	0
105384	HSPA8	Hspa8	0	0	0	0
96240	HSPB1	Hspb1	0.05552	0.0176	0	0.0039
96413	IDH1	Idh1	0.265	0.0411	0.0011	0.0011
96705	KRT8	Krt8	0.19706	0.0667	0.0017	0.0071
96759	LDHA	Ldha	0.09163	0.008	0.0013	0.0013
96836	LTA4H	Lta4h	0.19132	0.0121	0	0
97051	MDH1	Mdh1	0.12758	0.0107	0	0
97050	MDH2	Mdh2	0.08792	0.0153	0	0.0014
107717	MYH9	Myh9	0.01165	0.0035	0	0.0011
97464	P4HB	P4hb	0.08835	0.0178	0	0.0018
2135637	PARK7	Park7	0.1005	0.0078	0	0.0026
95834	PDIA3	Pdia3	0.14971	0.0173	0	0
97549	PFN1	Pfn1	0.29469	0.0249	0	0.0134
1933118	PGAM2	Pgam2	0.02754	0.0064	0	0
97555	PGK1	Pgk1	0.20731	0.0158	0	0
1913421	PGLS	Pgls	0.09575	0.0188	0.0018	0
97565	PGM1	Pgm2	0.10201	0.012	0.0026	0.0009
103080	PIGR	Pigr	0.47638	0.0876	0.0068	0.0024
99523	PRDX1	Prdx1	0.1014	0.0078	0	0
109486	PRDX2	Prdx2	0.12405	0.025	0	0
1859821	PRDX5	Prdx5	0.3221	0.0321	0.0046	0
894320	PRDX6	Prdx6	0.08072	0.0089	0	0
97828	PYGB	Pygb	0.11028	0.051	0	0
97842	RAB1A	Rab1	0.07614	0.0047	0	0
1928750	RAB2A	Rab2a	0.0001	0	0	0
891968	SERPINA1	Serpina1e	0.4603	0.0723	0.0011	0.0023
103123	SERPINB6	Serpinb6a	0.14886	0.0469	0	0.0103
98351	SOD1	Sod1	0.59912	0.0769	0	0
98821	TF	Trf	0.54147	0.0872	0.0013	0.002
3027002	TGM4	Tgm4	0.38754	0.0541	0.004	0.003
105992	TKT	Tkt	0.03005	0.0069	0.0007	0.0007
98797	TPI1	Tpi1	0.08996	0.0132	0	0
104890	TPT1	Tpt1	0.31717	0.0197	0	0
98865	TTR	Ttr	0.59375	0.0644	0.0067	0.0068
98874	TXN	Txn1	0.34466	0.02	0	0
99919	VCP	Vcp	0.02398	0.0023	0	0
1891917	YWHAB	Ywhab	0	0	0	0
894689	YWHAE	Ywhae	0.09136	0.0037	0	0
108109	YWHAG	Ywhag	0	0	0	0
109484	YWHAZ	Ywhaz	0	0	0	0

Bulbourethral Gland – maximum expression

mouse&d	HumanGeneName	mouse&gene	tree_ω	Ka	H_Ka	C_Ka
1890773	ACTN4	Actn4	0.00599	0.0026	0	0
1344405	AGR2	Agr2	0.23294	0.0144	0.0029	0
1929955	AKR1A1	Akr1a1	0.11113	0.0105	0	0.0015
96819	ANXA1	Anxa1	0.07163	0.0073	0	0
108481	ANXA11	Anxa11	0.61009	0.3073	0	0
1201378	ANXA3	Anxa3	0.21532	0.0291	0.0029	0.0044
106008	ANXA5	Anxa5	0.15992	0.009	0	0
2180167	APOA1BP	Apoa1bp	0.25795	0.0291	0.0016	0.0016
2178103	ARHGDIA	Arhgdia	0.26962	0.0308	0.0013	0.0027
1917600	BASP1	Basp1	0.19262	0.0193	0.0021	0
88262	CAP1	Cap1	0.19238	0.019	0.006	0
107185	CCT5	Cct5	0.0113	0.0016	0	0
107183	CCT8	Cct8	0.07093	0.0068	0	0.0025
88354	CDH1	Cdh1	0.19729	0.0339	0	0.0016
2388633	CLTC	Cltc	0.01865	0.0011	0	0
1913304	CNDP2	Cndp2	0.38803	0.8795	0.0033	0.0011
1354962	COPB2	Copb2	0.09465	0.0068	0.0009	0.0007
101932	CPE	Cpe	0.1066	0.0113	0	0.001
102553	CRISP3	Crisp1	0.43931	0.059	0.0037	0.0019
1915130	DCXR	Dcxr	0.23412	0.0535	0.0127	0
1914410	EEF1G	Eef1g	0.17534	0.0207	0.001	0
95288	EEF2	Eef2	0.00178	0.001	0	0.0006
99845	GDI2	Gdi2	0.06813	0.0087	0	0.0011
104967	GLG1	Glg1	0.04455	0.0055	0	0.0008
95773	GNAI3	Gnai3	0	0	0	0
95784	GNB2	Gnb2	0.03504	0.0063	0	0
101849	GNB2L1	Gnb2l1	0	0	0	0
1289257	GPD1L	Gpd1l	0.09575	0.0153	0	
95851	GSN	Gsn	0.10021	0.0193	0.0006	0.0006
1342273	GSTO1	Gsto1	0.27514	0.026	0.0018	0.0018
1321133	HINT1	Hint1	0.09701	0.0117	0	0
105384	HSPA8	Hspa8	0	0	0	0
1352757	IQGAP1	Iqgap1	0.05349	0.0049	0.0003	0
96705	KRT8	Krt8	0.19706	0.0667	0.0017	0.0071
97050	MDH2	Mdh2	0.08792	0.0153	0	0.0014
107717	MYH9	Myh9	0.01165	0.0035	0	0.0011
1261422	NAGA	Naga	0.15037	0.0265	0.0021	0
97388	NUCB1	Nucb1	0.12083	0.0256	0	0.0011
97475	PAM	Pam	0.28683	0.0204	0.001	0.0005
2135637	PARK7	Park7	0.1005	0.0078	0	0.0026
97553	PGD	Pgd	0.13151	0.0253	0	0.003
1913421	PGLS	Pgls	0.09575	0.0188	0.0018	0
103080	PIGR	Pigr	0.47638	0.0876	0.0068	0.0024
99523	PRDX1	Prdx1	0.1014	0.0078	0	0
1859821	PRDX5	Prdx5	0.3221	0.0321	0.0046	0
97783	PSAP	Psap	0.11398	0.0149	0.0009	0
1347006	PSMA6	Psma6	0.15024	0.0136	0	0
1915615	RAB14	Rab14	0	0	0	0
97842	RAB1A	Rab1	0.07614	0.0047	0	0
1923558	RAB1B	Rab1b	0.07787	0.0182	0	0.0042
1931295	RAB27B	Rab27b	0.21051	0.0152	0	0.0022
1928750	RAB2A	Rab2a	0.0001	0	0	0
97844	RAB3D	Rab3d	0.04423	0.0098	0.002	0
97887	RDX	Rdx	0.1668	0.0238	0	0
1096342	RHOA	Rhoa	0	0	0	0
1927636	RPLP0	Rplp0	0.04414	0.003	0	0
98351	SOD1	Sod1	0.59912	0.0769	0	0
1312985	TAGLN2	Tagln2	0.05075	0.007	0	0
1274789	TALDO1	Taldo1	0.12716	0.0172	0	0.0027
98535	TCP1	Tcp1	0.03	0.0032	0	0
105992	TKT	Tkt	0.03005	0.0069	0.0007	0.0007
104890	TPT1	Tpt1	0.31717	0.0197	0	0
98857	TSTA3	Tsta3	0.1166	0.0242	0.0013	0.0053
98874	TXN	Txn1	0.34466	0.02	0	0
1349450	VAT1	Vat1	0.16604	0.0311	0.0046	0.0034
99919	VCP	Vcp	0.02398	0.0023	0	0
1914951	WFDC2	Wfdc2	0.20458	0.0487	0	0
2180003	XPNPEP1	Xpnpep1	0.02849	0.0031	0.0008	0

Bulbourethral Gland

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*
1890773	ACTN4	Actn4	0.00599	0.0026	0	0
1344405	AGR2	Agr2	0.23294	0.0144	0.0029	0
1929955	AKR1A1	Akr1a1	0.11113	0.0105	0	0.0015
1353494	AKR1B1	Akr1b3	0.11948	0.0172	0.0014	0.0029
87991	ALB	Alb	0.38549	0.052	0.0023	0.0033
87994	ALDOA	Aldoa	0.02534	0.0054	0	0
96819	ANXA1	Anxa1	0.07163	0.0073	0	0
108481	ANXA11	Anxa11	0.61009	0.3073	0	0
88246	ANXA2	Anxa2	0.00787	0.0013	0	0
1201378	ANXA3	Anxa3	0.21532	0.0291	0.0029	0.0044
88030	ANXA4	Anxa4	0.16539	0.014	0.0014	0
106008	ANXA5	Anxa5	0.15992	0.009	0	0
88255	ANXA6	Anxa6	0.20573	0.0425	0.0019	0.0019
2180167	APOA1BP	Apoa1bp	0.25795	0.0291	0.0016	0.0016
2178103	ARHGDIA	Arhgdia	0.26962	0.0308	0.0013	0.0027
1917600	BASP1	Basp1	0.19262	0.0193	0.0021	0
88227	C3	C3	0.22609	0.044	0.0022	0.0046
88252	CALR	Calr	0.02978	0.0044	0	0
88262	CAP1	Cap1	0.19238	0.019	0.006	0
107185	CCT5	Cct5	0.0113	0.0016	0	0
107183	CCT8	Cct8	0.07093	0.0068	0	0.0025
106211	CDC42	Cdc42	0.09607	0.0022	0	0
88354	CDH1	Cdh1	0.19729	0.0339	0	0.0016
101757	CFL1	Cfl1	0.00954	0.0025	0	0
88407	CKB	Ckb	0.02772	0.0062	0	0
2388633	CLTC	Cltc	0.01865	0.0011	0	0
1913304	CNDP2	Cndp2	0.38803	0.8795	0.0033	0.0011
1354962	COPB2	Copb2	0.09465	0.0068	0.0009	0.0007
101932	CPE	Cpe	0.1066	0.0113	0	0.001
102553	CRISP3	Crisp1	0.43931	0.059	0.0037	0.0019
1915130	DCXR	Dcxr	0.23412	0.0535	0.0127	0
1298381	DDT	Ddt	0.14877	0.0333	0	0
1914410	EEF1G	Eef1g	0.17534	0.0207	0.001	0
95288	EEF2	Eef2	0.00178	0.001	0	0.0006
95485	FASN	Fasn	0.1235	0.0517	0.002	0.0022
2444336	FCGBP	Fcgbp	0.19151	0.0318	0.0049	0.0048
95669	GC	Gc	0.37888	0.0399	0.001	0.001
99845	GDI2	Gdi2	0.06813	0.0087	0	0.0011
104967	GLG1	Glg1	0.04455	0.0055	0	0.0008
95773	GNAI3	Gnai3	0	0	0	0
95784	GNB2	Gnb2	0.03504	0.0063	0	0
101849	GNB2L1	Gnb2l1	0	0	0	0
1289257	GPD1L	Gpd1l	0.09575	0.0153	0	
95797	GPI	Gpi1	0.09336	0.0184	0.0015	0.0045
95851	GSN	Gsn	0.10021	0.0193	0.0006	0.0006
1342273	GSTO1	Gsto1	0.27514	0.026	0.0018	0.0018
1321133	HINT1	Hint1	0.09701	0.0117	0	0
105112	HPX	Hpx	0.67457	0.1034	0.001	0
1342292	HSPA4	Hspa4	0.06868	0.006	0.0005	0.0005
95835	HSPA5	Hspa5	0.0487	0.0055	0	0
105384	HSPA8	Hspa8	0	0	0	0
96413	IDH1	Idh1	0.265	0.0411	0.0011	0.0011
1352757	IQGAP1	Iqgap1	0.05349	0.0049	0.0003	0
96705	KRT8	Krt8	0.19706	0.0667	0.0017	0.0071
1914238	LAP3	Lap3	0.38199	0.0922	0	0
96759	LDHA	Ldha	0.09163	0.008	0.0013	0.0013
97051	MDH1	Mdh1	0.12758	0.0107	0	0
97050	MDH2	Mdh2	0.08792	0.0153	0	0.0014

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
107717	MYH9	Myh9	0.01165	0.0035	0	0.0011	
1261422	NAGA	Naga	0.15037	0.0265	0.0021	0	
97388	NUCB1	Nucb1	0.12083	0.0256	0	0.0011	
1858179	NUCB2	Nucb2	0.49462	0.0611	0.0017	0	
97464	P4HB	P4hb	0.08835	0.0178	0	0.0018	
97475	PAM	Pam	0.28683	0.0204	0.001	0.0005	
2135637	PARK7	Park7	0.1005	0.0078	0	0.0026	
95834	PDIA3	Pdia3	0.14971	0.0173	0	0	
97549	PFN1	Pfn1	0.29469	0.0249	0	0.0134	
1933118	PGAM2	Pgam2	0.02754	0.0064	0	0	
97553	PGD	Pgd	0.13151	0.0253	0	0.003	
97555	PGK1	Pgk1	0.20731	0.0158	0	0	
1913421	PGLS	Pgls	0.09575	0.0188	0.0018	0	
97565	PGM1	Pgm2	0.10201	0.012	0.0026	0.0009	
1355330	PHGDH	Phgdh	0.08515	0.0123	0	0.0009	
103080	PIGR	Pigr	0.47638	0.0876	0.0068	0.0024	
97750	PPIB	Ppib	0.034	0.0044	0	0.0021	
99523	PRDX1	Prdx1	0.1014	0.0078	0	0	
109486	PRDX2	Prdx2	0.12405	0.025	0	0	
1859821	PRDX5	Prdx5	0.3221	0.0321	0.0046	0	
894320	PRDX6	Prdx6	0.08072	0.0089	0	0	
97783	PSAP	Psap	0.11398	0.0149	0.0009	0	
1347006	PSMA6	Psma6	0.15024	0.0136	0	0	
97828	PYGB	Pygb	0.11028	0.051	0	0	
1915615	RAB14	Rab14	0	0	0	0	
97842	RAB1A	Rab1	0.07614	0.0047	0	0	
1923558	RAB1B	Rab1b	0.07787	0.0182	0	0.0042	
1931295	RAB27B	Rab27b	0.21051	0.0152	0	0.0022	
1928750	RAB2A	Rab2a	0.0001	0	0	0	
97844	RAB3D	Rab3d	0.04423	0.0098	0.002	0	
97887	RDX	Rdx	0.1668	0.0238	0	0	
1096342	RHOA	Rhoa	0	0	0	0	
1927636	RPLP0	Rplp0	0.04414	0.003	0	0	
103123	SERPINB6	Serpinb6a	0.14886	0.0469	0	0.0103	
98351	SOD1	Sod1	0.59912	0.0769	0	0	
1312985	TAGLN2	Tagln2	0.05075	0.007	0	0	
1274789	TALDO1	Taldo1	0.12716	0.0172	0	0.0027	
98535	TCP1	Tcp1	0.03	0.0032	0	0	
98821	TF	Trf	0.54147	0.0872	0.0013	0.002	
3027002	TGM4	Tgm4	0.38754	0.0541	0.004	0.003	
105992	TKT	Tkt	0.03005	0.0069	0.0007	0.0007	
98797	TPI1	Tpi1	0.08996	0.0132	0	0	
104890	TPT1	Tpt1	0.31717	0.0197	0	0	
98857	TSTA3	Tsta3	0.1166	0.0242	0.0013	0.0053	
98874	TXN	Txn1	0.34466	0.02	0	0	
1349450	VAT1	Vat1	0.16604	0.0311	0.0046	0.0034	
98927	VCL	Vcl	0.07167	0.0055	0	0	
99919	VCP	Vcp	0.02398	0.0023	0	0	
1914951	WFDC2	Wfdc2	0.20458	0.0487	0	0	
2180003	XPNPEP1	Xpnpep1	0.02849	0.0031	0.0008	0	
894689	YWHAE	Ywhae	0.09136	0.0037	0	0	
109484	YWHAZ	Ywhaz	0	0	0	0	

Prostate – maximum expression

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
87874	ACE	Ace	0.10981	0.0333	0.0014	0.0057	
103251	ACLY	Acly	0.06161	0.0089	0.0004	0.0033	
2137706	ACTN1	Actn1	0.0318	0.0077	0	0	
87968	AHCY	Ahcy	0.20319	0.058	0	0	
1353494	AKR1B1	Akr1b3	0.11948	0.0172	0.0014	0.0029	
1353450	ALDH1A1	Aldh1a1	0.09454	0.0114	0	0	
88246	ANXA2	Anxa2	0.00787	0.0013	0	0	
88030	ANXA4	Anxa4	0.16539	0.014	0.0014	0	
103163	AZGP1	Azgp1	0.42468	0.0812	0	0.0015	
88252	CALR	Calr	0.02978	0.0044	0	0	
106222	CAPZA2	Capza2	0.05711	0.0033	0	0.0047	
104689	CCT4	Cct4	0.041	0.0035	0	0	
106211	CDC42	Cdc42	0.09607	0.0022	0	0	
101757	CFL1	Cfl1	0.00954	0.0025	0	0	
88407	CKB	Ckb	0.02772	0.0062	0	0	
88460	COL6A2	Col6a2	0.17475	0.0808	0.0008	0.0004	
102519	CST3	Cst3	0.07408	0.0173	0		
88561	CTSB	Ctsb	0.09991	0.0272	0.0013	0.0013	
1298381	DDT	Ddt	0.14877	0.0333	0	0	
95485	FASN	Fasn	0.1235	0.0517	0.002	0.0022	
2444336	FCGBP	Fcgbp	0.19151	0.0318	0.0049	0.0048	
1097667	GANAB	Ganab	0.21498	0.0177	0	0.002	
96231	HSPA1L	Hspa1l	0.03881	0.0472	0.0022	0.0007	
1342292	HSPA4	Hspa4	0.06868	0.006	0.0005	0.0005	
95835	HSPA5	Hspa5	0.0487	0.0055	0	0	
108030	HYOU1	Hyou1	0.12987	0.0148	0.0015	0.0024	
96413	IDH1	Idh1	0.265	0.0411	0.0011	0.0011	
1914238	LAP3	Lap3	0.38199	0.0922	0	0	
96763	LDHB	Ldhb	0	0	0	0	
97464	P4HB	P4hb	0.08835	0.0178	0	0.0018	
95834	PDIA3	Pdia3	0.14971	0.0173	0	0	
97549	PFN1	Pfn1	0.29469	0.0249	0	0.0134	
1355330	PHGDH	Phgdh	0.08515	0.0123	0	0.0009	
97750	PPIB	Ppib	0.034	0.0044	0	0.0021	
1859815	PRDX4	Prdx4	0.33071	0.0215	0	0.0079	
894320	PRDX6	Prdx6	0.08072	0.0089	0	0	
1347070	PSMA7	Psma7	0.06726	0.0096	0.0019	0	
97919	RNASE1	Rnase1	0.3914	0.0684	0.0057	0.0028	
96825	SELENBP1	Selenbp2	0.11919	0.0232	0.0018	0.0027	
891970	SERPINA1	Serpina1e	0.4603	0.0723	0.0011	0.0023	
98266	SORD	Sord	0.28128	0.0529	0.003	0.0051	
3027002	TGM4	Tgm4	0.38754	0.0541	0.004	0.003	
98865	TTR	Ttr	0.59375	0.0644	0.0067	0.0068	
98927	VCL	Vcl	0.07167	0.0055	0	0	
1891917	YWHAB	Ywhab	0	0	0	0	
894689	YWHAE	Ywhae	0.09136	0.0037	0	0	
109484	YWHAZ	Ywhaz	0	0	0	0	

Prostate

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
87874	ACE	Ace	0.10981	0.0333	0.0014	0.0057	
103251	ACLY	Acly	0.06161	0.0089	0.0004	0.0033	
2137706	ACTN1	Actn1	0.0318	0.0077	0	0	
1890773	ACTN4	Actn4	0.00599	0.0026	0	0	
1344405	AGR2	Agr2	0.23294	0.0144	0.0029	0	
87968	AHCY	Ahcy	0.20319	0.058	0	0	
1929955	AKR1A1	Akr1a1	0.11113	0.0105	0	0.0015	
1353494	AKR1B1	Akr1b3	0.11948	0.0172	0.0014	0.0029	
87991	ALB	Alb	0.38549	0.052	0.0023	0.0033	
1353450	ALDH1A1	Aldh1a1	0.09454	0.0114	0	0	
87994	ALDOA	Aldoa	0.02534	0.0054	0	0	
96819	ANXA1	Anxa1	0.07163	0.0073	0	0	
88246	ANXA2	Anxa2	0.00787	0.0013	0	0	
1201378	ANXA3	Anxa3	0.21532	0.0291	0.0029	0.0044	
88030	ANXA4	Anxa4	0.16539	0.014	0.0014	0	
106008	ANXA5	Anxa5	0.15992	0.009	0	0	
88255	ANXA6	Anxa6	0.20573	0.0425	0.0019	0.0019	
2178103	ARHGDIA	Arhgdia	0.26962	0.0308	0.0013	0.0027	
103163	AZGP1	Azgp1	0.42468	0.0812	0	0.0015	
88127	B2M	B2m	0.51482	0.0596	0	0.0039	
88227	C3	C3	0.22609	0.044	0.0022	0.0046	
88269	CA2	Car2	0.27904	0.0316	0.0018	0.0037	
88252	CALR	Calr	0.02978	0.0044	0	0	
106222	CAPZA2	Capza2	0.05711	0.0033	0	0.0047	
104689	CCT4	Cct4	0.041	0.0035	0	0	
107185	CCT5	Cct5	0.0113	0.0016	0	0	
106211	CDC42	Cdc42	0.09607	0.0022	0	0	
101757	CFL1	Cfl1	0.00954	0.0025	0	0	
88407	CKB	Ckb	0.02772	0.0062	0	0	
2388633	CLTC	Cltc	0.01865	0.0011	0	0	
88460	COL6A2	Col6a2	0.17475	0.0808	0.0008	0.0004	
1354962	COPB2	Copb2	0.09465	0.0068	0.0009	0.0007	
88476	CP	Cp	0.28965	0.0273	0.001	0.0012	
102519	CST3	Cst3	0.07408	0.0173	0		
88561	CTSB	Ctsb	0.09991	0.0272	0.0013	0.0013	
94865	DBI	Dbi	0.3187	0.046	0.0035	0	
1298381	DDT	Ddt	0.14877	0.0333	0	0	
1914410	EEF1G	Eef1g	0.17534	0.0207	0.001	0	
95288	EEF2	Eef2	0.00178	0.001	0	0.0006	
95485	FASN	Fasn	0.1235	0.0517	0.002	0.0022	
2444336	FCGBP	Fcgbp	0.19151	0.0318	0.0049	0.0048	
1097667	GANAB	Ganab	0.21498	0.0177	0	0.002	
95669	GC	Gc	0.37888	0.0399	0.001	0.001	
99845	GDI2	Gdi2	0.06813	0.0087	0	0.0011	
101849	GNB2L1	Gnb2l1	0	0	0	0	
95797	GPI	Gpi1	0.09336	0.0184	0.0015	0.0045	
95851	GSN	Gsn	0.10021	0.0193	0.0006	0.0006	
1321133	HINT1	Hint1	0.09701	0.0117	0	0	
105112	HPX	Hpx	0.67457	0.1034	0.001	0	
96231	HSPA1L	Hspa1l	0.03881	0.0472	0.0022	0.0007	
1342292	HSPA4	Hspa4	0.06868	0.006	0.0005	0.0005	
95835	HSPA5	Hspa5	0.0487	0.0055	0	0	
105384	HSPA8	Hspa8	0	0	0	0	
96240	HSPB1	Hspb1	0.05552	0.0176	0	0.0039	
108030	HYOU1	Hyou1	0.12987	0.0148	0.0015	0.0024	
96413	IDH1	Idh1	0.265	0.0411	0.0011	0.0011	
1352757	IQGAP1	Iqgap1	0.05349	0.0049	0.0003	0	
96705	KRT8	Krt8	0.19706	0.0667	0.0017	0.0071	

mouse&d	HumanGeneName	mouse&gene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*
1914238	LAP3	Lap3	0.38199	0.0922	0	0
96759	LDHA	Ldha	0.09163	0.008	0.0013	0.0013
96763	LDHB	Ldhb	0	0	0	0
96836	LTA4H	Lta4h	0.19132	0.0121	0	0
97051	MDH1	Mdh1	0.12758	0.0107	0	0
97050	MDH2	Mdh2	0.08792	0.0153	0	0.0014
107717	MYH9	Myh9	0.01165	0.0035	0	0.0011
97388	NUCB1	Nucb1	0.12083	0.0256	0	0.0011
1858179	NUCB2	Nucb2	0.49462	0.0611	0.0017	0
97464	P4HB	P4hb	0.08835	0.0178	0	0.0018
2135637	PARK7	Park7	0.1005	0.0078	0	0.0026
95834	PDIA3	Pdia3	0.14971	0.0173	0	0
97549	PFN1	Pfn1	0.29469	0.0249	0	0.0134
97553	PGD	Pgd	0.13151	0.0253	0	0.003
97555	PGK1	Pgk1	0.20731	0.0158	0	0
97565	PGM1	Pgm2	0.10201	0.012	0.0026	0.0009
1355330	PHGDH	Phgdh	0.08515	0.0123	0	0.0009
103080	PIGR	Pigr	0.47638	0.0876	0.0068	0.0024
97750	PPIB	Ppib	0.034	0.0044	0	0.0021
99523	PRDX1	Prdx1	0.1014	0.0078	0	0
109486	PRDX2	Prdx2	0.12405	0.025	0	0
1859815	PRDX4	Prdx4	0.33071	0.0215	0	0.0079
1859821	PRDX5	Prdx5	0.3221	0.0321	0.0046	0
894320	PRDX6	Prdx6	0.08072	0.0089	0	0
97783	PSAP	Psap	0.11398	0.0149	0.0009	0
1347006	PSMA6	Psma6	0.15024	0.0136	0	0
1347070	PSMA7	Psma7	0.06726	0.0096	0.0019	0
97828	PYGB	Pygb	0.11028	0.051	0	0
1915615	RAB14	Rab14	0	0	0	0
97842	RAB1A	Rab1	0.07614	0.0047	0	0
1923558	RAB1B	Rab1b	0.07787	0.0182	0	0.0042
1096342	RHOA	Rhoa	0	0	0	0
97919	RNASE1	Rnase1	0.3914	0.0684	0.0057	0.0028
1927636	RPLP0	Rplp0	0.04414	0.003	0	0
96825	SELENBP1	Selenbp2	0.11919	0.0232	0.0018	0.0027
891968	SERPINA1	Serpina1e	0.4603	0.0723	0.0011	0.0023
103123	SERPINB6	Serpinb6a	0.14886	0.0469	0	0.0103
98351	SOD1	Sod1	0.59912	0.0769	0	0
98266	SORD	Sord	0.28128	0.0529	0.003	0.0051
1274789	TALDO1	Taldo1	0.12716	0.0172	0	0.0027
98535	TCP1	Tcp1	0.03	0.0032	0	0
98821	TF	Trf	0.54147	0.0872	0.0013	0.002
3027002	TGM4	Tgm4	0.38754	0.0541	0.004	0.003
98752	TIMP1	Timp1	0.81715	0.0557	0.0064	0.005
105992	TKT	Tkt	0.03005	0.0069	0.0007	0.0007
98797	TPI1	Tpi1	0.08996	0.0132	0	0
104890	TPT1	Tpt1	0.31717	0.0197	0	0
98865	TTR	Ttr	0.59375	0.0644	0.0067	0.0068
98874	TXN	Txn1	0.34466	0.02	0	0
1349450	VAT1	Vat1	0.16604	0.0311	0.0046	0.0034
98927	VCL	Vcl	0.07167	0.0055	0	0
99919	VCP	Vcp	0.02398	0.0023	0	0
1891917	YWHAB	Ywhab	0	0	0	0
894689	YWHAE	Ywhae	0.09136	0.0037	0	0
108109	YWHAG	Ywhag	0	0	0	0
109484	YWHAZ	Ywhaz	0	0	0	0

Seminal Vesicle – maximum expression

mouse&d	HumanGeneName	mouse&ene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
88127	B2M	B2m	0.51482	0.0596	0	0.0039	
107286	MAN2B1	Man2b1	0.14342	0.0256	0.0018	0.0013	
1858179	NUCB2	Nucb2	0.49462	0.0611	0.0017	0	
98752	TIMP1	Timp1	0.81715	0.0557	0.0064	0.005	

Seminal Vesicle

mouse&d	HumanGeneName	mouse&ene	tree_*ω*	*Ka*	H_*Ka*	C_*Ka*	
87991	ALB	Alb	0.38549	0.052	0.0023	0.0033	
88127	B2M	B2m	0.51482	0.0596	0	0.0039	
102519	CST3	Cst3	0.07408	0.0173	0		
95835	HSPA5	Hspa5	0.0487	0.0055	0	0	
107286	MAN2B1	Man2b1	0.14342	0.0256	0.0018	0.0013	
97050	MDH2	Mdh2	0.08792	0.0153	0	0.0014	
1858179	NUCB2	Nucb2	0.49462	0.0611	0.0017	0	
97464	P4HB	P4hb	0.08835	0.0178	0	0.0018	
97750	PPIB	Ppib	0.034	0.0044	0	0.0021	
97783	PSAP	Psap	0.11398	0.0149	0.0009	0	
891970	SERPINA1	Serpina1e	0.4603	0.0723	0.0011	0.0023	
98821	TF	Trf	0.54147	0.0872	0.0013	0.002	
98752	TIMP1	Timp1	0.81715	0.0557	0.0064	0.005	
99919	VCP	Vcp	0.02398	0.0023	0	0	

Seminal Gene Ontology

uniform_ω	Gene	Level 1: Biological Processes
0.07671	ADAM10	apoptosis
0.51589	ADAM7	apoptosis
0.02918	CAPN1	apoptosis
0.06818	CAPNS1	apoptosis
0.2118	CLU	apoptosis
0.13329	CNTN3	apoptosis
0.33434	CRYZ	apoptosis
0.03312	CUL3	apoptosis
0.04061	DDR1	apoptosis
0.03005	DDR2/TKT	apoptosis
0.18122	DNASE1	apoptosis
0.33377	DNASE2	apoptosis
0.15929	EPHA5	apoptosis
0.54147	F3/TF	apoptosis
0.23325	FKBP4	apoptosis
0.22362	GSR	apoptosis
0.59968	LGALS3	apoptosis
0.17687	LGALS3BP	apoptosis
0.14864	NEO1	apoptosis
0.1105	NRCAM	apoptosis
0.03412	PDCD6IP	apoptosis
0	PPP1CC	apoptosis
0.04184	PPP2CA	apoptosis
0.03747	PPP5C	apoptosis
0.04119	SDK2	apoptosis
0.28128	SORD	apoptosis
0.09418	ST14	apoptosis
0.50285	TMPRSS2	apoptosis
0.3777	TNFSF10	apoptosis
0.22876	TP53I3	apoptosis
0.19238	TRAF3/CAP1	apoptosis
0.34466	TXN	apoptosis
0.1222	UBE2L3	apoptosis
0.11295	UBE2N	apoptosis
0.16604	VAT1	apoptosis
0.07671	ADAM10	cell adhesion
0.51589	ADAM7	cell adhesion
0.08923	ADAMTS1	cell adhesion
0.15136	ADAMTSL1	cell adhesion
0.28839	APOH	cell adhesion
0.19515	BCAN	cell adhesion
0.02656	BGN	cell adhesion
0.4675	C9	cell adhesion
0.08282	CD151	cell adhesion
0.45853	CD44	cell adhesion
0.1187	CD47	cell adhesion
0.08642	CD63	cell adhesion
0.01699	CD81	cell adhesion
0.08598	CD9	cell adhesion
0.3508	CFB	cell adhesion
0.05783	CLSTN1	cell adhesion
0.13329	CNTN3	cell adhesion
0.13809	CNTNAP2	cell adhesion
0.1314	COL12A1	cell adhesion
0.28163	COL18A1	cell adhesion
0.15215	COL6A1	cell adhesion
0.17475	COL6A2	cell adhesion
0.31564	COL9A1	cell adhesion
0.06913	COLEC12	cell adhesion
0.28965	CP	cell adhesion
0.09991	CTSB	cell adhesion
0.26689	CTSF	cell adhesion
0.17724	CTSH	cell adhesion
0.42717	CTSO	cell adhesion
0.23084	CTSZ	cell adhesion
0.21846	DAG1	cell adhesion
0.04061	DDR1	cell adhesion
0.03005	DDR2/TKT	cell adhesion
0.09572	EDIL3	cell adhesion
0.11517	EFEMP1	cell adhesion
0.5994	EGF	cell adhesion
0.15929	EPHA5	cell adhesion
0.35622	F11R	cell adhesion
0.12755	FBLN2	cell adhesion
0.19151	FCGBP	cell adhesion
0.04614	FMOD	cell adhesion
0.1145	FN1	cell adhesion
0.11006	GAS6	cell adhesion
0.04455	GLG1	cell adhesion
0.05502	GPC1	cell adhesion
0.17128	GPC4	cell adhesion
0.40563	GPR115	cell adhesion
0.20081	KAL1	cell adhesion
0.13874	LDLR	cell adhesion
0.59968	LGALS3	cell adhesion
0.17687	LGALS3BP	cell adhesion
0.28021	LRG1	cell adhesion
0.04607	LSAMP	cell adhesion
0.19117	MATN2	cell adhesion
0.03403	MFAP4	cell adhesion
0.37182	MUC5B	cell adhesion
0.33656	MUC6	cell adhesion
0.22725	NELL1	cell adhesion
0.14864	NEO1	cell adhesion
0.1105	NRCAM	cell adhesion
0.1187	NRP1	cell adhesion
0.02107	ODZ2	cell adhesion
0.12028	PLOD2	cell adhesion
0.10437	PLOD3	cell adhesion
0.0833	PTPRD	cell adhesion
0.04714	PTPRF	cell adhesion
0.43859	PTPRJ	cell adhesion
0.05222	PTPRS	cell adhesion
0.33887	RALA	cell adhesion
0.08639	RALB	cell adhesion
0	RAP1B	cell adhesion
0.07028	RTN4RL1	cell adhesion
0.42477	SDC1	cell adhesion
0.04119	SDK2	cell adhesion
0.1026	SEMA3C	cell adhesion
0.09798	SEMA3F	cell adhesion
0.11662	SEMA7A	cell adhesion
0.11038	SEZ6L2	cell adhesion
0.09964	SLIT2	cell adhesion
0.08682	TMEFF2	cell adhesion
0.12797	TPP2	cell adhesion
0.46352	VTN	cell adhesion
0.16405	VWF	cell adhesion
0.33426	A1BG	cell communication
0.07671	ADAM10	cell communication
0.51589	ADAM7	cell communication
0.08923	ADAMTS1	cell communication
0.15136	ADAMTSL1	cell communication
0.07163	ANXA1	cell communication
0.61009	ANXA11	cell communication
0.21532	ANXA3	cell communication
0.20573	ANXA6	cell communication
0.28839	APOH	cell communication

uniform_ω	Gene	Level 1: Biological Processes
0	ARF1	cell communication
0.26962	ARHGDIA	cell communication
0.02656	BGN	cell communication
0.18307	BPNT1	cell communication
0.22609	C3	cell communication
0.4675	C9	cell communication
0.06728	CACNA2D1	cell communication
0.19238	CAP1	cell communication
0.02918	CAPN1	cell communication
0.06818	CAPNS1	cell communication
0.36155	CD109	cell communication
0.08282	CD151	cell communication
0.45853	CD44	cell communication
0.08642	CD63	cell communication
0.01699	CD81	cell communication
0.08598	CD9	cell communication
0.09607	CDC42	cell communication
0.3508	CFB	cell communication
0.2248	CLIC1	cell communication
0.05783	CLSTN1	cell communication
0.01865	CLTC	cell communication
0.2118	CLU	cell communication
0.13329	CNTN3	cell communication
0.13809	CNTNAP2	cell communication
0.1314	COL12A1	cell communication
0.28163	COL18A1	cell communication
0.15215	COL6A1	cell communication
0.17475	COL6A2	cell communication
0.31564	COL9A1	cell communication
0.06913	COLEC12	cell communication
0.28965	CP	cell communication
0.18279	CPAMD8	cell communication
0.33434	CRYZ	cell communication
0.03312	CUL3	cell communication
0.21846	DAG1	cell communication
0.04061	DDR1	cell communication
0.03005	DDR2/TKT	cell communication
0.18122	DNASE1	cell communication
0.33377	DNASE2	cell communication
0.27757	DPP4	cell communication
0.09572	EDIL3	cell communication
0	EEF1A1	cell communication
0.17534	EEF1G	cell communication
0.11517	EFEMP1	cell communication
0.5994	EGF	cell communication
0.15929	EPHA5	cell communication
0.54147	F3/TF	cell communication
0.72136	FAM3B	cell communication
0.12755	FBLN2	cell communication
0.23325	FKBP4	cell communication
0.04614	FMOD	cell communication
0.1145	FN1	cell communication
0.11006	GAS6	cell communication
0.39784	GDF15	cell communication
0.32047	GLA	cell communication
0	GNAI3	cell communication
0.01164	GNB1	cell communication
0	GNB2L1	cell communication
0.13522	GNG12	cell communication
0.40563	GPR115	cell communication
0.19109	GPR56	cell communication
0.39159	GPR64	cell communication
0.09742	GPRC5C	cell communication
0.22362	GSR	cell communication
0.27514	GSTO1	cell communication
0.25068	GSTT1	cell communication
0.33622	GSTZ1	cell communication
0.35872	IL1R1	cell communication
0.06479	IL1RAP	cell communication
0.55601	IL1RL1	cell communication
0.19931	IL6ST	cell communication
0.04703	INHBB	cell communication
0.05349	IQGAP1	cell communication
0.18891	IQGAP2	cell communication
0.06355	LEFTY2	cell communication
0.59968	LGALS3	cell communication
0.17687	LGALS3BP	cell communication
0.21051	LIFR	cell communication
0.28021	LRG1	cell communication
0.13143	MARCKS	cell communication
0.19117	MATN2	cell communication
0.03403	MFAP4	cell communication
0.30424	MINPP1	cell communication
0.07672	MME	cell communication
0.01165	MYH9	cell communication
0.06255	MYO1C	cell communication
0.22725	NELL1	cell communication
0.14864	NEO1	cell communication
0.1105	NRCAM	cell communication
0.1187	NRP1	cell communication
0.02107	ODZ2	cell communication
0.02472	OLFM1	cell communication
0.36665	OLFM4	cell communication
0.03412	PDCD6IP	cell communication
0.28039	PDGFA	cell communication
0.06133	PLXNB2	cell communication
0.25775	PPAP2A	cell communication
0	PPP1CC	cell communication
0.04184	PPP2CA	cell communication
0.03747	PPP5C	cell communication
0.02182	PRKACA	cell communication
0.26782	PRKAR2A	cell communication
0.12775	PTGDS	cell communication
0.0833	PTPRD	cell communication
0.04714	PTPRF	cell communication
0.43859	PTPRJ	cell communication
0.05222	PTPRS	cell communication
0	RAB10	cell communication
0	RAB11B	cell communication
0.02735	RAB3B	cell communication
0.12088	RAC1	cell communication
0.33887	RALA	cell communication
0.08639	RALB	cell communication
0	RAP1B	cell communication
0	RHOA	cell communication
0.07028	RTN4RL1	cell communication
0.09238	S100A11	cell communication
0.42477	SDC1	cell communication
0.04119	SDK2	cell communication
0.1026	SEMA3C	cell communication
0.09798	SEMA3F	cell communication
0.11662	SEMA7A	cell communication
0.11038	SEZ6L2	cell communication
0.01088	SFN	cell communication
0.09929	SLC1A1	cell communication
0.09964	SLIT2	cell communication
0.28128	SORD	cell communication
0.09418	ST14	cell communication
0.06	SYT7	cell communication
0.01709	TGFB1	cell communication
0.01365	TGFB3	cell communication
0.18951	TGFBR3	cell communication
0.08682	TMEFF2	cell communication
0.50285	TMPRSS2	cell communication
0.3777	TNFSF10	cell communication
0.22876	TP53I3	cell communication
0.12797	TPP2	cell communication
0.19238	TRAF3/CAP1	cell communication
0.34466	TXN	cell communication
0.1222	UBE2L3	cell communication
0.11295	UBE2N	cell communication
0.16604	VAT1	cell communication
0.46352	VTN	cell communication
0	YWHAB	cell communication
0.09136	YWHAE	cell communication
0	YWHAG	cell communication
0.33806	YWHAQ	cell communication
0	YWHAZ	cell communication
0	ACTR1A	cell cycle
0.13329	CNTN3	cell cycle
0.03312	CUL3	cell cycle
0.04061	DDR1	cell cycle
0.03005	DDR2/TKT	cell cycle
0.5994	EGF	cell cycle
0.15929	EPHA5	cell cycle
0.23325	FKBP4	cell cycle
0.05349	IQGAP1	cell cycle
0.18891	IQGAP2	cell cycle
0.41834	KLK2	cell cycle
0.39957	KLK3	cell cycle
0.01165	MYH9	cell cycle
0.07453	NCAPG/CAPG	cell cycle

uniform_ω	Gene	Level 1: Biological Processes
0.14864	NEO1	cell cycle
0.1105	NRCAM	cell cycle
0.28039	PDGFA	cell cycle
0	PPP1CC	cell cycle
0.05014	PPP1R7	cell cycle
0.04184	PPP2CA	cell cycle
0.03747	PPP5C	cell cycle
0.21771	PRKACA	cell cycle
0.05075	PSMD2	cell cycle
0.0833	PTPRD	cell cycle
0.04714	PTPRF	cell cycle
0.43859	PTPRJ	cell cycle
0.05222	PTPRS	cell cycle
0	RAB10	cell cycle
0	RAB11B	cell cycle
0.02735	RAB3B	cell cycle
0.09238	S100A11	cell cycle
0.04119	SDK2	cell cycle
0.01088	SFN	cell cycle
0.07015	TUBB1	cell cycle
0.34466	TXN	cell cycle
0.11295	UBE2N	cell cycle
0	YWHAB	cell cycle
0.09136	YWHAE	cell cycle
0	YWHAG	cell cycle
0.33806	YWHAQ	cell cycle
0	YWHAZ	cell cycle
0	ACTR1A	cellular component organization
0.07453	CAPG	cellular component organization
0.08727	CAPZA1	cellular component organization
0.05711	CAPZA2	cellular component organization
0.46787	CAPZB	cellular component organization
0.00954	CFL1	cellular component organization
0.1314	COL12A1	cellular component organization
0.28163	COL18A1	cellular component organization
0.15215	COL6A1	cellular component organization
0.17475	COL6A2	cellular component organization
0.31564	COL9A1	cellular component organization
0.06913	COLEC12	cellular component organization
0.19151	FCGBP	cellular component organization
0.1145	FN1	cellular component organization
0.10021	GSN	cellular component organization
0	HIST2H2BE	cellular component organization
0.11737	KRT1	cellular component organization
0.20231	KRT10	cellular component organization
0.06082	KRT5	cellular component organization
0.19706	KRT8	cellular component organization
0.4345	KRT9	cellular component organization
0.02083	LCP1	cellular component organization
0.19117	MATN2	cellular component organization
0.03403	MFAP4	cellular component organization
0.37182	MUC5B	cellular component organization
0.33656	MUC6	cellular component organization
0.01165	MYH9	cellular component organization
0.06255	MYO1C	cellular component organization
0.02472	OLFM1	cellular component organization
0.36665	OLFM4	cellular component organization
0.28039	PDGFA	cellular component organization
0.43859	PTPRJ	cellular component organization
0.1668	RDX	cellular component organization
0.11153	SPON2	cellular component organization
0.07015	TUBB1	cellular component organization
0.07167	VCL	cellular component organization
0.16405	VWF	cellular component organization
0.33426	A1BG	cellular process
0	ACTR1A	cellular process
0.07671	ADAM10	cellular process
0.51589	ADAM7	cellular process
0.08923	ADAMTS1	cellular process
0.15136	ADAMTSL1	cellular process
0.07163	ANXA1	cellular process
0.61009	ANXA11	cellular process
0.21532	ANXA3	cellular process
0.20573	ANXA6	cellular process
0.28839	APOH	cellular process
0	ARF1	cellular process
0.26962	ARHGDIA	cellular process
0.19515	BCAN	cellular process
0.02656	BGN	cellular process
0.18307	BPNT1	cellular process
0.22609	C3	cellular process
0.4675	C9	cellular process
0.06728	CACNA2D1	cellular process
0.19238	CAP1	cellular process
0.07453	CAPG	cellular process
0.02918	CAPN1	cellular process
0.06818	CAPNS1	cellular process
0.08727	CAPZA1	cellular process
0.05711	CAPZA2	cellular process
0.46787	CAPZB	cellular process
0.36155	CD109	cellular process
0.08282	CD151	cellular process
0.45853	CD44	cellular process
0.1187	CD47	cellular process
0.08642	CD63	cellular process
0.01699	CD81	cellular process
0.08598	CD9	cellular process
0.09607	CDC42	cellular process
0.3508	CFB	cellular process
0.00954	CFL1	cellular process
0.2248	CLIC1	cellular process
0.05783	CLSTN1	cellular process
0.01865	CLTC	cellular process
0.2118	CLU	cellular process
0.13329	CNTN3	cellular process
0.13809	CNTNAP2	cellular process
0.1314	COL12A1	cellular process
0.28163	COL18A1	cellular process
0.15215	COL6A1	cellular process
0.17475	COL6A2	cellular process
0.31564	COL9A1	cellular process
0.06913	COLEC12	cellular process
0.28965	CP	cellular process
0.18279	CPAMD8	cellular process
0.33434	CRYZ	cellular process
0.09991	CTSB	cellular process
0.26689	CTSF	cellular process
0.17724	CTSH	cellular process
0.42717	CTSO	cellular process
0.23084	CTSZ	cellular process
0.03312	CUL3	cellular process
0.21846	DAG1	cellular process
0.04061	DDR1	cellular process
0.03005	DDR2/TKT	cellular process
0.18122	DNASE1	cellular process
0.33377	DNASE2	cellular process
0.27757	DPP4	cellular process
0.09572	EDIL3	cellular process
0	EEF1A1	cellular process
0.17534	EEF1G	cellular process
0.11517	EFEMP1	cellular process
0.5994	EGF	cellular process
0.15929	EPHA5	cellular process
0.35622	F11R	cellular process
0.54147	F3/TF	cellular process
0.72136	FAM3B	cellular process
0.12755	FBLN2	cellular process
0.19151	FCGBP	cellular process
0.23325	FKBP4	cellular process
0.04614	FMOD	cellular process
0.1145	FN1	cellular process
0.11006	GAS6	cellular process
0.39784	GDF15	cellular process
0.32047	GLA	cellular process
0.04455	GLG1	cellular process
0	GNAI3	cellular process
0.01164	GNB1	cellular process
0	GNB2L1	cellular process
0.13522	GNG12	cellular process
0.05502	GPC1	cellular process
0.17128	GPC4	cellular process
0.40563	GPR115	cellular process
0.19109	GPR56	cellular process
0.39159	GPR64	cellular process
0.09742	GPRC5C	cellular process
0.10021	GSN	cellular process
0.22362	GSR	cellular process
0.27514	GSTO1	cellular process
0.25068	GSTT1	cellular process
0.33622	GSTZ1	cellular process
0	HIST2H2BE	cellular process
0.35872	IL1R1	cellular process

uniform_ω	Gene	Level 1: Biological Processes
0.06479	IL1RAP	cellular process
0.55601	IL1RL1	cellular process
0.19931	IL6ST	cellular process
0.04703	INHBB	cellular process
0.05349	IQGAP1	cellular process
0.18891	IQGAP2	cellular process
0.20081	KAL1	cellular process
0.11737	KRT1	cellular process
0.20231	KRT10	cellular process
0.06082	KRT5	cellular process
0.19706	KRT8	cellular process
0.4345	KRT9	cellular process
0.02083	LCP1	cellular process
0.13874	LDLR	cellular process
0.06355	LEFTY2	cellular process
0.59968	LGALS3	cellular process
0.17687	LGALS3BP	cellular process
0.21051	LIFR	cellular process
0.28021	LRG1	cellular process
0.04607	LSAMP	cellular process
0.13143	MARCKS	cellular process
0.19117	MATN2	cellular process
0.03403	MFAP4	cellular process
0.30424	MINPP1	cellular process
0.07672	MME	cellular process
0.37182	MUC5B	cellular process
0.33656	MUC6	cellular process
0.01165	MYH9	cellular process
0.06255	MYO1C	cellular process
0.22725	NELL1	cellular process
0.14864	NEO1	cellular process
0.1105	NRCAM	cellular process
0.1187	NRP1	cellular process
0.02107	ODZ2	cellular process
0.02472	OLFM1	cellular process
0.36665	OLFM4	cellular process
0.03412	PDCD6IP	cellular process
0.28039	PDGFA	cellular process
0.12028	PLOD2	cellular process
0.10437	PLOD3	cellular process
0.06133	PLXNB2	cellular process
0.25775	PPAP2A	cellular process
0	PPP1CC	cellular process
0.05014	PPP1R7	cellular process
0.04184	PPP2CA	cellular process
0.03747	PPP5C	cellular process
0.02182	PRKACA	cellular process
0.26782	PRKAR2A	cellular process
0.12775	PTGDS	cellular process
0.0833	PTPRD	cellular process
0.04714	PTPRF	cellular process
0.43859	PTPRJ	cellular process
0.05222	PTPRS	cellular process
0	RAB10	cellular process
0	RAB11B	cellular process
0.02735	RAB3B	cellular process
0.12088	RAC1	cellular process
0.33887	RALA	cellular process
0.08639	RALB	cellular process
0	RAP1B	cellular process
0.1668	RDX	cellular process
0	RHOA	cellular process
0.07028	RTN4RL1	cellular process
0.09238	S100A11	cellular process
0.42477	SDC1	cellular process
0.04119	SDK2	cellular process
0.1026	SEMA3C	cellular process
0.09798	SEMA3F	cellular process
0.11662	SEMA7A	cellular process
0.11038	SEZ6L2	cellular process
0.01088	SFN	cellular process
0.09929	SLC1A1	cellular process
0.09964	SLIT2	cellular process
0.28128	SORD	cellular process
0.11153	SPON2	cellular process
0.09418	ST14	cellular process
0.06	SYT7	cellular process
0.01709	TGFB1	cellular process
0.01365	TGFB3	cellular process
0.18951	TGFBR3	cellular process
0.08682	TMEFF2	cellular process
0.50285	TMPRSS2	cellular process
0.3777	TNFSF10	cellular process
0.22876	TP53I3	cellular process
0.12797	TPP2	cellular process
0.19238	TRAF3/CAP1	cellular process
0.07015	TUBB1	cellular process
0.34466	TXN	cellular process
0.1222	UBE2L3	cellular process
0.11295	UBE2N	cellular process
0.16604	VAT1	cellular process
0.07167	VCL	cellular process
0.46352	VTN	cellular process
0.16405	VWF	cellular process
0	YWHAB	cellular process
0.09136	YWHAE	cellular process
0	YWHAG	cellular process
0.33806	YWHAQ	cellular process
0	YWHAZ	cellular process
0.11253	ACP5	developmental process
0	ACTR1A	developmental process
0.07671	ADAM10	developmental process
0.51589	ADAM7	developmental process
0.08923	ADAMTS1	developmental process
0.15136	ADAMTSL1	developmental process
1.26483	ANG	developmental process
0.19262	BASP1	developmental process
0.07453	CAPG	developmental process
0.08727	CAPZA1	developmental process
0.05711	CAPZA2	developmental process
0.46787	CAPZB	developmental process
0.00954	CFL1	developmental process
0.1314	COL12A1	developmental process
0.28163	COL18A1	developmental process
0.15215	COL6A1	developmental process
0.17475	COL6A2	developmental process
0.31564	COL9A1	developmental process
0.06913	COLEC12	developmental process
0.07909	DDAH1	developmental process
0.04061	DDR1	developmental process
0.03005	DDR2/TKT	developmental process
0.09572	EDIL3	developmental process
0.11517	EFEMP1	developmental process
0.04856	EFHD2	developmental process
0.15929	EPHA5	developmental process
0.12755	FBLN2	developmental process
0.19151	FCGBP	developmental process
0.04614	FMOD	developmental process
0.1145	FN1	developmental process
0.11006	GAS6	developmental process
0.39784	GDF15	developmental process
0.40563	GPR115	developmental process
0.19109	GPR56	developmental process
0.39159	GPR64	developmental process
0.10021	GSN	developmental process
2.36478	IGKC	developmental process
0.19931	IL6ST	developmental process
0.04703	INHBB	developmental process
0.41834	KLK2	developmental process
0.39957	KLK3	developmental process
0.11737	KRT1	developmental process
0.20231	KRT10	developmental process
0.06082	KRT5	developmental process
0.19706	KRT8	developmental process
0.4345	KRT9	developmental process
0.02083	LCP1	developmental process
0.06355	LEFTY2	developmental process
0.17687	LGALS3BP	developmental process
0.21051	LIFR	developmental process
0.04607	LSAMP	developmental process
0.19117	MATN2	developmental process
0.03403	MFAP4	developmental process
0.37182	MUC5B	developmental process
0.33656	MUC6	developmental process
0.28683	MYCBP2/PAM	developmental process
0.01165	MYH9	developmental process
0.06255	MYO1C	developmental process
0.22725	NELL1	developmental process
0.14864	NEO1	developmental process
0.1105	NRCAM	developmental process
0.1187	NRP1	developmental process
0.02107	ODZ2	developmental process

uniform_ω	Gene	Level 1: Biological Processes
0.02472	OLFM1	developmental process
0.36665	OLFM4	developmental process
0.28039	PDGFA	developmental process
0.06133	PLXNB2	developmental process
0.0833	PTPRD	developmental process
0.04714	PTPRF	developmental process
0.43859	PTPRJ	developmental process
0.05222	PTPRS	developmental process
0.33887	RALA	developmental process
0.08639	RALB	developmental process
0.1668	RDX	developmental process
0.09263	RELN	developmental process
0.3914	RNASE1	developmental process
0.07028	RTN4RL1	developmental process
0.00916	RUVBL2	developmental process
0.42477	SDC1	developmental process
0.04119	SDK2	developmental process
0.1026	SEMA3C	developmental process
0.09798	SEMA3F	developmental process
0.11662	SEMA7A	developmental process
0.09964	SLIT2	developmental process
0.23664	SMPD1	developmental process
0.34902	SMPDL3A	developmental process
0.43209	SMPDL3B	developmental process
0.11153	SPON2	developmental process
0.01709	TGFB1	developmental process
0.01365	TGFB3	developmental process
0.08682	TMEFF2	developmental process
0.3777	TNFSF10	developmental process
0.19238	TRAF3/CAP1	developmental process
0.07015	TUBB1	developmental process
0.07167	VCL	developmental process
0.16405	VWF	developmental process
0.06161	ACLY	generation of precursor metabolites and energy
0.25119	CAT	generation of precursor metabolites and energy
0.34622	CYB561	generation of precursor metabolites and energy
0.2849	CYB5R2	generation of precursor metabolites and energy
0.22362	GSR	generation of precursor metabolites and energy
0.265	IDH1	generation of precursor metabolites and energy
0.09163	LDHA	generation of precursor metabolites and energy
0.18715	LDHC	generation of precursor metabolites and energy
0.08792	MDH2	generation of precursor metabolites and energy
0.34466	TXN	generation of precursor metabolites and energy
0.04163	UGDH	generation of precursor metabolites and energy
0.23294	AGR2	homeostatic process
0.12083	NUCB1	homeostatic process
0.49462	NUCB2	homeostatic process
0.0833	PTPRD	homeostatic process
0.04714	PTPRF	homeostatic process
0.05222	PTPRS	homeostatic process
0.33426	A1BG	immune system process
0.17234	ABP1	immune system process
0.16497	AMBP	immune system process
0.15789	ANTXR2	immune system process
0.28839	APOH	immune system process
0.22162	Arsa1	immune system process
0.42468	AZGP1	immune system process
0.51482	B2M	immune system process
0.02656	BGN	immune system process
0.2419	BPIL1	immune system process
0.28272	C1RL	immune system process
0.22609	C3	immune system process
0.4675	C9	immune system process
1.17322	CAMP	immune system process
0.25119	CAT	immune system process
0.36155	CD109	immune system process
0.43576	CD14	immune system process
0.08282	CD151	immune system process
0.45853	CD44	immune system process
2.49128	CD59	immune system process
0.08642	CD63	immune system process
0.01699	CD81	immune system process
0.08598	CD9	immune system process
0.3508	CFB	immune system process
0.2248	CLIC1	immune system process
0.13329	CNTN3	immune system process
0.13809	CNTNAP2	immune system process
0.1314	COL12A1	immune system process
0.28163	COL18A1	immune system process
0.15215	COL6A1	immune system process
0.17475	COL6A2	immune system process
0.31564	COL9A1	immune system process
0.06913	COLEC12	immune system process
0.12853	COMP	immune system process
0.28965	CP	immune system process
0.18279	CPAMD8	immune system process
0.60043	CRISP1	immune system process
0.09991	CTSB	immune system process
0.26689	CTSF	immune system process
0.17724	CTSH	immune system process
0.42717	CTSO	immune system process
0.23084	CTSZ	immune system process
0.04061	DDR1	immune system process
0.03005	DDR2/TKT	immune system process
0.41566	DNAJB9	immune system process
0.05636	DNAJC3	immune system process
0.27757	DPP4	immune system process
0.09572	EDIL3	immune system process
0.17534	EEF1G	immune system process
0.11517	EFEMP1	immune system process
0.15929	EPHA5	immune system process
0.35622	F11R	immune system process
0.54147	F3/TF	immune system process
0.12755	FBLN2	immune system process
0.19151	FCGBP	immune system process
0.23325	FKBP4	immune system process
0.04614	FMOD	immune system process
0.1145	FN1	immune system process
0.16557	FUT3	immune system process
0.37888	GGCX/GC	immune system process
0.4432	GM2A	immune system process
0.40563	GPR115	immune system process
0.17703	GPX3	immune system process
0.22362	GSR	immune system process
0.10633	GSTM3	immune system process
0.27514	GSTO1	immune system process
0.11791	GSTP1	immune system process
0.25068	GSTT1	immune system process
0.33622	GSTZ1	immune system process
0.03881	HSPA1L	immune system process
0.06868	HSPA4	immune system process
0.0487	HSPA5	immune system process
0	HSPA8	immune system process
0.05552	HSPB1	immune system process
0.12987	HYOU1	immune system process
0.28039	IGHG2	immune system process
0.19341	IGHG4	immune system process
2.36478	IGKC	immune system process
0.35872	IL1R1	immune system process
0.06479	IL1RAP	immune system process
0.55601	IL1RL1	immune system process
0.19931	IL6ST	immune system process
0.41834	KLK2	immune system process
0.39957	KLK3	immune system process
0.59968	LGALS3	immune system process
0.17687	LGALS3BP	immune system process
0.21051	LIFR	immune system process
0.28021	LRG1	immune system process
0.19132	LTA4H	immune system process
0.77421	LYZ	immune system process
0.19117	MATN2	immune system process
0.03403	MFAP4	immune system process
0.13639	MPST	immune system process
0.37182	MUC5B	immune system process
0.33656	MUC6	immune system process
0	NAPA	immune system process
0.22725	NELL1	immune system process
0.14864	NEO1	immune system process
0.1105	NRCAM	immune system process
0.1187	NRP1	immune system process
0.34271	ORM1	immune system process
0.39559	ORM2	immune system process
0.1005	PARK7	immune system process
0.15509	PGC	immune system process
0.37912	PGCP	immune system process
0.10346	PI15	immune system process
0.47638	PIGR	immune system process
0.36576	PLA2G7	immune system process
0.04806	PPIA	immune system process
0.034	PPIB	immune system process
0.22018	PPIC	immune system process
0	PPP1CC	immune system process

uniform_ω	Gene	Level 1: Biological Processes
0.04184	PPP2CA	immune system process
0.03747	PPP5C	immune system process
0.1014	PRDX1	immune system process
0.12405	PRDX2	immune system process
0.33071	PRDX4	immune system process
0.3221	PRDX5	immune system process
0.08072	PRDX6	immune system process
0.0833	PTPRD	immune system process
0.04714	PTPRF	immune system process
0.43859	PTPRJ	immune system process
0.05222	PTPRS	immune system process
0.07028	RTN4RL1	immune system process
0.09238	S100A11	immune system process
0.42477	SDC1	immune system process
0.04119	SDK2	immune system process
0.11919	SELENBP1	immune system process
0.1026	SEMA3C	immune system process
0.09798	SEMA3F	immune system process
0.11662	SEMA7A	immune system process
0.71077	SEPP1	immune system process
0.11038	SEZ6L2	immune system process
0.09964	SLIT2	immune system process
0.65389	SPACA3	immune system process
0.27985	SPINT1	immune system process
1.11091	SPINT3	immune system process
0.09418	ST14	immune system process
0.55887	TFPI2	immune system process
0.04402	THBS1	immune system process
0.06881	THBS2	immune system process
0.13337	THBS4	immune system process
0.08682	TMEFF2	immune system process
0.50285	TMPRSS2	immune system process
0.3777	TNFSF10	immune system process
0.31717	TPT1	immune system process
0.19238	TRAF3/CAP1	immune system process
0	TSN	immune system process
0.34466	TXN	immune system process
0.16405	VWF	immune system process
0.63099	WFDC8	immune system process
0.09809	A4GALT	metabolic process
0.17234	ABP1	metabolic process
0.50645	ACAT2	metabolic process
0.10981	ACE	metabolic process
0.66947	ACE2	metabolic process
0.06161	ACLY	metabolic process
0.11253	ACP5	metabolic process
0.73724	ACPP	metabolic process
0.40141	ACR	metabolic process
0.3842	ACYP1	metabolic process
0.07671	ADAM10	metabolic process
0.51589	ADAM7	metabolic process
0.08923	ADAMTS1	metabolic process
0.15136	ADAMTSL1	metabolic process
0.47452	AGA	metabolic process
0.23294	AGR2	metabolic process
0.23471	AGT	metabolic process
0.23471	AGXT/AGT	metabolic process
0.11113	AKR1A1	metabolic process
0.11948	AKR1B1	metabolic process
0.1908	AKR7A2	metabolic process
0.24398	ALAD	metabolic process
0.09454	ALDH1A1	metabolic process
0.16655	ALDH7A1	metabolic process
0.18802	ALDH9A1	metabolic process
0.02534	ALDOA	metabolic process
0.09505	ALDOC	metabolic process
0.16497	AMBP	metabolic process
1.26483	ANG	metabolic process
0.21071	ANPEP	metabolic process
0.07163	ANXA1	metabolic process
0.61009	ANXA11	metabolic process
0.21532	ANXA3	metabolic process
0.20573	ANXA6	metabolic process
0.08984	APEH	metabolic process
0.50302	APOA2	metabolic process
0.50294	APOB	metabolic process
1.85478	APOD	metabolic process
0.21988	APOE	metabolic process
0.28839	APOH	metabolic process
0.28671	ASRGL1	metabolic process
0.2536	B4GALT1	metabolic process
0.33034	B4GALT4	metabolic process
0.2419	BPIL1	metabolic process
0.18307	BPNT1	metabolic process
0.28272	C1RL	metabolic process
0.22609	C3	metabolic process
0.4675	C9	metabolic process
0.27904	CA2	metabolic process
0.61962	CA4	metabolic process
0.24573	CA6	metabolic process
0.16147	CACYBP	metabolic process
0.02978	CALR	metabolic process
0.02918	CAPN1	metabolic process
0.06818	CAPNS1	metabolic process
0.25119	CAT	metabolic process
0.03	CCT1/TCP1	metabolic process
0.00897	CCT2	metabolic process
0.24102	CCT3	metabolic process
0.041	CCT4	metabolic process
0.0113	CCT5	metabolic process
0.05102	CCT7	metabolic process
0.07093	CCT8	metabolic process
0.36155	CD109	metabolic process
0.84752	CD38	metabolic process
0.3508	CFB	metabolic process
0.00954	CFL1	metabolic process
0.02772	CKB	metabolic process
0.2248	CLIC1	metabolic process
0.10332	CNDP2	metabolic process
0.13329	CNTN3	metabolic process
0.13809	CNTNAP2	metabolic process
0.1314	COL12A1	metabolic process
0.28163	COL18A1	metabolic process
0.15215	COL6A1	metabolic process
0.17475	COL6A2	metabolic process
0.31564	COL9A1	metabolic process
0.28965	CP	metabolic process
0.18279	CPAMD8	metabolic process
0.28376	CPD	metabolic process
0.1066	CPE	metabolic process
0.23619	CPM	metabolic process
0.44663	CPO	metabolic process
0.44663	CPOX/CPO	metabolic process
0.47714	CPVL	metabolic process
0.0753	CPZ	metabolic process
0.25119	CRAT/CAT	metabolic process
0.33434	CRYZ	metabolic process
0.4454	CST1	metabolic process
0.07408	CST3	metabolic process
0.14608	CST6	metabolic process
0.33236	CTBS	metabolic process
0.09991	CTSB	metabolic process
0.07036	CTSD	metabolic process
0.26689	CTSF	metabolic process
0.17724	CTSH	metabolic process
0.42717	CTSO	metabolic process
0.23084	CTSZ	metabolic process
0.03312	CUL3	metabolic process
0.2849	CYB5R2	metabolic process
0.3187	DBI	metabolic process
0.23412	DCXR	metabolic process
0.04061	DDR1	metabolic process
0.03005	DDR2/TKT	metabolic process
0.41566	DNAJB9	metabolic process
0.05636	DNAJC3	metabolic process
0.18122	DNASE1	metabolic process
0.33377	DNASE2	metabolic process
0.38552	DPEP3	metabolic process
0.27757	DPP4	metabolic process
0.11549	DPP7	metabolic process
0.09572	EDIL3	metabolic process
0	EEF1A1	metabolic process
0.17534	EEF1G	metabolic process
0.11517	EFEMP1	metabolic process
0.5994	EGF	metabolic process
0.01082	ENO1	metabolic process
0.15929	EPHA5	metabolic process
0.22022	EXTL2	metabolic process
0.1235	FASN	metabolic process
0.12755	FBLN2	metabolic process

uniform_ω	Gene	Level 1: Biological Processes	uniform_ω	Gene	Level 1: Biological Processes
0.07692	FBP1	metabolic process	0.05326	MMP2	metabolic process
0.24122	FDPS	metabolic process	0.295	MMP7	metabolic process
0.10285	FH	metabolic process	0.17907	MPI	metabolic process
0.23325	FKBP4	metabolic process	0.13639	MPST	metabolic process
0.3166	FOLH1	metabolic process	0.28683	MYCBP2/PAM	metabolic process
0.25481	FUCA1	metabolic process	0.08384	NAGLU	metabolic process
0.22975	FUCA2	metabolic process	0	NAPA	metabolic process
0.16557	FUT3	metabolic process	0.32047	NAT8/GLA	metabolic process
0.12394	GAA	metabolic process	0.22725	NELL1	metabolic process
0.23822	GALC	metabolic process	0.14864	NEO1	metabolic process
0.12852	GALNS	metabolic process	0.14015	NEU1	metabolic process
0.11878	GALNT6	metabolic process	0.02462	NME3	metabolic process
0.14096	GALNT7	metabolic process	0.37191	NP	metabolic process
0.21498	GANAB	metabolic process	0.07267	NPC2	metabolic process
0.0398	GAPDH	metabolic process	0.11108	NPEPPS	metabolic process
0.21675	GAPDHS	metabolic process	0.1105	NRCAM	metabolic process
0.57864	GBA	metabolic process	0.1187	NRP1	metabolic process
0.37888	GGCX/GC	metabolic process	0.02107	ODZ2	metabolic process
0.11826	GGT1	metabolic process	0.02472	OLFM1	metabolic process
0.32047	GLA	metabolic process	0.36665	OLFM4	metabolic process
0.44713	GLB1	metabolic process	0.08835	P4HB	metabolic process
0.47739	GLB1L	metabolic process	0.27061	PAICS	metabolic process
0.14205	GLO1	metabolic process	0.28683	PAM	metabolic process
0.25119	GLYAT/CAT	metabolic process	0.1005	PARK7	metabolic process
0.4432	GM2A	metabolic process	0.12522	PCMT1	metabolic process
0.09519	GMPPA	metabolic process	0.14971	PDIA3	metabolic process
0.04066	GNPDA1	metabolic process	0.20845	PFAS	metabolic process
0.12664	GNPTG	metabolic process	0.06371	PFKP	metabolic process
0.13572	GNS	metabolic process	0.02754	PGAM2	metabolic process
0.10364	GOT1	metabolic process	0.15509	PGC	metabolic process
0.09575	GPD1L	metabolic process	0.37912	PGCP	metabolic process
0.09336	GPI	metabolic process	0.13151	PGD	metabolic process
0.17703	GPX3	metabolic process	0.20731	PGK1	metabolic process
0.22933	GRHPR	metabolic process	0.20829	PGK2	metabolic process
0.22362	GSR	metabolic process	0.09575	PGLS	metabolic process
0.27514	GSTO1	metabolic process	0.10201	PGM1	metabolic process
0.25068	GSTT1	metabolic process	0.3495	PGM2	metabolic process
0.33622	GSTZ1	metabolic process	0.08515	PHGDH	metabolic process
0.27561	GUSB	metabolic process	0.08676	PITPNA	metabolic process
0.25007	HDHD2	metabolic process	0.16829	PKM2	metabolic process
0.17335	HEBP2	metabolic process	0.40009	PLA1A	metabolic process
0.20408	HEXA	metabolic process	0.36576	PLA2G7	metabolic process
0.4545	HEXB	metabolic process	0.12028	PLOD2	metabolic process
0	HIST2H2BE	metabolic process	0.10437	PLOD3	metabolic process
0.29012	HPRT1	metabolic process	0.06133	PLXNB2	metabolic process
0.22527	HRSP12	metabolic process	0.25775	PPAP2A	metabolic process
0.03881	HSPA1L	metabolic process	0.04806	PPIA	metabolic process
0.06868	HSPA4	metabolic process	0.034	PPIB	metabolic process
0.0487	HSPA5	metabolic process	0.22018	PPIC	metabolic process
0	HSPA8	metabolic process	0	PPP1CC	metabolic process
0.05552	HSPB1	metabolic process	0.04184	PPP2CA	metabolic process
0.12987	HYOU1	metabolic process	0.34304	PPP2R4	metabolic process
0.0866	IDE	metabolic process	0.03747	PPP5C	metabolic process
0.265	IDH1	metabolic process	0.12499	PPT1	metabolic process
0.28544	IDI1	metabolic process	0.4072	PRCP	metabolic process
0.28007	IDUA	metabolic process	0.1014	PRDX1	metabolic process
0.21116	ITIH5	metabolic process	0.12405	PRDX2	metabolic process
0.41834	KLK2	metabolic process	0.33071	PRDX4	metabolic process
0.39957	KLK3	metabolic process	0.3221	PRDX5	metabolic process
0.15986	LAMP1	metabolic process	0.08072	PRDX6	metabolic process
0.46213	LAMP2	metabolic process	0.02182	PRKACA	metabolic process
0.38199	LAP3	metabolic process	0.26782	PRKAR2A	metabolic process
0.09163	LDHA	metabolic process	0.11368	PRKCSH	metabolic process
0.18715	LDHC	metabolic process	0.25859	PRSS22	metabolic process
0.17687	LGALS3BP	metabolic process	0.11398	PSAP	metabolic process
0.17889	LGMN	metabolic process	0.14332	PSAT1	metabolic process
0.52468	LIPA	metabolic process	0.05462	PSMA1	metabolic process
0.21196	LIPG	metabolic process	0.19882	PSMA2	metabolic process
0.66784	LIPI	metabolic process	0.22828	PSMA3	metabolic process
0.34041	LNPEP	metabolic process	0.02917	PSMA4	metabolic process
0.08979	LPL	metabolic process	0	PSMA5	metabolic process
0.19132	LTA4H	metabolic process	0.15024	PSMA6	metabolic process
0.77421	LYZ	metabolic process	0.06726	PSMA7	metabolic process
0.21517	MAN2A1	metabolic process	0.12317	PSMB1	metabolic process
0.14342	MAN2B1	metabolic process	0.16208	PSMB2	metabolic process
0.25926	MAN2B2	metabolic process	0.08328	PSMB4	metabolic process
0.2677	MANBA	metabolic process	0.06972	PSMB5	metabolic process
0.08792	MDH2	metabolic process	0.08442	PSMB6	metabolic process
0.21447	MGAM	metabolic process	0.07857	PSMB7	metabolic process
0.07672	MME	metabolic process	0.40269	PSMB8	metabolic process
0.08387	MMP14	metabolic process	0	PSMD14	metabolic process

uniform_ω	Gene	Level 1: Biological Processes
0.05075	PSMD2	metabolic process
0.12775	PTGDS	metabolic process
0.0833	PTPRD	metabolic process
0.04714	PTPRF	metabolic process
0.43859	PTPRJ	metabolic process
0.05222	PTPRS	metabolic process
0.06875	PURA	metabolic process
0.11028	PYGB	metabolic process
0.24935	QPCT	metabolic process
0.13207	RAD23B	metabolic process
0.01088	REXO2/SFN	metabolic process
0.3914	RNASE1	metabolic process
0.23948	RNASET2	metabolic process
0.04414	RPLP0	metabolic process
0.00916	RUVBL2	metabolic process
0.09238	S100A11	metabolic process
0.28463	SCPEP1	metabolic process
0.04119	SDK2	metabolic process
0.71077	SEPP1	metabolic process
0.4603	SERPINA1	metabolic process
0.69942	SERPINA3	metabolic process
0.31022	SERPINA4	metabolic process
0.21902	SERPINA5	metabolic process
0.35446	SERPINA6	metabolic process
0.15915	SERPINB5	metabolic process
0.14886	SERPINB6	metabolic process
0.37296	SERPINC1	metabolic process
0.13839	SERPINF1	metabolic process
0.35049	SERPING1	metabolic process
0.24428	SERPINI1	metabolic process
0.11038	SEZ6L2	metabolic process
0.27066	SI	metabolic process
0.22735	SIL1	metabolic process
0.09929	SLC1A1	metabolic process
0.09964	SLIT2	metabolic process
0.55658	SLPI	metabolic process
0.23664	SMPD1	metabolic process
0.34902	SMPDL3A	metabolic process
0.43209	SMPDL3B	metabolic process
0.23779	SMS	metabolic process
0.50645	SOAT2/ACAT2	metabolic process
0.28128	SORD	metabolic process
0.10077	SORL1	metabolic process
0.14231	SORT1	metabolic process
0.65389	SPACA3	metabolic process
1.33875	SPINK2	metabolic process
0.27985	SPINT1	metabolic process
1.11091	SPINT3	metabolic process
0.09418	ST14	metabolic process
0.12716	TALDO1	metabolic process
0.55887	TFPI2	metabolic process
0.21664	TFRC	metabolic process
0.38754	TGM4	metabolic process
0.81715	TIMP1	metabolic process
0.03019	TIMP2	metabolic process
0.02181	TIMP3	metabolic process
0.03005	TKT	metabolic process
0.50285	TMPRSS2	metabolic process
0.08296	TOR1B	metabolic process
0.22876	TP53I3	metabolic process
0.08996	TPI1	metabolic process
0.12797	TPP2	metabolic process
0	TSN	metabolic process
0.1166	TSTA3	metabolic process
0.34466	TXN	metabolic process
0.1222	UBE2L3	metabolic process
0.11295	UBE2N	metabolic process
0.1394	UGCGL1	metabolic process
0.04163	UGDH	metabolic process
0.09211	USP14	metabolic process
0.16604	VAT1	metabolic process
0.02398	VCP	metabolic process
0.20458	WFDC2	metabolic process
0.63099	WFDC8	metabolic process
0.02849	XPNPEP1	metabolic process
0.40141	ACR	reproduction
0.07671	ADAM10	reproduction
0.51589	ADAM7	reproduction
0.08923	ADAMTS1	reproduction
0.15136	ADAMTSL1	reproduction
0.28272	C1RL	reproduction
0.08282	CD151	reproduction
0.08642	CD63	reproduction
0.01699	CD81	reproduction
0.08598	CD9	reproduction
0.60043	CRISP1	reproduction
0.04061	DDR1	reproduction
0.03005	DDR2/TKT	reproduction
0.5994	EGF	reproduction
0.14843	ELSPBP1	reproduction
0.15929	EPHA5	reproduction
0.89891	FAM12A	reproduction
0.56441	FAM12B	reproduction
0.19151	FCGBP	reproduction
0.39784	GDF15	reproduction
0.41834	KLK2	reproduction
0.39957	KLK3	reproduction
0.13874	LDLR	reproduction
0.37182	MUC5B	reproduction
0.33656	MUC6	reproduction
0.10346	PI15	reproduction
0.90477	SEMG1	reproduction
1.07914	SEMG2	reproduction
0.09418	ST14	reproduction
0.50285	TMPRSS2	reproduction
0.09211	USP14	reproduction
0.16405	VWF	reproduction
0.34036	ZPBP	reproduction
0.33426	A1BG	response to stimulus
0.16497	AMBP	response to stimulus
0.66684	APCS	response to stimulus
0.28839	APOH	response to stimulus
0.22162	Arsa1	response to stimulus
0.42468	AZGP1	response to stimulus
0.51482	B2M	response to stimulus
0.2419	BPIL1	response to stimulus
0.28272	C1RL	response to stimulus
0.22609	C3	response to stimulus
0.4675	C9	response to stimulus
1.17322	CAMP	response to stimulus
0.36155	CD109	response to stimulus
0.08282	CD151	response to stimulus
0.1187	CD47	response to stimulus
0.08642	CD63	response to stimulus
0.01699	CD81	response to stimulus
0.08598	CD9	response to stimulus
0.3508	CFB	response to stimulus
0.2248	CLIC1	response to stimulus
0.1314	COL12A1	response to stimulus
0.28163	COL18A1	response to stimulus
0.15215	COL6A1	response to stimulus
0.17475	COL6A2	response to stimulus
0.31564	COL9A1	response to stimulus
0.06913	COLEC12	response to stimulus
0.12853	COMP	response to stimulus
0.18279	CPAMD8	response to stimulus
0.09991	CTSB	response to stimulus
0.26689	CTSF	response to stimulus
0.17724	CTSH	response to stimulus
0.42717	CTSO	response to stimulus
0.23084	CTSZ	response to stimulus
0.41566	DNAJB9	response to stimulus
0.05636	DNAJC3	response to stimulus
0.27757	DPP4	response to stimulus
0.17534	EEF1G	response to stimulus
0.54147	F3/TF	response to stimulus
0.19151	FCGBP	response to stimulus
0.23325	FKBP4	response to stimulus
0.37888	GGCX/GC	response to stimulus
0.17703	GPX3	response to stimulus
0.10633	GSTM3	response to stimulus
0.27514	GSTO1	response to stimulus
0.11791	GSTP1	response to stimulus
0.25068	GSTT1	response to stimulus
0.33622	GSTZ1	response to stimulus
0.03881	HSPA1L	response to stimulus
0.06868	HSPA4	response to stimulus
0.0487	HSPA5	response to stimulus
0	HSPA8	response to stimulus
0.05552	HSPB1	response to stimulus
0.12987	HYOU1	response to stimulus
0.28039	IGHG2	response to stimulus

uniform_ω	Gene	Level 1: Biological Processes
0.19341	IGHG4	response to stimulus
1.05716	IGJ	response to stimulus
2.36478	IGKC	response to stimulus
0.19931	IL6ST	response to stimulus
0.41834	KLK2	response to stimulus
0.39957	KLK3	response to stimulus
0.17687	LGALS3BP	response to stimulus
0.21051	LIFR	response to stimulus
0.77421	LYZ	response to stimulus
0.19117	MATN2	response to stimulus
0.13639	MPST	response to stimulus
0.37182	MUC5B	response to stimulus
0.33656	MUC6	response to stimulus
0	NAPA	response to stimulus
0.1005	PARK7	response to stimulus
0.15509	PGC	response to stimulus
0.37912	PGCP	response to stimulus
0.47638	PIGR	response to stimulus
0	PPP1CC	response to stimulus
0.04184	PPP2CA	response to stimulus
0.03747	PPP5C	response to stimulus
0.09238	S100A11	response to stimulus
0.11038	SEZ6L2	response to stimulus
0.65389	SPACA3	response to stimulus
0.27985	SPINT1	response to stimulus
1.11091	SPINT3	response to stimulus
0.09418	ST14	response to stimulus
0.55887	TFPI2	response to stimulus
0.04402	THBS1	response to stimulus
0.06881	THBS2	response to stimulus
0.13337	THBS4	response to stimulus
0.50285	TMPRSS2	response to stimulus
0.3777	TNFSF10	response to stimulus
0.34466	TXN	response to stimulus
0.16405	VWF	response to stimulus
0.63099	WFDC8	response to stimulus
0.07671	ADAM10	system process
0.51589	ADAM7	system process
0.19262	BASP1	system process
0.28272	C1RL	system process
0.06728	CACNA2D1	system process
0.08282	CD151	system process
0.08642	CD63	system process
0.01699	CD81	system process
0.08598	CD9	system process
0.02772	CKB	system process
0.01865	CLTC	system process
0.13329	CNTN3	system process
0.13809	CNTNAP2	system process
0.28965	CP	system process
0.27757	DPP4	system process
0.09572	EDIL3	system process
0.11517	EFEMP1	system process
0.12755	FBLN2	system process
0.19151	FCGBP	system process
0.23325	FKBP4	system process
0.04614	FMOD	system process
0.1145	FN1	system process
0.01164	GNB1	system process
0.40563	GPR115	system process
0.19109	GPR56	system process
0.39159	GPR64	system process
0.05552	HSPB1	system process
0.20081	KAL1	system process
0.17687	LGALS3BP	system process
0.28021	LRG1	system process
0.19117	MATN2	system process
0.03403	MFAP4	system process
0.37182	MUC5B	system process
0.33656	MUC6	system process
0.01165	MYH9	system process
0.06255	MYO1C	system process
0.14864	NEO1	system process
0.1105	NRCAM	system process
0.1187	NRP1	system process
0.08676	PITPNA	system process
0.21771	PRKACA	system process
0.12775	PTGDS	system process
0	RAB10	system process
0	RAB11B	system process
0.02735	RAB3B	system process
0.33887	RALA	system process
0.08639	RALB	system process
0.04119	SDK2	system process
0.16604	SLC18A1/VAT1	system process
0.09929	SLC1A1	system process
0.09964	SLIT2	system process
0.09418	ST14	system process
0.06	SYT7	system process
0.08682	TMEFF2	system process
0.50285	TMPRSS2	system process
0.08296	TOR1B	system process
0.11253	ACP5	transport
0	ACTR1A	transport
0.07163	ANXA1	transport
0.61009	ANXA11	transport
0.21532	ANXA3	transport
0.20573	ANXA6	transport
0.50302	APOA2	transport
0.50294	APOB	transport
1.85478	APOD	transport
0.21988	APOE	transport
0	ARF1	transport
0.22162	Arsa1	transport
0.19262	BASP1	transport
0.2419	BPIL1	transport
0.06728	CACNA2D1	transport
0.09607	CDC42	transport
0.2248	CLIC1	transport
0.01865	CLTC	transport
0.13809	CNTNAP2	transport
0.1314	COL12A1	transport
0.28163	COL18A1	transport
0.15215	COL6A1	transport
0.17475	COL6A2	transport
0.31564	COL9A1	transport
0.06913	COLEC12	transport
0.09465	COPB2	transport
0.28965	CP	transport
0.3187	DBI	transport
0.27757	DPP4	transport
0.09572	EDIL3	transport
0.17534	EEF1G	transport
0.1145	FN1	transport
0.06923	FTH1	transport
0.11006	GAS6	transport
0.04455	GLG1	transport
0	GNB2L1	transport
0.40563	GPR115	transport
0.27514	GSTO1	transport
0.25068	GSTT1	transport
0.33622	GSTZ1	transport
0.22362	IGF2R	transport
0.02703	KPNB1	transport
0.15986	LAMP1	transport
0.17687	LGALS3BP	transport
0.03762	LMAN2	transport
0.08979	LPL	transport
0.03403	MFAP4	transport
0.13639	MPST	transport
0.11398	MTCH1/PSAP	transport
0.01165	MYH9	transport
0.06255	MYO1C	transport
0	NAPA	transport
0.22725	NELL1	transport
0.07267	NPC2	transport
0.1187	NRP1	transport
0.24164	NUTF2	transport
0.02107	ODZ2	transport
0.02472	OLFM1	transport
0.36665	OLFM4	transport
0.47638	PIGR	transport
0.08676	PITPNA	transport
0.04806	PPIA	transport
0.034	PPIB	transport
0.22018	PPIC	transport
0.25088	PROM2	transport
0.11398	PSAP	transport
0.12775	PTGDS	transport
0.0833	PTPRD	transport
0.04714	PTPRF	transport
0.43859	PTPRJ	transport

uniform_ω	Gene	Level 1: Biological Processes	uniform_ω	Gene	Level 1: Biological Processes
0.05222	PTPRS	transport			
0	RAB10	transport			
0	RAB11B	transport			
0.02735	RAB3B	transport			
0.12088	RAC1	transport			
0.33887	RALA	transport			
0.08639	RALB	transport			
0	RAP1B	transport			
0	RHOA	transport			
0.14582	SDCBP	transport			
0.17189	SDCBP2	transport			
0.29309	SLC15A2	transport			
0.16604	SLC18A1/VAT1	transport			
0.09929	SLC1A1	transport			
0.17158	SLC44A4	transport			
0.10077	SORL1	transport			
0.14231	SORT1	transport			
0.06	SYT7	transport			
0.54147	TF	transport			
0.21664	TFRC	transport			
0.59375	TTR	transport			
0.07015	TUBB1	transport			
0.02398	VCP	transport			
0.05097	VPS28	transport			

Control Gene Ontology

uniform_ω	Gene	Level.1:.Biological.Process
0.44471	ADAM29	apoptosis
0.16305	ADAM9	apoptosis
0.40953	ADH1A	apoptosis
0.09743	ADRA1B	apoptosis
0.08569	APC2	apoptosis
0.08569	APC2/ANAPC2	apoptosis
0.24802	ARHGAP4	apoptosis
0.3139	CAPN11	apoptosis
0.07595	CARD11	apoptosis
0.42606	CASP8	apoptosis
0.19809	CHL1	apoptosis
0.3206	CISH	apoptosis
0.19901	CNTN6	apoptosis
0.02051	EPHB3	apoptosis
0.28362	FLT3	apoptosis
0.01978	GADD45A	apoptosis
0.79254	IFNA2	apoptosis
0.44695	IL10RA	apoptosis
0.68451	IL19	apoptosis
	LGALS7	apoptosis
0.24546	LTK	apoptosis
0.05879	MAGEA8	apoptosis
0.31908	MAGEB3	apoptosis
0.30916	MAP2	apoptosis
0.13548	MDM4	apoptosis
0.05829	OAZ2	apoptosis
0.33672	ODR4/C1orf27	apoptosis
0.11671	PRRG1	apoptosis
0.32214	ROBO4	apoptosis
0.04994	ROR2	apoptosis
0.03661	STAT5B	apoptosis
0.16329	TNS3	apoptosis
0.38503	TRAIP	apoptosis
0.5884	TTF1	apoptosis
0.44471	ADAM29	cell adhesion
0.16305	ADAM9	cell adhesion
0.10182	ADAMTS8	cell adhesion
0.7904	CEACAM6	cell adhesion
0.19809	CHL1	cell adhesion
0.58328	CLEC4E	cell adhesion
0.19901	CNTN6	cell adhesion
0.22552	COL20A1	cell adhesion
0.08985	COL5A2	cell adhesion
0.02051	EPHB3	cell adhesion
0.28362	FLT3	cell adhesion
0.71596	GP1BA	cell adhesion
0.14252	ITGB8	cell adhesion
0.0704	JAG2	cell adhesion
0.32378	KLRG2	cell adhesion
0.04283	LRRTM3	cell adhesion
0.24546	LTK	cell adhesion
0.07245	MEGF10	cell adhesion
0.02587	NLGN3	cell adhesion
0.04162	PCDH7	cell adhesion
0.29576	PCDHA1	cell adhesion
0.17195	PCDHA3	cell adhesion
0.27942	PCDHB5	cell adhesion
0.32214	ROBO4	cell adhesion
0.04994	ROR2	cell adhesion
0.10758	RTN4RL2	cell adhesion
0.13293	SEMA4B	cell adhesion
0.04865	SEMA6B	cell adhesion
0.06266	SLIT1	cell adhesion
0.24717	SUSD3	cell adhesion
0.064	TSPAN15	cell adhesion
1.69742	TSPAN8	cell adhesion

uniform_ω	Gene	Level.1:.Biological.Process
0.44471	ADAM29	cell communication
0.16305	ADAM9	cell communication
0.10182	ADAMTS8	cell communication
0.40953	ADH1A	cell communication
0.09743	ADRA1B	cell communication
0.08569	APC2	cell communication
0.08569	APC2/ANAPC2	cell communication
0.24802	ARHGAP4	cell communication
0.31762	ASPH	cell communication
0.25319	BLNK	cell communication
0.14347	C1QTNF7	cell communication
0.3139	CAPN11	cell communication
0.10233	CAPN7	cell communication
0.07595	CARD11	cell communication
0.42606	CASP8	cell communication
0.03265	CAV1	cell communication
0.35182	CCL24	cell communication
0.39503	CCRL1	cell communication
0.00621	CDC37	cell communication
0.01091	CDK9	cell communication
0.7904	CEACAM6	cell communication
0.19809	CHL1	cell communication
0.2921	CHM	cell communication
0.3206	CISH	cell communication
0.58328	CLEC4E	cell communication
0.09218	CNTFR	cell communication
0.19901	CNTN6	cell communication
0.22552	COL20A1	cell communication
0.08985	COL5A2	cell communication
0.04779	CORO1C	cell communication
0.08145	CXCR5	cell communication
0.16564	DNAJC24	cell communication
0.37881	DNAJC30	cell communication
0.90695	DNAJC5G	cell communication
0.0001	DUSP1	cell communication
0.23925	EBI3	cell communication
0.0406	ECEL1	cell communication
0.29914	EFS	cell communication
0.23113	ELF4	cell communication
0.02051	EPHB3	cell communication
0.71925	FCRL2	cell communication
0.27381	FGF2	cell communication
0.28362	FLT3	cell communication
0.58545	FXYD3	cell communication
0.01978	GADD45A	cell communication
0.24368	GCGR	cell communication
0.05652	GJA4	cell communication
0.07131	GNAO1	cell communication
0.05255	GNAT2	cell communication
0.71596	GP1BA	cell communication
0.10446	GPR176	cell communication
0.22396	GPR39	cell communication
0.0197	GRIK3	cell communication
0.0001	GUCA1B	cell communication
0.0199	HM13	cell communication
0.79254	IFNA2	cell communication
0.44695	IL10RA	cell communication
0.68451	IL19	cell communication
0.06408	ILKAP	cell communication
0.14252	ITGB8	cell communication
0.0704	JAG2	cell communication
0.02316	KCNB1	cell communication
0.04569	KCNG2	cell communication
0.32378	KLRG2	cell communication
0.98035	LAIR1	cell communication
	LGALS7	cell communication
0.15342	LPAR3	cell communication

uniform_ω	Gene	Level.1:.Biological.Process	uniform_ω	Gene	Level.1:.Biological.Process
0.41602	LRRC2	cell communication	0.13497	STX2	cell communication
0.78222	LRRC27	cell communication	0.24717	SUSD3	cell communication
0.04283	LRRTM3	cell communication	0.02962	SV2B	cell communication
0.24546	LTK	cell communication	0.34558	SYNJ2BP	cell communication
0.05879	MAGEA8	cell communication	0.1945	TACR2	cell communication
0.31908	MAGEB3	cell communication	0.06219	TBXA2R	cell communication
0.30916	MAP2	cell communication	0.03844	THY1	cell communication
0.09101	MARK2	cell communication	0.16329	TNS3	cell communication
0.13548	MDM4	cell communication	0.38503	TRAIP	cell communication
0.07245	MEGF10	cell communication	0.1087	TRIM39	cell communication
0.29627	MOCS3	cell communication	0.064	TSPAN15	cell communication
0.40455	MRGPRD	cell communication	1.69742	TSPAN8	cell communication
0.08977	MRGPRE	cell communication	0.10263	TSSK2	cell communication
0.49329	MS4A7	cell communication	0.5521	TSSK4	cell communication
0.29918	MTG1	cell communication	0.57975	TTC29	cell communication
0.02587	NLGN3	cell communication	0.5884	TTF1	cell communication
1.32221	NPFF	cell communication	0.09537	WDFY2	cell communication
0.11288	NPFFR1	cell communication	0.2632	WISP3	cell communication
0.0435	NPY1R	cell communication	0.09507	WSB2	cell communication
0.06886	NPY5R	cell communication	0.08569	APC2	cell cycle
0.0573	NR1D2	cell communication	0.08569	APC2/ANAPC2	cell cycle
0.23094	NR1I3	cell communication	0.24802	ARHGAP4	cell cycle
0.03019	NR2C2	cell communication	0.11789	ASCC3	cell cycle
0.05829	OAZ2	cell communication	0.7671	BCCIP	cell cycle
0.33672	ODR4/C1orf27	cell communication	0.25128	CCNB1	cell cycle
0.04162	PCDH7	cell communication	0.06302	CDC20	cell cycle
0.29576	PCDHA1	cell communication	0.09586	CDC23	cell cycle
0.17195	PCDHA3	cell communication	0.00621	CDC37	cell cycle
0.27942	PCDHB5	cell communication	0.01091	CDK9	cell cycle
0.04152	PDK3	cell communication	0.19809	CHL1	cell cycle
0.51372	PER3	cell communication	0.19809	CHL1/DDX11	cell cycle
0.14508	PIP4K2C	cell communication	0.19901	CNTN6	cell cycle
0.35402	PLAU	cell communication	0.04779	CORO1C	cell cycle
0.31859	PLB1	cell communication	0.15138	DNAI2	cell cycle
0.09634	PLCB1	cell communication	0.12622	DNAJC17	cell cycle
0.11674	PLCH2	cell communication	0.16564	DNAJC24	cell cycle
0.09085	PLK2	cell communication	0.37881	DNAJC30	cell cycle
0.28141	PPM1E	cell communication	0.90695	DNAJC5G	cell cycle
0.12621	PPM1K	cell communication	0.0001	DUSP1	cell cycle
0.28141	PPM1M/PPM1E	cell communication	0.23113	ELF4	cell cycle
0.02783	PRKCD	cell communication	0.02051	EPHB3	cell cycle
0.06779	PRPF4B	cell communication	0.02168	FBXL12	cell cycle
0.11671	PRRG1	cell communication	0.27381	FGF2	cell cycle
0.31202	RAB17	cell communication	0.28362	FLT3	cell cycle
0.10056	RALGDS	cell communication	0.02275	FOSB	cell cycle
0.54877	RBP7	cell communication	0.01962	FZR1	cell cycle
0.12665	RCN2	cell communication	0.01978	GADD45A	cell cycle
0.37106	RGS18	cell communication	0.21798	GMNN	cell cycle
0.08965	RGS8	cell communication	0.16507	HNRNPD	cell cycle
0.00865	RHOB	cell communication	0.19851	KLHDC4	cell cycle
0.32214	ROBO4	cell communication	0.27676	L3MBTL/L3MBTI	cell cycle
0.04994	ROR2	cell communication	0.24546	LTK	cell cycle
0.10758	RTN4RL2	cell communication	0.35669	MPHOSPH9	cell cycle
0.0001	S100A4	cell communication	0.49329	MS4A7	cell cycle
0.07308	S1PR3	cell communication	0.02587	NLGN3	cell cycle
0.04253	SCN1B	cell communication	0.03019	NR2C2	cell cycle
0.2481	SCT	cell communication	0.15016	ORC2	cell cycle
0.1843	SDC2	cell communication	0.09085	PLK2	cell cycle
0.19743	SDSL	cell communication	0.06779	PRPF4B	cell cycle
0.13293	SEMA4B	cell communication	0.31202	RAB17	cell cycle
0.04865	SEMA6B	cell communication	0.03208	RAE1	cell cycle
0.0472	SFRP1	cell communication	0.10056	RALGDS	cell cycle
0.07005	SLC6A4	cell communication	0.32214	ROBO4	cell cycle
0.06266	SLIT1	cell communication	0.04994	ROR2	cell cycle
0.08137	SOCS4	cell communication	0.0001	S100A4	cell cycle
0.06607	SPIB	cell communication	0.34749	SDAD1	cell cycle
0.03661	STAT5B	cell communication	0.09617	SMC2	cell cycle

uniform_ω	Gene	Level.1:.Biological.Process	uniform_ω	Gene	Level.1:.Biological.Process
0.06607	SPIB	cell cycle	0.42606	CASP8	cellular process
0.04941	TBCB	cell cycle	0.03265	CAV1	cellular process
0.16329	TNS3	cell cycle	0.35182	CCL24	cellular process
0.2615	TOP3A	cell cycle	0.25128	CCNB1	cellular process
0.1087	TRIM39	cell cycle	0.39503	CCRL1	cellular process
0.10263	TSSK2	cell cycle	0.06302	CDC20	cellular process
0.5521	TSSK4	cell cycle	0.09586	CDC23	cellular process
0.57975	TTC29	cell cycle	0.00621	CDC37	cellular process
0.5884	TTF1	cell cycle	0.01091	CDK9	cellular process
0.16238	TUBB	cell cycle	0.7904	CEACAM6	cellular process
0.39106	WDR63	cell cycle	0.19809	CHL1	cellular process
0.2632	WISP3	cell cycle	0.19809	CHL1/DDX11	cellular process
0.14347	C1QTNF7	cellular component organization	0.2921	CHM	cellular process
0.00621	CDC37	cellular component organization	0.1641	CHRDL2	cellular process
0.22552	COL20A1	cellular component organization	0.3206	CISH	cellular process
0.08985	COL5A2	cellular component organization	0.58328	CLEC4E	cellular process
0.04779	CORO1C	cellular component organization	0.09218	CNTFR	cellular process
0.94067	CYLC1	cellular component organization	0.19901	CNTN6	cellular process
0.15138	DNAI2	cellular component organization	0.22552	COL20A1	cellular process
0.01706	EPB49	cellular component organization	0.08985	COL5A2	cellular process
0.32992	H2AFB3	cellular component organization	0.04779	CORO1C	cellular process
0.0001	HIST1H2AJ	cellular component organization	0.08145	CXCR5	cellular process
0.21687	KRT36	cellular component organization	0.94067	CYLC1	cellular process
0.27676	L3MBTL/L3MBTI	cellular component organization	0.15138	DNAI2	cellular process
0.15996	LDB3	cellular component organization	0.12622	DNAJC17	cellular process
0.02486	LHX2	cellular component organization	0.16564	DNAJC24	cellular process
0.30916	MAP2	cellular component organization	0.37881	DNAJC30	cellular process
0.09101	MARK2	cellular component organization	0.90695	DNAJC5G	cellular process
0.03199	MIER1	cellular component organization	0.0001	DUSP1	cellular process
0.15926	MPZL2	cellular component organization	0.23925	EBI3	cellular process
0.04162	PCDH7	cellular component organization	0.0406	ECEL1	cellular process
0.29576	PCDHA1	cellular component organization	0.29914	EFS	cellular process
0.17195	PCDHA3	cellular component organization	0.23113	ELF4	cellular process
0.27942	PCDHB5	cellular component organization	0.01706	EPB49	cellular process
0.07234	PLP1	cellular component organization	0.02051	EPHB3	cellular process
0.03425	PLS3	cellular component organization	0.02168	FBXL12	cellular process
0.16826	RBBP7	cellular component organization	0.71925	FCRL2	cellular process
0.15954	SHPRH	cellular component organization	0.27381	FGF2	cellular process
0.11363	SLC4A4	cellular component organization	0.28362	FLT3	cellular process
0.09617	SMC2	cellular component organization	0.02275	FOSB	cellular process
0.0001	SUV39H1	cellular component organization	0.58545	FXYD3	cellular process
0.38996	SYNPO2L	cellular component organization	0.01962	FZR1	cellular process
0.05219	TBC1D17	cellular component organization	0.01978	GADD45A	cellular process
0.0128	TBC1D9	cellular component organization	0.24368	GCGR	cellular process
0.04941	TBCB	cellular component organization	0.05652	GJA4	cellular process
0.14052	TEKT5	cellular component organization	0.21798	GMNN	cellular process
0.1903	TJP2	cellular component organization	0.07131	GNAO1	cellular process
0.10263	TSSK2	cellular component organization	0.05255	GNAT2	cellular process
0.5521	TSSK4	cellular component organization	0.71596	GP1BA	cellular process
0.16238	TUBB	cellular component organization	0.10446	GPR176	cellular process
0.39106	WDR63	cellular component organization	0.22396	GPR39	cellular process
0.44471	ADAM29	cellular process	0.0197	GRIK3	cellular process
0.16305	ADAM9	cellular process	0.0001	GUCA1B	cellular process
0.10182	ADAMTS8	cellular process	0.32992	H2AFB3	cellular process
0.40953	ADH1A	cellular process	0.0001	HIST1H2AJ	cellular process
0.09743	ADRA1B	cellular process	0.0199	HM13	cellular process
0.08569	APC2	cellular process	0.16507	HNRNPD	cellular process
0.08569	APC2/ANAPC2	cellular process	0.08087	HRH3	cellular process
0.24802	ARHGAP4	cellular process	0.79254	IFNA2	cellular process
0.11789	ASCC3	cellular process	0.44695	IL10RA	cellular process
0.31762	ASPH	cellular process	0.68451	IL19	cellular process
0.7671	BCCIP	cellular process	0.06408	ILKAP	cellular process
0.25319	BLNK	cellular process	0.14252	ITGB8	cellular process
0.14347	C1QTNF7	cellular process	0.0704	JAG2	cellular process
0.3139	CAPN11	cellular process	0.19363	JAM2	cellular process
0.10233	CAPN7	cellular process	0.02316	KCNB1	cellular process
0.07595	CARD11	cellular process	0.04569	KCNG2	cellular process

uniform_ω	Gene	Level.1:.Biological.Process
0.19851	KLHDC4	cellular process
0.32378	KLRG2	cellular process
0.21687	KRT36	cellular process
0.27676	L3MBTL/L3MBTl	cellular process
0.98035	LAIR1	cellular process
0.15996	LDB3	cellular process
	LGALS7	cellular process
0.02486	LHX2	cellular process
0.15342	LPAR3	cellular process
0.41602	LRRC2	cellular process
0.78222	LRRC27	cellular process
0.04283	LRRTM3	cellular process
0.24546	LTK	cellular process
0.05879	MAGEA8	cellular process
0.75453	MAGEB3	cellular process
0.30916	MAP2	cellular process
0.09101	MARK2	cellular process
0.13548	MDM4	cellular process
0.07245	MEGF10	cellular process
0.03199	MIER1	cellular process
0.29627	MOCS3	cellular process
0.35669	MPHOSPH9	cellular process
0.15926	MPZL2	cellular process
0.40455	MRGPRD	cellular process
0.08977	MRGPRE	cellular process
0.49329	MS4A7	cellular process
0.29918	MTG1	cellular process
0.02587	NLGN3	cellular process
1.32221	NPFF	cellular process
0.11288	NPFFR1	cellular process
0.0435	NPY1R	cellular process
0.06886	NPY5R	cellular process
0.0573	NR1D2	cellular process
0.23094	NR1I3	cellular process
0.03019	NR2C2	cellular process
0.05829	OAZ2	cellular process
0.33672	ODR4/C1orf27	cellular process
0.15016	ORC2	cellular process
0.04162	PCDH7	cellular process
0.29576	PCDHA1	cellular process
0.17195	PCDHA3	cellular process
0.27942	PCDHB5	cellular process
0.04152	PDK3	cellular process
0.51372	PER3	cellular process
0.14508	PIP4K2C	cellular process
0.35402	PLAU	cellular process
0.31859	PLB1	cellular process
0.09634	PLCB1	cellular process
0.11674	PLCH2	cellular process
0.09085	PLK2	cellular process
0.07234	PLP1	cellular process
0.03425	PLS3	cellular process
0.28141	PPM1E	cellular process
0.12621	PPM1K	cellular process
0.28141	PPM1M/PPM1E	cellular process
0.02783	PRKCD	cellular process
0.06779	PRPF4B	cellular process
0.11671	PRRG1	cellular process
0.31202	RAB17	cellular process
0.03208	RAE1	cellular process
0.10056	RALGDS	cellular process
0.07865	RAP1GAP2/GAR	cellular process
0.16826	RBBP7	cellular process
0.54877	RBP7	cellular process
0.12665	RCN2	cellular process
0.37106	RGS18	cellular process
0.08965	RGS8	cellular process
0.00865	RHOB	cellular process
0.32214	ROBO4	cellular process
0.04994	ROR2	cellular process
0.10758	RTN4RL2	cellular process
0.0001	S100A4	cellular process
0.07308	S1PR3	cellular process
0.04253	SCN1B	cellular process
0.2481	SCT	cellular process
0.34749	SDAD1	cellular process
0.1843	SDC2	cellular process
0.19743	SDSL	cellular process
0.13293	SEMA4B	cellular process
0.04865	SEMA6B	cellular process
0.0472	SFRP1	cellular process
0.15954	SHPRH	cellular process
0.06162	SIPA1	cellular process
0.11363	SLC4A4	cellular process
0.07005	SLC6A4	cellular process
0.07005	SLC6A4	cellular process
0.07005	SLC6A4	cellular process
0.06266	SLIT1	cellular process
0.09617	SMC2	cellular process
0.08137	SOCS4	cellular process
0.06607	SPIB	cellular process
0.03661	STAT5B	cellular process
0.13497	STX2	cellular process
0.24717	SUSD3	cellular process
0.0001	SUV39H1	cellular process
0.02962	SV2B	cellular process
0.34558	SYNJ2BP	cellular process
0.38996	SYNPO2L	cellular process
0.1945	TACR2	cellular process
0.05219	TBC1D17	cellular process
0.0128	TBC1D9	cellular process
0.04941	TBCB	cellular process
0.06219	TBXA2R	cellular process
0.14052	TEKT5	cellular process
0.03844	THY1	cellular process
0.1903	TJP2	cellular process
0.16329	TNS3	cellular process
0.2615	TOP3A	cellular process
0.38503	TRAIP	cellular process
0.1087	TRIM39	cellular process
0.064	TSPAN15	cellular process
1.69742	TSPAN8	cellular process
0.10263	TSSK2	cellular process
0.5521	TSSK4	cellular process
0.57975	TTC29	cellular process
0.5884	TTF1	cellular process
0.16238	TUBB	cellular process
0.59697	VSIG1	cellular process
0.09537	WDFY2	cellular process
0.39106	WDR63	cellular process
0.2632	WISP3	cellular process
0.09507	WSB2	cellular process
0.44471	ADAM29	developmental process
0.16305	ADAM9	developmental process
0.10182	ADAMTS8	developmental process
0.10357	BCL9L	developmental process
0.09663	C1orf43	developmental process
0.14347	C1QTNF7	developmental process
0.00621	CDC37	developmental process
0.19809	CHL1	developmental process
0.1641	CHRDL2	developmental process
0.3206	CISH	developmental process
0.09218	CNTFR	developmental process
0.19901	CNTN6	developmental process

uniform_ω	Gene	Level.1:.Biological.Process	uniform_ω	Gene	Level.1:.Biological.Process
0.22552	COL20A1	developmental process	0.04941	TBCB	developmental process
0.08985	COL5A2	developmental process	0.00823	TBR1	developmental process
0.04779	CORO1C	developmental process	0.14052	TEKT5	developmental process
0.94067	CYLC1	developmental process	0.1903	TJP2	developmental process
0.194	DBX1	developmental process	0.1087	TRIM39	developmental process
0.27729	DLX6	developmental process	0.10263	TSSK2	developmental process
0.15138	DNAI2	developmental process	0.16238	TUBB	developmental process
0.0001	DUSP1	developmental process	0.47646	VPREB1	developmental process
0.23925	EBI3	developmental process	0.20814	WDR5B	developmental process
0.23113	ELF4	developmental process	0.39106	WDR63	developmental process
0.02597	EPAS1/HLF	developmental process	0.2632	WISP3	developmental process
0.01706	EPB49	developmental process	0.09507	WSB2	developmental process
0.02051	EPHB3	developmental process	0.28034	ALOX15	generation of precursor metabolites and energy
0.27381	FGF2	developmental process	0.74972	COX5B	generation of precursor metabolites and energy
0.28362	FLT3	developmental process	0.54142	CYP3A5	generation of precursor metabolites and energy
0.02275	FOSB	developmental process	0.23863	CYP4F11	generation of precursor metabolites and energy
0.24368	GCGR	developmental process	0.21395	DHTKD1	generation of precursor metabolites and energy
0.71596	GP1BA	developmental process	0.20438	DMGDH	generation of precursor metabolites and energy
0.03351	GSC	developmental process	0.1696	GCDH	generation of precursor metabolites and energy
0.02211	HES5	developmental process	0.02629	GFOD2	generation of precursor metabolites and energy
0.29903	HEYL	developmental process	0.05195	ME2	generation of precursor metabolites and energy
0.16507	HNRNPD	developmental process	0.2592	NDUFA6	generation of precursor metabolites and energy
0.34715	IRX6	developmental process	0.22614	SDHA	generation of precursor metabolites and energy
0.0704	JAG2	developmental process	0.31096	ATP10D	homeostatic process
0.21687	KRT36	developmental process	0.3206	CISH	homeostatic process
0.15996	LDB3	developmental process	0.08985	COL5A2	homeostatic process
0.02486	LHX2	developmental process	0.24368	GCGR	homeostatic process
0.04283	LRRTM3	developmental process	0.08137	SOCS4	homeostatic process
0.24546	LTK	developmental process	0.28618	ABCB11	Immune system process
0.30916	MAP2	developmental process	0.06569	ABHD4	Immune system process
0.09101	MARK2	developmental process	0.53826	ACSM1	Immune system process
0.08903	MBNL2	developmental process	0.13916	AHSA1	Immune system process
0.07245	MEGF10	developmental process	0.28034	ALOX15	Immune system process
0.03199	MIER1	developmental process	0.14347	C1QTNF7	Immune system process
0.15926	MPZL2	developmental process	0.35182	CCL24	Immune system process
0.5884	NKX2-1/TTF1	developmental process	0.39503	CCRL1	Immune system process
0.02587	NLGN3	developmental process	0.7195	CD300C	Immune system process
0.0573	NR1D2	developmental process	0.44299	CD69	Immune system process
0.23094	NR1I3	developmental process	0.01091	CDK9	Immune system process
0.19401	PAFAH1B1	developmental process	0.19809	CHL1	Immune system process
0.03506	PAX9	developmental process	0.3206	CISH	Immune system process
0.04162	PCDH7	developmental process	0.58328	CLEC4E	Immune system process
0.29576	PCDHA1	developmental process	0.09218	CNTFR	Immune system process
0.17195	PCDHA3	developmental process	0.19901	CNTN6	Immune system process
0.27942	PCDHB5	developmental process	0.22552	COL20A1	Immune system process
0.09085	PLK2	developmental process	0.08985	COL5A2	Immune system process
0.07234	PLP1	developmental process	0.08145	CXCR5	Immune system process
0.03425	PLS3	developmental process	0.62793	DDTL	Immune system process
0.07697	POGK	developmental process	0.12622	DNAJC17	Immune system process
0.14517	PYGO2	developmental process	0.16564	DNAJC24	Immune system process
0.54877	RBP7	developmental process	0.37881	DNAJC30	Immune system process
0.37106	RGS18	developmental process	0.90695	DNAJC5G	Immune system process
0.08965	RGS8	developmental process	0.0001	DUSP1	Immune system process
0.32214	ROBO4	developmental process	0.23925	EBI3	Immune system process
0.04994	ROR2	developmental process	0.23113	ELF4	Immune system process
0.10758	RTN4RL2	developmental process	0.02051	EPHB3	Immune system process
0.1843	SDC2	developmental process	0.02168	FBXL12	Immune system process
0.13293	SEMA4B	developmental process	0.71925	FCRL2	Immune system process
0.04865	SEMA6B	developmental process	0.28362	FLT3	Immune system process
0.11363	SLC4A4	developmental process	0.02275	FOSB	Immune system process
0.06266	SLIT1	developmental process	0.01978	GADD45A	Immune system process
0.08137	SOCS4	developmental process	0.68287	GIMAP2	Immune system process
0.06607	SPIB	developmental process	0.71596	GP1BA	Immune system process
0.03661	STAT5B	developmental process	0.22396	GPR39	Immune system process
0.38996	SYNPO2L	developmental process	0.08087	HRH3	Immune system process
0.05219	TBC1D17	developmental process	0.16616	HSPB2	Immune system process
0.0128	TBC1D9	developmental process	0.79254	IFNA2	Immune system process

uniform_ω	Gene	Level.1:.Biological.Process	uniform_ω	Gene	Level.1:.Biological.Process
0.44695	IL10RA	Immune system process	0.28034	ALOX15	metabolic process
0.68451	IL19	Immune system process	0.08569	APC2/ANAPC2	metabolic process
0.09154	IRF8	Immune system process	0.08569	APC2/APOC2	metabolic process
0.14252	ITGB8	Immune system process	0.35525	APOBEC1	metabolic process
0.0704	JAG2	Immune system process	0.31252	ARV1	metabolic process
0.19363	JAM2	Immune system process	0.11789	ASCC3	metabolic process
0.19851	KLHDC4	Immune system process	0.07034	ASH2L	metabolic process
0.32378	KLRG2	Immune system process	0.31762	ASPH	metabolic process
0.98035	LAIR1	Immune system process	0.23109	ATAD2	metabolic process
0.05879	LGALS7	Immune system process	0.31096	ATP10D	metabolic process
0.02486	LHX2	Immune system process	0.0594	B4GALT5	metabolic process
0.41602	LRRC2	Immune system process	0.39057	C10orf11	metabolic process
0.78222	LRRC27	Immune system process	0.53333	C12orf5	metabolic process
0.04283	LRRTM3	Immune system process	0.14347	C1QTNF7	metabolic process
0.24546	LTK	Immune system process	0.01332	CA10	metabolic process
0.2101	MOAP1	Immune system process	0.4998	CA5A	metabolic process
0.49477	MPV17L	Immune system process	0.3139	CAPN11	metabolic process
0.49329	MS4A7	Immune system process	0.10233	CAPN7	metabolic process
0.2631	MSRB2	Immune system process	0.3361	CAPS2	metabolic process
0.0435	NPY1R	Immune system process	0.42606	CASP8	metabolic process
0.0573	NR1D2	Immune system process	0.03265	CAV1	metabolic process
0.23094	NR1I3	Immune system process	0.24962	CD2AP	metabolic process
0.31658	NUP88	Immune system process	0.06302	CDC20	metabolic process
1.0655	OAS1	Immune system process	0.09586	CDC23	metabolic process
0.35402	PLAU	Immune system process	0.00621	CDC37	metabolic process
0.09085	PLK2	Immune system process	0.01091	CDK9	metabolic process
0.13351	PNMA1	Immune system process	0.38003	CEBPZ	metabolic process
0.32185	PPIG	Immune system process	0.19809	CHL1	metabolic process
0.01826	PPP2R2C	Immune system process	0.19809	CHL1/DDX11	metabolic process
0.06779	PRPF4B	Immune system process	0.07547	CHST2	metabolic process
0.11671	PRRG1	Immune system process	0.28245	CHST4	metabolic process
0.04825	RBCK1	Immune system process	0.13393	CLK4	metabolic process
0.16529	RNF216	Immune system process	0.31914	CMBL	metabolic process
0.32214	ROBO4	Immune system process	0.19901	CNTN6	metabolic process
0.04994	ROR2	Immune system process	0.22552	COL20A1	metabolic process
0.10758	RTN4RL2	Immune system process	0.08985	COL5A2	metabolic process
0.0001	S100A4	Immune system process	0.09887	COPS4	metabolic process
0.1843	SDC2	Immune system process	0.63308	COQ3	metabolic process
0.13293	SEMA4B	Immune system process	0.16552	CPA5	metabolic process
0.04865	SEMA6B	Immune system process	0.51219	CPB2	metabolic process
0.06266	SLIT1	Immune system process	0.13443	CPT1B	metabolic process
0.06607	SPIB	Immune system process	0.54142	CYP3A5	metabolic process
0.14793	SQSTM1	Immune system process	0.23863	CYP4F11	metabolic process
0.03661	STAT5B	Immune system process	0.00665	CYTH1	metabolic process
0.0001	STUB1	Immune system process	0.194	DBX1	metabolic process
0.24717	SUSD3	Immune system process	0.02566	DCTN6	metabolic process
0.1945	TACR2	Immune system process	0.10933	DDB2	metabolic process
0.06219	TBXA2R	Immune system process	0.25792	DGAT1	metabolic process
0.18326	TNFAIP8L3	Immune system process	0.33835	DHRS7	metabolic process
0.16329	TNS3	Immune system process	0.21395	DHTKD1	metabolic process
0.064	TSPAN15	Immune system process	0.27729	DLX6	metabolic process
1.69742	TSPAN8	Immune system process	0.20438	DMGDH	metabolic process
0.10263	TSSK2	Immune system process	0.15138	DNAI2	metabolic process
0.5521	TSSK4	Immune system process	0.12622	DNAJC17	metabolic process
0.47646	VPREB1	Immune system process	0.16564	DNAJC24	metabolic process
0.59697	VSIG1	Immune system process	0.37881	DNAJC30	metabolic process
0.15138	DNAI2	localization	0.90695	DNAJC5G	metabolic process
0.19401	PAFAH1B1	localization	0.12032	DRAP1	metabolic process
0.03208	RAE1	localization	0.0001	DUSP1	metabolic process
0.11993	SEC13	localization	0.0406	ECEL1	metabolic process
0.20814	WDR5B	localization	0.02379	EIF2C2	metabolic process
0.39106	WDR63	localization	0.0001	EIF2C4	metabolic process
0.28618	ABCB11	metabolic process	0.23113	ELF4	metabolic process
0.13009	ABCD3	metabolic process	0.10166	ENOPH1	metabolic process
0.06569	ABHD4	metabolic process	0.02597	EPAS1/HLF	metabolic process
0.2554	ACOT12	metabolic process	0.02051	EPHB3	metabolic process
0.53826	ACSM1	metabolic process	0.05756	ERCC3	metabolic process
0.44471	ADAM29	metabolic process	0.37276	FAAH2	metabolic process
0.16305	ADAM9	metabolic process	0.1293	FBL	metabolic process
0.10182	ADAMTS8	metabolic process	0.02168	FBXL12	metabolic process
0.22183	ADAT2	metabolic process	0.17813	FGGY	metabolic process
0.40953	ADH1A	metabolic process	0.28362	FLT3	metabolic process
0.07626	AGPAT2	metabolic process	0.02275	FOSB	metabolic process
0.13916	AHSA1	metabolic process	0.27228	FTSJ2	metabolic process
0.11748	ALDH1A3	metabolic process	0.01962	FZR1	metabolic process

uniform_ω	Gene	Level.1:.Biological.Process
0.21468	G6PC	metabolic process
0.01978	GADD45A	metabolic process
0.39561	GAL3ST4	metabolic process
0.19299	GALNT12	metabolic process
0.1696	GCDH	metabolic process
0.12391	GCK	metabolic process
0.02629	GFOD2	metabolic process
0.51996	GLYAT	metabolic process
0.21798	GMNN	metabolic process
0.23519	GNPAT	metabolic process
0.04079	GPT2	metabolic process
0.03351	GSC	metabolic process
0.24456	GUCY2F	metabolic process
0.32992	H2AFB3	metabolic process
0.44281	HELB	metabolic process
0.02211	HES5	metabolic process
0.29903	HEYL	metabolic process
0.0001	HIST1H2AJ	metabolic process
0.02597	HLF	metabolic process
0.24855	HMGCR	metabolic process
0.16507	HNRNPD	metabolic process
0.03584	HNRPLL	metabolic process
0.28111	HSD17B3	metabolic process
0.16616	HSPB2	metabolic process
0.00945	HSPBP1	metabolic process
0.38557	ICT1	metabolic process
0.06408	ILKAP	metabolic process
0.09154	IRF8	metabolic process
0.34715	IRX6	metabolic process
0.04974	ISYNA1	metabolic process
0.0704	JAG2	metabolic process
0.19851	KLHDC4	metabolic process
0.45969	KMO	metabolic process
0.27676	L3MBTL/L3MBTI	metabolic process
0.02486	LHX2	metabolic process
0.40303	LIPH	metabolic process
0.76638	LRPPRC	metabolic process
0.41602	LRRC2	metabolic process
0.78222	LRRC27	metabolic process
0.01271	LSM7	metabolic process
0.24546	LTK	metabolic process
0.12391	MAP4K2/GCK	metabolic process
0.09243	MAP4K3	metabolic process
0.0812	MAP4K4	metabolic process
0.09101	MARK2	metabolic process
0.05471	MAT2A	metabolic process
0.05409	MBTPS2	metabolic process
0.05195	ME2	metabolic process
0.03199	MIER1	metabolic process
0.07658	MLLT6	metabolic process
0.21341	MLXIPL	metabolic process
0.29627	MOCS3	metabolic process
0.49477	MPV17L	metabolic process
0.26008	MRPL20	metabolic process
0.29047	MRPL21	metabolic process
0.36544	MRPL43	metabolic process
0.2631	MSRB2	metabolic process
0.29918	MTG1	metabolic process
0.84182	MTIF3	metabolic process
0.06662	NCOR2	metabolic process
0.5884	NKX2-1/TTF1	metabolic process
0.02587	NLGN3	metabolic process
0.0573	NR1D2	metabolic process
0.23094	NR1I3	metabolic process
0.03019	NR2C2	metabolic process
0.32474	NSUN3	metabolic process
1.0655	OAS1	metabolic process
0.05829	OAZ2	metabolic process
0.33672	ODR4/C1orf27	metabolic process
0.15016	ORC2	metabolic process
0.04459	OVOL2	metabolic process
0.20957	PADI1	metabolic process
0.19401	PAFAH1B1	metabolic process
0.03506	PAX9	metabolic process
0.04152	PDK3	metabolic process
0.51372	PER3	metabolic process
0.03469	PGAM1	metabolic process
0.00964	PIAS1	metabolic process
0.58822	PIGA	metabolic process
0.14508	PIP4K2C	metabolic process
0.08239	PITPNM1	metabolic process
0.35402	PLAU	metabolic process
0.09634	PLCB1	metabolic process
0.11674	PLCH2	metabolic process
0.09085	PLK2	metabolic process
0.13825	PNKP	metabolic process
0.61214	PNLIPRP3	metabolic process
0.24036	PNPLA7	metabolic process
0.19903	PNPT1	metabolic process
0.07697	POGK	metabolic process
0.07162	POLR2F	metabolic process
0.09881	POU2F2	metabolic process
0.32185	PPIG	metabolic process
0.28141	PPM1E	metabolic process
0.12621	PPM1K	metabolic process
0.28141	PPM1M/PPM1E	metabolic process
0.11377	PPP1R12A	metabolic process
0.01826	PPP2R2C	metabolic process
0.02783	PRKCD	metabolic process
0.02662	PRMT6	metabolic process
0.06779	PRPF4B	metabolic process
0.11671	PRRG1	metabolic process
0.02592	PSMD4	metabolic process
0.13632	PSMD9	metabolic process
0.14517	PYGO2	metabolic process
0.18157	RABGGTA	metabolic process
0.03208	RAE1	metabolic process
0.14204	RBBP6	metabolic process
0.16826	RBBP7	metabolic process
0.04825	RBCK1	metabolic process
0.54877	RBP7	metabolic process
0.15548	RFX7	metabolic process
0.0001	RNF11	metabolic process
0.16529	RNF216	metabolic process
0.15787	RNF34	metabolic process
0.32214	ROBO4	metabolic process
0.04994	ROR2	metabolic process
0.34186	RPL23A	metabolic process
0.19832	RPL26	metabolic process
0.144	RPS12	metabolic process
0.0001	RPS23	metabolic process
0.22614	SDHA	metabolic process
0.19743	SDSL	metabolic process
0.11993	SEC13	metabolic process
0.07534	SEC14L5	metabolic process
	SELI	metabolic process
	SERPINA3	metabolic process
0.14247	SHMT2	metabolic process
0.15954	SHPRH	metabolic process
0.0515	SIX6	metabolic process
0.02267	SLC22A17	metabolic process
0.0302	SLC25A23	metabolic process
0.0749	SLC35C1	metabolic process
0.27837	SLC45A2	metabolic process
0.10763	SLC5A3	metabolic process
0.07005	SLC6A4	metabolic process
0.05471	SLC7A14	metabolic process
0.06266	SLIT1	metabolic process
0.09617	SMC2	metabolic process
0.24785	SMC5	metabolic process
0.0001	SNRPA1	metabolic process
0.21479	SOAT2	metabolic process
0.06607	SPIB	metabolic process
0.14793	SQSTM1	metabolic process
0.03661	STAT5B	metabolic process
0.0001	STUB1	metabolic process
0.06703	SULF2	metabolic process
0.24717	SUSD3	metabolic process
0.0001	SUV39H1	metabolic process
0.04941	TBCB	metabolic process

uniform_ω	Gene	Level.1:.Biological.Process
0.00823	TBR1	metabolic process
0.38492	TFEC	metabolic process
0.07911	TGM1	metabolic process
0.16329	TNS3	metabolic process
0.2615	TOP3A	metabolic process
0.38503	TRAIP	metabolic process
0.1087	TRIM39	metabolic process
0.10263	TSSK2	metabolic process
0.5521	TSSK4	metabolic process
0.5884	TTF1	metabolic process
0.20965	TTLL9	metabolic process
0.31256	TXNDC11	metabolic process
0.07336	UPF2	metabolic process
0.21049	USP1	metabolic process
0.39733	USP18	metabolic process
0.90656	USP26	metabolic process
0.01015	USP7	metabolic process
0.06752	WDR33	metabolic process
0.20814	WDR5B	metabolic process
0.39106	WDR63	metabolic process
0.03828	YTHDC1	metabolic process
0.81373	ZBP1/IGF2BP1	metabolic process
0.17502	ZBTB38	metabolic process
0.87814	ZFP37	metabolic process
0.41787	ZFP57	metabolic process
0.60373	ZNF117	metabolic process
0.34854	ZNF157	metabolic process
0.46068	ZNF192	metabolic process
	ZNF197	metabolic process
0.46875	ZNF20	metabolic process
0.32765	ZNF235	metabolic process
0.07994	ZNF275	metabolic process
0.47462	ZNF30	metabolic process
0.49188	ZNF302	metabolic process
0.19381	ZNF324B	metabolic process
0.35099	ZNF528	metabolic process
0.44193	ZNF540	metabolic process
0.65825	ZNF561	metabolic process
0.14679	ZNF569	metabolic process
0.08974	ZNF570	metabolic process
0.05399	ZNF574	metabolic process
0.26699	ZNF575	metabolic process
0.12998	ZNF592	metabolic process
0.18908	ZNF625	metabolic process
0.21862	ZNF652	metabolic process
0.20302	ZNRD1	metabolic process
0.0406	ECEL1	regulation of biological processes
1.32221	NPFF	regulation of biological processes
0.06219	TBXA2R	regulation of biological processes
0.44471	ADAM29	reproduction
0.16305	ADAM9	reproduction
0.10182	ADAMTS8	reproduction
0.1641	CHRDL2	reproduction
0.02051	EPHB3	reproduction
0.28362	FLT3	reproduction
0.16507	HNRNPD	reproduction
0.19851	KLHDC4	reproduction
0.24546	LTK	reproduction
0.31908	MAGEA8	reproduction
0.75453	MAGEB3	reproduction
0.04994	ROR2	reproduction
0.1087	TRIM39	reproduction
0.064	TSPAN15	reproduction
1.69742	TSPAN8	reproduction
0.10263	TSSK2	reproduction
0.5521	TSSK4	reproduction
0.21049	USP1	reproduction
0.39733	USP18	reproduction
0.90656	USP26	reproduction
0.01015	USP7	reproduction
0.87814	ZFP37	reproduction
0.41787	ZFP57	reproduction
0.34854	ZNF157	reproduction
0.46068	ZNF192	reproduction
0.46875	ZNF20	reproduction
0.32765	ZNF235	reproduction
0.35099	ZNF528	reproduction
0.65825	ZNF561	reproduction
0.08974	ZNF570	reproduction
0.12998	ZNF592	reproduction
0.18908	ZNF625	reproduction
0.28618	ABCB11	response to stimulus
0.06569	ABHD4	response to stimulus
0.13916	AHSA1	response to stimulus
0.28034	ALOX15	response to stimulus
0.14347	C1QTNF7	response to stimulus
0.35182	CCL24	response to stimulus
0.39503	CCRL1	response to stimulus
0.7195	CD300C	response to stimulus
0.44299	CD69	response to stimulus
0.01091	CDK9	response to stimulus
0.3206	CISH	response to stimulus
0.58328	CLEC4E	response to stimulus
0.09218	CNTFR	response to stimulus
0.22552	COL20A1	response to stimulus
0.08985	COL5A2	response to stimulus
0.08145	CXCR5	response to stimulus
0.12622	DNAJC17	response to stimulus
0.16564	DNAJC24	response to stimulus
0.37881	DNAJC30	response to stimulus
0.90695	DNAJC5G	response to stimulus
0.0001	DUSP1	response to stimulus
0.23925	EBI3	response to stimulus
0.23113	ELF4	response to stimulus
0.71925	FCRL2	response to stimulus
0.28362	FLT3	response to stimulus
0.02275	FOSB	response to stimulus
0.01978	GADD45A	response to stimulus
0.08087	HRH3	response to stimulus
0.16616	HSPB2	response to stimulus
0.79254	IFNA2	response to stimulus
0.44695	IL10RA	response to stimulus
0.68451	IL19	response to stimulus
0.09154	IRF8	response to stimulus
0.14252	ITGB8	response to stimulus
0.32378	KLRG2	response to stimulus
0.98035	LAIR1	response to stimulus
0.02486	LHX2	response to stimulus
0.49329	MS4A7	response to stimulus
0.2631	MSRB2	response to stimulus
0.0573	NR1D2	response to stimulus
0.23094	NR1I3	response to stimulus
0.31658	NUP88	response to stimulus
1.0655	OAS1	response to stimulus
0.35402	PLAU	response to stimulus
0.09085	PLK2	response to stimulus
0.01826	PPP2R2C	response to stimulus
0.06779	PRPF4B	response to stimulus
0.0001	S100A4	response to stimulus
0.06607	SPIB	response to stimulus
0.14793	SQSTM1	response to stimulus
0.03661	STAT5B	response to stimulus
0.0001	STUB1	response to stimulus
0.24717	SUSD3	response to stimulus
0.1945	TACR2	response to stimulus
0.06219	TBXA2R	response to stimulus
0.18326	TNFAIP8L3	response to stimulus
0.064	TSPAN15	response to stimulus
1.69742	TSPAN8	response to stimulus
0.10263	TSSK2	response to stimulus
0.5521	TSSK4	response to stimulus
0.47646	VPREB1	response to stimulus
0.24264	ACCN1	system process
0.44471	ADAM29	system process
0.16305	ADAM9	system process
0.09743	ADRA1B	system process
0.39503	CCRL1	system process
0.19809	CHL1	system process
0.2921	CHM	system process
0.19901	CNTN6	system process

uniform_ω	Gene	Level.1:.Biological.Process
0.08985	COL5A2	system process
0.08145	CXCR5	system process
0.33835	DHRS7	system process
0.16564	DNAJC24	system process
0.37881	DNAJC30	system process
0.90695	DNAJC5G	system process
0.0406	ECEL1	system process
0.24368	GCGR	system process
0.10446	GPR176	system process
0.22396	GPR39	system process
0.0197	GRIK3	system process
0.0001	GUCA1B	system process
0.16507	HNRNPD	system process
0.08087	HRH3	system process
0.28111	HSD17B3	system process
0.16616	HSPB2	system process
0.02316	KCNB1	system process
0.04569	KCNG2	system process
0.03396	KCNJ9	system process
0.15996	LDB3	system process
0.15342	LPAR3	system process
0.40455	MRGPRD	system process
0.08977	MRGPRE	system process
0.11479	MYL6B	system process
0.02587	NLGN3	system process
1.32221	NPFF	system process
0.11288	NPFFR1	system process
0.0435	NPY1R	system process
0.06886	NPY5R	system process
0.03019	NR2C2	system process
0.04162	PCDH7	system process
0.08239	PITPNM1	system process
0.07234	PLP1	system process
0.24036	PNPLA7	system process
0.31202	RAB17	system process
0.16529	RNF216	system process
0.32214	ROBO4	system process
0.07308	S1PR3	system process
0.04253	SCN1B	system process
0.19743	SDSL	system process
0.07227	SLC24A4	system process
0.07005	SLC6A4	system process
0.06266	SLIT1	system process
0.13497	STX2	system process
0.02962	SV2B	system process
0.1945	TACR2	system process
0.01342	TAGLN	system process
0.06219	TBXA2R	system process
0.1087	TRIM39	system process
0.064	TSPAN15	system process
1.69742	TSPAN8	system process
0.10263	TSSK2	system process
0.5521	TSSK4	system process
0.57975	TTC29	system process
0.14659	UNC13C	system process
0.81373	ZBP1/IGF2BP1	system process
0.28618	ABCB11	transport
0.13009	ABCD3	transport
0.24264	ACCN1	transport
0.08569	APC2/APOC2	transport
0.05611	ARCN1	transport
0.11307	ARL6IP1	transport
0.31252	ARV1	transport
0.31096	ATP10D	transport
0.30585	BET1	transport
0.14347	C1QTNF7	transport
0.33835	CACNG8/CACN(	transport
0.03265	CAV1	transport
0.7195	CD300C	transport
0.2921	CHM	transport
0.0001	CHMP5	transport
0.3206	CISH	transport
0.05529	CLCN4	transport
0.58328	CLEC4E	transport
0.22552	COL20A1	transport

uniform_ω	Gene	Level.1:.Biological.Process
0.08985	COL5A2	transport
0.04779	CORO1C	transport
0.00665	CYTH1	transport
0.31257	DDHD2	transport
0.15138	DNAI2	transport
0.16564	DNAJC24	transport
0.37881	DNAJC30	transport
0.90695	DNAJC5G	transport
0.07754	DSCR3	transport
0.04897	ERC1	transport
0.11806	FOLR2	transport
0.58545	FXYD3	transport
0.0197	GRIK3	transport
0.0704	JAG2	transport
0.02316	KCNB1	transport
0.04569	KCNG2	transport
0.03396	KCNJ9	transport
0.32378	KLRG2	transport
0.76638	LRPPRC	transport
0.07245	MEGF10	transport
0.15926	MPZL2	transport
0.29918	MTG1	transport
0.31658	NUP88	transport
0.0001	NXT1	transport
0.08239	PITPNM1	transport
0.32185	PPIG	transport
0.31202	RAB17	transport
0.16826	RBBP7	transport
0.54877	RBP7	transport
0.00865	RHOB	transport
0.04253	SCN1B	transport
0.11993	SEC13	transport
0.07534	SEC14L5	transport
0.08908	SLC16A8	transport
0.02267	SLC22A17	transport
0.07227	SLC24A4	transport
0.0302	SLC25A23	transport
0.27658	SLC31A1	transport
0.0749	SLC35C1	transport
0.27837	SLC45A2	transport
0.11363	SLC4A4	transport
0.10763	SLC5A3	transport
0.07005	SLC6A4	transport
0.05471	SLC7A14	transport
0.08137	SOCS4	transport
0.13497	STX2	transport
0.34558	SYNJ2BP	transport
0.05219	TBC1D17	transport
0.0128	TBC1D9	transport
0.04941	TBCB	transport
0.06219	TBXA2R	transport
0.06661	TMED4	transport
0.38503	TRAIP	transport
0.1087	TRIM39	transport
0.0886	TTYH1	transport
0.16238	TUBB	transport
0.14659	UNC13C	transport
0.07923	VPS52	transport
0.09537	WDFY2	transport
0.39106	WDR63	transport

Appendix 3: Sequence alignments from Chapter 4

Sequence alignment of the 5' putative proximal promoter region of the hominoids used in the *in vitro* expression study

```
SEMG1_Human           AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAA 60
SEMG1_Chimpanzee      AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAA 60
SEMG1_Bonobo          AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAA 60
SEMG1_Gorilla         AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAA 60
SEMG1_Orangutan       AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTGTCTAA 60
SEMG1_Gibbon          AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAA 60
SEMG1_Macaque         AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGCGTTCTATCTAA 60
SEMG2_Human           AAAACAGAATGTGTCTCAGGATTACTTT-AAAACAAGACAAAGTATAGAGTTATACCTAA 59
SEMG2_Chimpanzee      AAAACAGAATGTGTCTCAGGATTACTTT-AAAACAAGACAAAGGATAGAGTTATACCTAA 59
SEMG2_Bonobo          AAAACAGAATGTGTCTCAGGATTACTTT-AAAACAAGACAAAGGATAGAGTTATACCTAA 59
SEMG2_Gorilla         AAAACAGAATGTGTCTCAGGATTACTTT-AAAACAAGACAAAGTATAGAGTTATACCTAA 59
SEMG2_Orangutan       AAAACAGAATGTGTCTCAGGATTACTTT-AAAACAAGACGAAGTACAGAGTTATACCTAA 59
SEMG2_Gibbon          AAAACAGAATGTGTCTCAGGATTATTTT-AAAACAAGACAAAGTATA--GTTATATCTAA 57
SEMG2_Macaque         AAAACAGAATGTGTCTCAGGATTATTTT-AAAACAAGATGAAGTACAGAGTTATACCTAA 59
                      **** **** ******** *** * *** ******* *  *** *    *** *  ****

SEMG1_Human           AATAGAGTATTTAAATTATTGCATCATGAAGGGAAACTCACATTTAGAATATAAAGGCAT 120
SEMG1_Chimpanzee      AATAGAGTATTTAAATTGTTGCATCATGAAGGGAAACTCACATTTAGAATATAAAGGCAT 120
SEMG1_Bonobo          AATAGAGTATTTAAATTGTTGCATCATGAAGGGAAACTCACATTTAGAATATAAAGGCAT 120
SEMG1_Gorilla         AATAGAATATTTAAATTATTGCATCATGAAGGGAAACTCACATTTAGAATATAAAGGCAT 120
SEMG1_Orangutan       AATAGAGTATTTAAATTATTACATCATGAAGGGAAACTCACATTTAGAATATAAAGGCAT 120
SEMG1_Gibbon          AACAGAGTATTTAAATTATTGCATCATGAAGGGAAACTCACTTTTAGAATATAAAGGCAT 120
SEMG1_Macaque         AATAGAATATTTAATTTATTACATCATGAAGGCAAACTCACATTTAGAATATAAAGGCAT 120
SEMG2_Human           AATTTAGTATTTAAGTTATTGGATCA-GAAAGGAAACTCGCATTTAGAGTATGAAGGCAT 118
SEMG2_Chimpanzee      AATTTAATATTTAAGTTATTGCATCA-GAAAGGAAACTCGCATTTAGAATATGAAGGCAT 118
SEMG2_Bonobo          AATTTAGTATTTAAGTTATTGCATCA-GAAAGGAAACTCGCATTTAGAGTATGAAGGCAT 118
SEMG2_Gorilla         AATTTAGTATTTAAGTTATTGCATCA-GAAAGGAAACTCGCATTTAGAGTATGAAGGCAT 118
SEMG2_Orangutan       AATGTAGTATTTAAGTTACTGCATCA-GAAAGGAAACTCGCATTTAGAGTATGAAGGCAT 118
SEMG2_Gibbon          AATTGAGTATTTAAGTTATTGCATCA-GAAAGGAAACTCACATTTAAAATATGAAGGCAT 116
SEMG2_Macaque         AATTGAGTATTTAAGTGATGGCATCA-GAAAGGAAACTC-CATTTAGAATATGAAGGCAT 117
                      **   * ******* *      **** *** * ****** * **** * *** *******

SEMG1_Human           TCTCAGAAACCAATTGCTTTTGTAGCCTGAAGCCAGTCTCTTTCCTACTTTTGTCTATAA 180
SEMG1_Chimpanzee      TCTCAGAAACCAATTGCTTTTGTAGCCCGAAGCCAGTCTCTTTCCTACTTTTGTCTATAA 180
SEMG1_Bonobo          TCTCAGAAACCAATTGCTTTTGTAGCCCGAAGCCAGTCTCTTTCCTACTTTTGTCTATAA 180
SEMG1_Gorilla         TCTCAGAAACCAATTGCTTTTGTAGCCTGAAGCCAGTCTCTTTCCTACTTTTGTCTATAA 180
SEMG1_Orangutan       TCTCAGAAACCAATTGCTTTTGTAGCCTGAAGCTAGTCTCTTTCCTACTTTTGTCTATAA 180
SEMG1_Gibbon          TCTCAGAAACCAATTGCTTTTGTAGCCTGAAGCTAGTCTCTTTCCTACTTTTGTCTGTAA 180
SEMG1_Macaque         TCTCAGAAACCAATTACTTTTGTAGCCTGAAGCTAATCTCTTTCCTACTTTCATCTAAAA 180
SEMG2_Human           TGTCAGCCACCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCGGACTGAAT 178
SEMG2_Chimpanzee      TGTCAGCCACCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCAGACTGAAT 178
SEMG2_Bonobo          TGTCAGCCACCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCAGACTGAAT 178
SEMG2_Gorilla         TGTCAGCCAYCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCAAACTGAAT 178
SEMG2_Orangutan       TGTCAGCCACCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCTGGACTGAAT 178
SEMG2_Gibbon          TGTCAGCCACCAATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCGGACTGAAT 176
SEMG2_Macaque         AGTCAGCCACCAGTTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCGGACTGAAT 177
                        ****  * ** ** ******** ** ***** * **** ********     **  *

SEMG1_Human           ---TTCTGTAAAATTAAAGTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGC 237
SEMG1_Chimpanzee      ---TTCTGTAAAATTAAAGTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGC 237
SEMG1_Bonobo          ---TTCTGTAAAATTAAAGTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGC 237
SEMG1_Gorilla         ---TTCTGTAAAATTAAAGTGATCTGGCATGATGATCTAAAAGGACTGACAAAAATTTGC 237
SEMG1_Orangutan       ---TTCCGTAAAATGAAAGTGAGC-GGCATGATGATCTACAAGGACTGATAAAAATTTGC 236
SEMG1_Gibbon          ---TTCCATAAAATGAAAGTGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGC 237
SEMG1_Macaque         ---TTCCGTAAAATGCAAGTGATCTGGCATGATGATCAACAAGGACTGATAAAAATTTGC 237
SEMG2_Human           TTCTTCTGTATAATGCAAGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGC 238
SEMG2_Chimpanzee      TTCTTCTGTATAATGCAAGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGC 238
SEMG2_Bonobo          TTCTTCTGTATAATGCAAGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGC 238
SEMG2_Gorilla         TTSTTCTGTATAATGCAAACGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGC 238
```

```
SEMG2_Orangutan       TTCTTCTGTATAATGCAAGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGC 238
SEMG2_Gibbon          TTCTTCTGTATAATGCAAGTGATCTGGCATGAAGATATACAAAGACTGATAAAATTTTGC 236
SEMG2_Macaque         GTCTTCTGTGTAATGCAAGCGATCTGGCTTGATGATATACAAGGACCGATAAAATTTTGC 237
                         ***  *  ***  **  ** * *** *** ***  * ** *** ** **** *****



SEMG1_Human           TGGGGCTGCCAGAAG-AAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG1_Chimpanzee      TGGGGCTGCCAGAAG-AAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG1_Bonobo          TGGGGCTGCCAGAAG-AAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG1_Gorilla         TGGGGCTGCCAGAAG-GAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG1_Orangutan       TGGGGCTTCCAGAAG-AAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 280
SEMG1_Gibbon          TGGGGCTTCCAGAAG-AAAGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG1_Macaque         TGAGGCTTCCAGAAG-AAGGAAAA--TGCCTTTGACATTATGT-----TG--------CT 281
SEMG2_Human           TGGGGATTCTGAAAGTAAAAAAAA-TTGCCTTTGATATTATGTCCCCATGCTAAGTCCCT 297
SEMG2_Chimpanzee      TGGGGATTCTGGAAGTAAAAAAAA-TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCT 297
SEMG2_Bonobo          TGGGGATTCTGGAAGTAAAAAAAA-TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCT 297
SEMG2_Gorilla         TGGGGATTCTGGAAGTAAAAAAAAATTGCCTTTGACATTATGTCCCCATGCTAAGTCCCT 298
SEMG2_Orangutan       TGGGGATTCTGGAAGTAAAAAAAA-TTGCCTTTAACATTATGTCCCCATGCTAAGTCCCT 297
SEMG2_Gibbon          TGGGGATTCTGGAAGTAAAAAAAA-TTGCCTTTGACATTATGTTCCCATGCTAAGTCCCT 295
SEMG2_Macaque         TGGGGATTCTGGAAGCAAAAAAAAATTGCCTTTGACATTATGTCCCCTTGCTAAGTCCCT 297
                      ** ** * *   ***  *  ****  ******* * *******     **        **

SEMG1_Human           GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAG 341
SEMG1_Chimpanzee      GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAG 341
SEMG1_Bonobo          GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAG 341
SEMG1_Gorilla         GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAG 341
SEMG1_Orangutan       GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGACATTTACTGATAAG 340
SEMG1_Gibbon          GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAG 341
SEMG1_Macaque         GGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAA 341
SEMG2_Human           GGGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGCTGGCATTTACTAATAAG 357
SEMG2_Chimpanzee      GGGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTTACTAATAAG 357
SEMG2_Bonobo          GGGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTTACTAATAAG 357
SEMG2_Gorilla         GGGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTTACTAATAAG 358
SEMG2_Orangutan       GGGGACTTTGACATTATTCCCCACTGAGCAGGGGCGAGGAAGTTGGCATTTACTAATAAG 357
SEMG2_Gibbon          GGGAACTTTGACATTATCTCCCACTGAGCAGGGGCGAYGAAGTTGGCATTTACTAATAAG 355
SEMG2_Macaque         GGGGACTTTGACATTATCCCCCACTGAGCAGTGGCGAGGAAGTTGGCATTTACTAATAAG 357
                      *** ** ***** ** *  * **** ***** ** ** **** ** ******** ****

SEMG1_Human           CTAAGAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACTCAAGGA 401
SEMG1_Chimpanzee      CTAAGAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTTACTCAAGGA 401
SEMG1_Bonobo          CTAAGAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTTACTCAAGGA 401
SEMG1_Gorilla         CTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACTCAAGGA 401
SEMG1_Orangutan       CTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACTCAAGGA 400
SEMG1_Gibbon          CTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCATCCATGGCACACTCACTCAAGGA 401
SEMG1_Macaque         CTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACCTTCACTCAAGGA 401
SEMG2_Human           CTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCATAGCACACCCACTCAAGGA 417
SEMG2_Chimpanzee      CTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCATAGCACACCCACTCAAGGA 417
SEMG2_Bonobo          CTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCATAGCACACCCACTCAAGGA 417
SEMG2_Gorilla         CTATGAAAGGGCAGTACCTTTTGACATTTCAGCTCCACCCATAGCACACCCACTCAAGGA 418
SEMG2_Orangutan       CTATGAAAGGGCAGTGCCTTTTCACATTTCAGCTCCACCCATGGCACACCCACTCAAGGA 417
SEMG2_Gibbon          CTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCATGGCACACCCACTCAAGGA 415
SEMG2_Macaque         CTATGAAAGGGGGGAGCCTTTTGACATTTCAGCTCCACCCATGGCACACCCACTCAAGGA 417
                      *** **** *   *  ******   **** ******* **** ****    *********

SEMG1_Human           AGATATAAATGACAAGGTCGGCTCAGCTCTCAGACAAGGTTTTCCAAGCAAGATGAAGCC 461
SEMG1_Chimpanzee      AGATATAAATTACAAGGTCCGCTCAGCTCTCAGACAAGGTTTTCCAAGCAAGATGAAGCC 461
SEMG1_Bonobo          AGATATAAATGACAAGGTCCGCTCAGCTCTCAGACAAGGTTTTCCAAGCAAGATGAAGCC 461
SEMG1_Gorilla         AGATATAAATGACAAGGTCCGCTCAGCTGTCAGACAAGGTTTTCCAAGCAAGATGAAACC 461
SEMG1_Orangutan       AGATATAAATGACAAGGTCCGCTCAGTTCTCAGACAAGGTTTTTCAAGCAAGATGAAGCC 460
SEMG1_Gibbon          AGATATAAATGACAAGGTCTGCTTAGCTCTCAGACAAGGTTTGCCAAGCAAGATGAAGCC 461
SEMG1_Macaque         AGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGCTTTCCAAGCAAGATGAAGCC 461
SEMG2_Human           ACATATAAATGAAGAGATCCGCTCAGTTCTCAGACAAGATTTTTCAAGCAAGATGAAGTC 477
SEMG2_Chimpanzee      ACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAAGATTTTTCAAGCAAGATGAAGTC 477
SEMG2_Bonobo          ACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAAGATTTTTCAAGCAAGATGAAGTC 477
```

```
SEMG2_Gorilla         ACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAAGATTTTTCAAGCAAGATGAAGTC 478
SEMG2_Orangutan       ACATATAAATGAAGAGATCCGCTGAGCTCTCAGACAAGATTTTTCAAGCAAGATGAAGTC 477
SEMG2_Gibbon          ACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAAGATTTTTCGAGCAAGATGAAGTC 475
SEMG2_Macaque         ACATATAAATGA-GAGATCCCCTCCGGTCTCAGACAAGATTTTTCAAGCAAAATGAAGTC 476
                      * ******** *  ** **  **  * * *********  **  * ***** *****  *
```

```
SEMG1_Human           CAACATCATCTTTGTACTTT--- 481
SEMG1_Chimpanzee      CAACATCATCTTTGTACTTT--- 481
SEMG1_Bonobo          CAACATCATCTTTGTACTTT--- 481
SEMG1_Gorilla         CAACATCATCTTTGTACTTT--- 481
SEMG1_Orangutan       CAACATCATCTTTGTACTTT--- 480
SEMG1_Gibbon          CAACATCATCTTTGTACTTT--- 481
SEMG1_Macaque         CAACATCATCTTTGTACTTT--- 481
SEMG2_Human           CATCATCCTCTTTGTCCTTTCCC 500
SEMG2_Chimpanzee      CATCATCCTCTTTGTCCTTTCCC 500
SEMG2_Bonobo          CATCATCCTCTTTGTCCTTTCCC 500
SEMG2_Gorilla         CATCATCCTCTTTGTCCTTTCCC 501
SEMG2_Orangutan       CATCATCCTCTTTGTCCTTTCCC 500
SEMG2_Gibbon          CATCATCCTCTTTGTCCTTTCCC 498
SEMG2_Macaque         CATCATCCTCTTTGTCCTTTCCC 499
                      ** **** ******* ****
```

All species *SEMG1* alignment

Seqeunce alignment of *SEMG1* sequences generated in house for *in vitro* study in combination with species data obtained from Hurle et al. (2007, through GENBANK)

```
SEMG1_Human                     AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Chimpanzee                AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Bonobo                    AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Gorilla                   AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Orangutan                 AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Gibbon                    AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Macaque                   AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Papio_anubis              AAAATAGATCGTGTCTCAAGATCATTTTTAAAACAAAAGGA--AGTATGG 48
SEMG1_Chlorocebus_aethiops      AAAATAGATCGTGTCTCAAGATCATTTTTAAGACAAAAGGA--AGTATGG 48
SEMG1_Colobus_guereza           AAAATAGAACGTGTCTCAAGACCATTTTTAAAACAAGAGGA--AGTATGG 48
SEMG1_Saguinus_oedipus          AAAATAGAATGTGTCTCAAGATCATTTTTAAAACAAAAAAAAAAGTATGG 50
SEMG1_Callithrix_jacchus        AAAATAGAATGTGTCTCAAGATCATTTTTAAAACAAAAAAA--AGTATGG 48
SEMG1_Saimiri_boliviensis       AAAATAGAATGTGTCTCAAGATCATTTTTAAAACAAAAAAA---GTATGA 47
Aotus_nancymaae_SEMG            AAAATAGAATGTGTCTCAAGATCATTTTTAAACCAAAAAAA--AGTATGG 48
                                ********  *********** *********  *** *  *   ***** 

SEMG1_Human                     AGTTCTATCTAAAATAGAGTATTTAAATTATTGCATCATGAAGGGAAACT 98
SEMG1_Chimpanzee                AGTTCTATCTAAAATAGAGTATTTAAATTGTTGCATCATGAAGGGAAACT 98
SEMG1_Bonobo                    AGTTCTATCTAAAATAGAGTATTTAAATTGTTGCATCATGAAGGGAAACT 98
SEMG1_Gorilla                   AGTTCTATCTAAAATAGAATATTTAAATTATTGCATCATGAAGGGAAACT 98
SEMG1_Orangutan                 AGTTCTGTCTAAAATAGAGTATTTAAATTATTACATCATGAAGGGAAACT 98
SEMG1_Gibbon                    AGTTCTATCTAAAACAGAGTATTTAAATTATTGCATCATGAAGGGAAACT 98
SEMG1_Macaque                   CGTTCTATCTAAAATAGAATATTTAATTTATTACATCATGAAGGCAAACT 98
SEMG1_Papio_anubis              CGTTCTATCTAAAATAGAATATTTAATTTATTACATCATGAAGGCAAACT 98
SEMG1_Chlorocebus_aethiops      AGTTCTATCTAAAATAGAATATTTAATGTATTACATCATGAAGGCAAACT 98
SEMG1_Colobus_guereza           AGTTCTATCTAAAATAGAATATTTAATTTATTACATCATGAAGGCAAACT 98
SEMG1_Saguinus_oedipus          AGTTCTATCTAAAATAGAGTATTTAAATTATTATACCATAAAGGGAAACT 100
SEMG1_Callithrix_jacchus        AGTTCTATCTA-----GAGTATTTAAATTATTATACCATAAAGGAAAACT 93
SEMG1_Saimiri_boliviensis       AGTTCTATCTAAAATAGAGTATTTAAATTATTATACCATAAAGAGAAACT 97
Aotus_nancymaae_SEMG            AGTTCTACCTAAAATAGAGTATTTAAATTATTATACCATAAAGGGAAACT 98
                                 *****  ***     ** *******  * **  * *** ***  ***** 

SEMG1_Human                     CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCT 148
SEMG1_Chimpanzee                CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCC 148
SEMG1_Bonobo                    CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCC 148
SEMG1_Gorilla                   CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCT 148
SEMG1_Orangutan                 CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCT 148
SEMG1_Gibbon                    CACTTTTAGAATATAAAGGCATTCTCAGAAACCAATTGCTTTTGTAGCCT 148
SEMG1_Macaque                   CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTACTTTTGTAGCCT 148
SEMG1_Papio_anubis              CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTACTTTTGTAGCCT 148
SEMG1_Chlorocebus_aethiops      CACATTTAGAACATAAAGGCATTCTCAGAAACCAATTACTTTTGTAGCCT 148
SEMG1_Colobus_guereza           CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTACTTTTGTAGCCT 148
SEMG1_Saguinus_oedipus          CACATTTAGAATATAAAGGCATTCTCAGAAACCAATTACTTT-GTAACCT 149
SEMG1_Callithrix_jacchus        CACATTTAGAATATAAAGGCATTCTCAGAAACCAATCACTTT-GTAACCT 142
SEMG1_Saimiri_boliviensis       CACATTTAGAATATAAAGGCGTTCTCAGAAACCAATTACTTT-GTAACCT 146
Aotus_nancymaae_SEMG            CACATTTAGAATATAAAGGCGTCCTCAGAAACAAATTACTTT-GTAACCT 147
                                *** ******* ******** * ********* ***  **** *** ** 

SEMG1_Human                     GAAGCCAGT---CTCTTTCCTACTTTTGTCTATAATTCTGTAAAATTAAA 195
SEMG1_Chimpanzee                GAAGCCAGT---CTCTTTCCTACTTTTGTCTATAATTCTGTAAAATTAAA 195
SEMG1_Bonobo                    GAAGCCAGT---CTCTTTCCTACTTTTGTCTATAATTCTGTAAAATTAAA 195
SEMG1_Gorilla                   GAAGCCAGT---CTCTTTCCTACTTTTGTCTATAATTCTGTAAAATTAAA 195
SEMG1_Orangutan                 GAAGCTAGT---CTCTTTCCTACTTTTGTCTATAATTCCGTAAAATGAAA 195
SEMG1_Gibbon                    GAAGCTAGT---CTCTTTCCTACTTTTGTCTGTAATTCCATAAAATGAAA 195
SEMG1_Macaque                   GAAGCTAAT---CTCTTTCCTACTTTCATCTAAAATTCCGTAAAATGCAA 195
SEMG1_Papio_anubis              GAAGCTAAT---CTCTTTCCTACTTTCGTCTAAAATTCCGTAAAATGCAA 195
SEMG1_Chlorocebus_aethiops      GAAGCTAAT---CTCTTTCCTACTTTCGTCTAAAATTCCGTAAAACGCAA 195
SEMG1_Colobus_guereza           GAAGCTAAT---CTCTTTCCTACTTTCGTCTAAAATTCTGTAAAATGCAA 195
SEMG1_Saguinus_oedipus          GAAGTTAGTTTACTCTTTCCTACTTCTGTCTATACTTCCATAAAATGAAA 199
SEMG1_Callithrix_jacchus        GAAGTTAGT---CTCTTTCCTGCTTTTGTCTATAGTTCCATAAAATGCAA 189
```

```
SEMG1_Saimiri_boliviensis       AAAGTTAGT---CTCTTTCCTCCTTTTGTCTATACTTCCATAAAATACAA 193
Aotus_nancymaae_SEMG            GAAGTTAGT---CTCTTTCCTACTTTTGTCTATACGTCCATAAAATGCAA 194
                                 ***  * *   ********* ***   ***  *  **  *****   **


SEMG1_Human                     GTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGCTGGGGCTG 245
SEMG1_Chimpanzee                GTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGCTGGGGCTG 245
SEMG1_Bonobo                    GTGATCTGGCATGATGATCTAAAAGGACTGATAAAAATTTGCTGGGGCTG 245
SEMG1_Gorilla                   GTGATCTGGCATGATGATCTAAAAGGACTGACAAAAATTTGCTGGGGCTG 245
SEMG1_Orangutan                 GTGAGC-GGCATGATGATCTACAAGGACTGATAAAAATTTGCTGGGGCTT 244
SEMG1_Gibbon                    GTGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGCTGGGGCTT 245
SEMG1_Macaque                   GTGATCTGGCATGATGATCAACAAGGACTGATAAAAATTTGCTGAGGCTT 245
SEMG1_Papio_anubis              GTGATCTGGCATGATGATCAACAAGGACTGATAAAAATTTGCTGAGGCTT 245
SEMG1_Chlorocebus_aethiops      GTGATCTGGCATGATGATCAAAAAGGACTGATAAAGATTTGCTGAGGCTT 245
SEMG1_Colobus_guereza           ATGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGCTGAGGCTT 245
SEMG1_Saguinus_oedipus          GTGATCTGGCATGATAATCTACAAGGACTCACAAACATTTGCTGTGGCTT 249
SEMG1_Callithrix_jacchus        GTGATCTGGCATGATAATCTACAAGGACTCATAAACATTTGCTGTGGCTT 239
SEMG1_Saimiri_boliviensis       ATGATCTGGCATGATAATCTACAAGGACTCATAAAAATTTGCTGTGGCTT 243
Aotus_nancymaae_SEMG            GTGATCTG-CATGATAATCTACAAGGACTCATAAAAATTTGCTGTGGCTT 243
                                 *** * * ****** *** * ******* * *** ******** ****

SEMG1_Human                     CCAGAAGAAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Chimpanzee                CCAGAAGAAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Bonobo                    CCAGAAGAAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Gorilla                   CCAGAAGGAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Orangutan                 CCAGAAGAAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 294
SEMG1_Gibbon                    CCAGAAGAAAGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Macaque                   CCAGAAGAAGGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Papio_anubis              CCAGAAGAAGGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Chlorocebus_aethiops      CCAGAAGAAGGAAAATGCCTTTGACATTATGTTGCTGGGGACATTGACTT 295
SEMG1_Colobus_guereza           CCAGAAGAAGGAAAATGCCTTTGACATTACGTTGCTGGGGACATTGACTT 295
SEMG1_Saguinus_oedipus          CCAGAAGAAAGAAAATGCCTTTGACATTATGTCGCTGGGGACATTGACT- 298
SEMG1_Callithrix_jacchus        CCAGAAGAAAGAAAATGCCTTTGACATTATGTCACTGGGGACATTGACT- 288
SEMG1_Saimiri_boliviensis       CCAGAAGAAAGAAAATGACTTTGACATTATGTGGCTGGGGACATTGACT- 292
Aotus_nancymaae_SEMG            CCAGAAGAAAGAAAATGCCTTTGACGTTATGTCGTTGGGGGCATTGACT- 292
                                ******* * ******* ******* *** **   ***** ********

SEMG1_Human                     TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Chimpanzee                TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Bonobo                    TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Gorilla                   TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Orangutan                 TGTCCCACACTCAGCAGGGGTGAGGAAGTTGACATTTACTGATAAGCTAA 344
SEMG1_Gibbon                    TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Macaque                   TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAACTAA 345
SEMG1_Papio_anubis              TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAACTAA 345
SEMG1_Chlorocebus_aethiops      TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Colobus_guereza           TGTCCCACACTCAGCAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAA 345
SEMG1_Saguinus_oedipus          -ATCTCATACTCAGCAGGGGTGAGGAAGTTTCCATTTACTGATAAGCTAA 347
SEMG1_Callithrix_jacchus        -ACCTCATACTCAGCAGGGGTGAGGAAGTTTCCATTTACTGATAAGCTAA 337
SEMG1_Saimiri_boliviensis       -ATCTCATACTCAGCAGGGGTGAGGAAGTTTCCATTTACTGATAAGCTAA 341
Aotus_nancymaae_SEMG            -ATGTCATACTCAGCAGGGGTGAGGAAGTTTCCATTTACTGATAAGCTAA 341
                                     ** **********************  ************* ****

SEMG1_Human                     GAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACT 395
SEMG1_Chimpanzee                GAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTTACT 395
SEMG1_Bonobo                    GAAAAGTCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTTACT 395
SEMG1_Gorilla                   GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACT 395
SEMG1_Orangutan                 GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACACTCACT 394
SEMG1_Gibbon                    GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCATCCATGGCACACTCACT 395
SEMG1_Macaque                   GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACCTTCACT 395
SEMG1_Papio_anubis              GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACCTTCACT 395
SEMG1_Chlorocebus_aethiops      GAAAAGGCAGTGCCTTTTGTAATTTAATCTCCACCCATGACACATTCACT 395
SEMG1_Colobus_guereza           GAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACATTCACT 395
SEMG1_Saguinus_oedipus          GAAAAGGCAAGGTCTTTCGTAATTTAAGCTCCACCCGTGGCACATGCACT 397
SEMG1_Callithrix_jacchus        GAAAAGGCAAGACCTTTCATAATTTAAGTTCCACCCGTGGCACAAGCACT 387
```

```
SEMG1_Saimiri_boliviensis       GAAAAGGCAATGTTTTTCGTAATTTAAGCTCCACCCATGGCACATGCACT 391
Aotus_nancymaae_SEMG            GAAAAGGCAATGCCTTTCGTAATTTAAGCTCCACCCGTGGCACATGCACT 391
                                ****** **     ***  ********  **** ** ** ***    ***
```

```
SEMG1_Human                     CAAGGAAGATATAAATGACAAGGTCGGCTCAGCTCTCAGACAAGGTTTTC 445
SEMG1_Chimpanzee                CAAGGAAGATATAAATTACAAGGTCCGCTCAGCTCTCAGACAAGGTTTTC 445
SEMG1_Bonobo                    CAAGGAAGATATAAATGACAAGGTCCGCTCAGCTCTCAGACAAGGTTTTC 445
SEMG1_Gorilla                   CAAGGAAGATATAAATGACAAGGTCCGCTCAGCTGTCAGACAAGGTTTTC 445
SEMG1_Orangutan                 CAAGGAAGATATAAATGACAAGGTCCGCTCAGTTCTCAGACAAGGTTTTT 444
SEMG1_Gibbon                    CAAGGAAGATATAAATGACAAGGTCTGCTTAGCTCTCAGACAAGGTTTGC 445
SEMG1_Macaque                   CAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGCTTTC 445
SEMG1_Papio_anubis              CAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGCTTTC 445
SEMG1_Chlorocebus_aethiops      CAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACCAGGCTTTC 445
SEMG1_Colobus_guereza           CAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGCTTTC 445
SEMG1_Saguinus_oedipus          CAAGGAAAATATAAATGACAAGGTCCACTCGACTCTCAGACAAGGTTTTT 447
SEMG1_Callithrix_jacchus        CAAGGAAAATATAAATGACATGGTCCACTCGACTCTCAGACAAGGTTTTC 437
SEMG1_Saimiri_boliviensis       CAAGAAAAATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGTTTTC 441
Aotus_nancymaae_SEMG            CAAGGAAAATATAAATGACAAGATCCACTCTACTCTGAGACAAGGTTTTC 441
                                **** ** ******** *** * **  **    * * **** *** **
```

```
SEMG1_Human                     CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 481
SEMG1_Chimpanzee                CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 481
SEMG1_Bonobo                    CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 481
SEMG1_Gorilla                   CAAGCAAGATGAAACCCAACATCATCTTTGTACTTT--- 481
SEMG1_Orangutan                 CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 480
SEMG1_Gibbon                    CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 481
SEMG1_Macaque                   CAAGCAAGATGAAGCCCAACATCATCTTTGTACTTT--- 481
SEMG1_Papio_anubis              CAAGCAAGATGAAGCCCAACATCATCTTCGTACTTT--- 481
SEMG1_Chlorocebus_aethiops      CAAGCAAGATGAAGCCCAACATCATCTTCGTACTTT--- 481
SEMG1_Colobus_guereza           CAAGCAAGATGAAGCCCAACATCATCTTCGTACTTT--- 481
SEMG1_Saguinus_oedipus          CAAGCAAGATGAAGCCCATCATCTTTCTCGTACTTT--- 483
SEMG1_Callithrix_jacchus        CAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTT--- 473
SEMG1_Saimiri_boliviensis       CAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTT--- 477
Aotus_nancymaae_SEMG            CAAGCAAGATGAAGCCCATCATCTTCTTTGTACTTTCCC 480
                                ************* **** **** *  * *******
```

All species *SEMG2* alignment

Seqeunce alignment of *SEMG2* sequences generated in house for *in vitro* study in combination with species data obtained from Hurle et al. (2007, through GENBANK)

```
SEMG2_Human                     AAAACAGAATGTGTCTCAGGATTACTTTAAAACAAGACAAAGTATAGAGT 50
SEMG2_Chimpanzee                AAAACAGAATGTGTCTCAGGATTACTTTAAAACAAGACAAAGGATAGAGT 50
SEMG2_Bonobo                    AAAACAGAATGTGTCTCAGGATTACTTTAAAACAAGACAAAGGATAGAGT 50
SEMG2_Gorilla                   AAAACAGAATGTGTCTCAGGATTACTTTAAAACAAGACAAAGTATAGAGT 50
SEMG2_Orangutan                 AAAACAGAATGTGTCTCAGGATTACTTTAAAACAAGACGAAGTACAGAGT 50
SEMG2_Gibbon                    AAAACAGAATGTGTCTCAGGATTATTTTAAAACAAGACAAAGTATA--GT 48
SEMG2_Macaque                   AAAACAGAATGTGTCTCAGGATTATTTTAAAACAAGATGAAGTACAGAGT 50
SEMG2_Papio_anubis              AAAACAGAATATATCTCAGGATTATTTTAAAACAAGATGAAGTACAGAGT 50
SEMG2_Chlorocebus_aethiops      AAAACAGAATGCATCTCAGGATTATTTTAAAACAAGATGAAGTACAGAGT 50
SEMG2_Colobus_guereza           AAAACAGAATGCATCTCAGGATTATTTTAAAACAAGGTGAAGTACAGAGT 50
SEMG2_Callithrix_jacchus        AAAACAGAATGTGTCTTAGGATTATTTTAAAACAAGACAAAATACAGAGT 50
SEMG2_Saimiri_boliviensis       AAAACAGAATGTGTCTTAGGATTATTTTAAAACAAGACGAAGTACAGAGT 50
                                **********   *** ******* **********   **  * *  **

SEMG2_Human                     TATACCTAAAATTTAGTATTTAAGTTATTGGATCAGAAAGGAAACTCGCA 100
SEMG2_Chimpanzee                TATACCTAAAATTTAATATTTAAGTTATTGCATCAGAAAGGAAACTCGCA 100
SEMG2_Bonobo                    TATACCTAAAATTTAGTATTTAAGTTATTGCATCAGAAAGGAAACTCGCA 100
SEMG2_Gorilla                   TATACCTAAAATTTAGTATTTAAGTTATTGCATCAGAAAGGAAACTCGCA 100
SEMG2_Orangutan                 TATACCTAAAATGTAGTATTTAAGTTACTGCATCAGAAAGGAAACTCGCA 100
SEMG2_Gibbon                    TATATCTAAAATTGAGTATTTAAGTTATTGCATCAGAAAGGAAACTCACA 98
SEMG2_Macaque                   TATACCTAAAATTGAGTATTTAAGTGATGGCATCAGAAAGGAAACTC-CA 99
SEMG2_Papio_anubis              TATACCTAAA-TTGAGTATTTAAGTGATGGCATCAGAAAGGAAAC-C-CA 97
SEMG2_Chlorocebus_aethiops      TATACCTAAA-TTGAGTATTTAAGTGATGGCATCAGAAAAGAAAC-C-CA 97
SEMG2_Colobus_guereza           TATACCTAAAATTGAGTATTTAAGTGATGGCATCAGAAAGGAAAC-C-T- 97
SEMG2_Callithrix_jacchus        TACATCTAAAATTGGATTTTTAAATCATTGCATCAGAAAGGAAACTCACG 100
SEMG2_Saimiri_boliviensis       TATACCTAAAATTGGGTTTTTTAATTATTGCATCAGAAAGGAAACTCACG 100
                                ** * ***** *    * *** * * *  * ******** ***** *

SEMG2_Human                     TTTAGAGTATGAAGGCATTGTCAGCCACCAATTACTTTTGTAACCTGAAG 150
SEMG2_Chimpanzee                TTTAGAATATGAAGGCATTGTCAGCCACCAATTACTTTTGTAACCTGAAG 150
SEMG2_Bonobo                    TTTAGAGTATGAAGGCATTGTCAGCCACCAATTACTTTTGTAACCTGAAG 150
SEMG2_Gorilla                   TTTAGAGTATGAAGGCATTGTCAGCCAYCAATTACTTTTGTAACCTGAAG 150
SEMG2_Orangutan                 TTTAGAGTATGAAGGCATTGTCAGCCACCAATTACTTTTGTAACCTGAAG 150
SEMG2_Gibbon                    TTTAAAATATGAAGGCATTGTCAGCCACCAATTACTTTTGTAACCTGAAG 148
SEMG2_Macaque                   TTTAGAATATGAAGGCATAGTCAGCCACCAGTTACTTTTGTAACCTGAAG 149
SEMG2_Papio_anubis              TTTAGAATATGAAGGCATAGTCAGCCACCAGTTACTTTTGTAACCTGAAG 147
SEMG2_Chlorocebus_aethiops      TTTAGAATATGAAGGCATAGTCAGCCACCAATTACTTTTGTAACCTGAAG 147
SEMG2_Colobus_guereza           -------------GGCATAGTCAGCCACCAGTTACTTTTGTAACCTGAAG 134
SEMG2_Callithrix_jacchus        TTTAGAATAAGAAGGCATTGCCAGCCACCAGTTACTTTTGTAACCTGAAG 150
SEMG2_Saimiri_boliviensis       TTTAGTATAAGAAGGCATTGCCAGCCACCAATTACTTTTGTAACCTGAAG 150
                                           ***** * ****** ** ******************

SEMG2_Human                     CTAGTCTCCTTCCTACTCCGGACTGAATTTCTTCTGTATAATGCAAGCGA 200
SEMG2_Chimpanzee                CTAGTCTCCTTCCTACTCCAGACTGAATTTCTTCTGTATAATGCAAGCGA 200
SEMG2_Bonobo                    CTAGTCTCCTTCCTACTCCAGACTGAATTTCTTCTGTATAATGCAAGCGA 200
SEMG2_Gorilla                   CTAGTCTCCTTCCTACTCCAAACTGAATTTSTTCTGTATAATGCAAACGA 200
SEMG2_Orangutan                 CTAGTCTCCTTCCTACTCTGGACTGAATTTCTTCTGTATAATGCAAGCGA 200
SEMG2_Gibbon                    CTAGTCTCCTTCCTACTCCGGACTGAATTTCTTCTGTATAATGCAAGTGA 198
SEMG2_Macaque                   CTAGTCTCCTTCCTACTCCGGACTGAATGTCTTCTGTGTAATGCAAGCGA 199
SEMG2_Papio_anubis              CTAGTCTCCTTCCTACTCCGGACTGAATGTCTTCTGTGTAATGCAAGCGA 197
SEMG2_Chlorocebus_aethiops      CTGGTCTCCTTCCTACTCTGGACTGAATGTCTTCTGTGTAATGCAAGCGA 197
SEMG2_Colobus_guereza           CTAGTCTCCTTCCTACTCCGAACTGAATGTCTTCTGTGTAATGCAAGCGA 184
SEMG2_Callithrix_jacchus        CTAGTCTCCTTCCCACTCTAGACTGAATTTCTTCTGTAAACTACAAGCAA 200
SEMG2_Saimiri_boliviensis       CTAGTCTCCTTCCTACTCTAGACTGAATTTCTTCTGTAAGATGCAAGCAA 200
                                ** ********** ****   ******* * ******    * ***   *
```

```
SEMG2_Human                     TCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGA 250
SEMG2_Chimpanzee                TCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGG 250
SEMG2_Bonobo                    TCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGG 250
SEMG2_Gorilla                   TCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGG 250
SEMG2_Orangutan                 TCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGG 250
SEMG2_Gibbon                    TCTGGCATGAAGATATACAAAGACTGATAAAATTTTGCTGGGGATTCTGG 248
SEMG2_Macaque                   TCTGGCTTGATGATATACAAGGACCGATAAAATTTTGCTGGGGATTCTGG 249
SEMG2_Papio_anubis              TCTGGCTTGATGATATACAAGGACAGATAAAATTTTGCTGGGGATTCTGG 247
SEMG2_Chlorocebus_aethiops      TCTGGCTTGATGATATACAAGGACCGATAAAATTTTGCTGGGGATTCTGG 247
SEMG2_Colobus_guereza           TCTGGCTTGATGATATACAAGGACCGATAAAATTTTGCTGGGGATTCTGG 234
SEMG2_Callithrix_jacchus        CTTGGCATGATGATATGCAAGTTCTGATAAAATTT-GCTGGGGATTGGGG 249
SEMG2_Saimiri_boliviensis       TCTGGCATGATGACATACAAGGACTGATAAAATTT-GCTGGGGATTCAGG 249
                                  **** *** ** ** ***   * ********** **********  *

SEMG2_Human                     AAGTAAAAAAAA--TTGCCTTTGATATTATGTCCCCATGCTAAGTCCCTG 298
SEMG2_Chimpanzee                AAGTAAAAAAAA--TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 298
SEMG2_Bonobo                    AAGTAAAAAAAA--TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 298
SEMG2_Gorilla                   AAGTAAAAAAAAA-TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 299
SEMG2_Orangutan                 AAGTAAAAAAAA--TTGCCTTTAACATTATGTCCCCATGCTAAGTCCCTG 298
SEMG2_Gibbon                    AAGTAAAAAAAA--TTGCCTTTGACATTATGTTCCCATGCTAAGTCCCTG 296
SEMG2_Macaque                   AAGCAAAAAAAAA-TTGCCTTTGACATTATGTCCCCTTGCTAAGTCCCTG 298
SEMG2_Papio_anubis              AAGCAAAAAAAAA-TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 296
SEMG2_Chlorocebus_aethiops      AAGCAAAAAAAAAATTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 297
SEMG2_Colobus_guereza           AAGTAAAAAAAA--TTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTG 282
SEMG2_Callithrix_jacchus        AAGTAAAAAAA---TTGCCTTTGACGTTATGTCCCCGTGCTAAGTCCCTG 296
SEMG2_Saimiri_boliviensis       AAGTAAAAAAA---TTGCCTTTGACGTTATGTCCCCGTGCTAAGTCCCTG 296
                                *** *******   ******** *  ****** *** **************

SEMG2_Human                     GGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGCTGGCATTT 348
SEMG2_Chimpanzee                GGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTT 348
SEMG2_Bonobo                    GGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTT 348
SEMG2_Gorilla                   GGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGGCATTT 349
SEMG2_Orangutan                 GGGACTTTGACATTATTCCCCACTGAGCAGGGGCGAGGAAGTTGGCATTT 348
SEMG2_Gibbon                    GGAACTTTGACATTATCTCCCACTGAGCAGGGGCGAYGAAGTTGGCATTT 346
SEMG2_Macaque                   GGGACTTTGACATTATCCCCCACTGAGCAGTGGCGAGGAAGTTGGCATTT 348
SEMG2_Papio_anubis              GGGACTTTGACATTATCCCCCACTGAGCAGTGGCGAGGAAGTGGGCATTT 346
SEMG2_Chlorocebus_aethiops      GGGACTTTGACATTATCCCCCACTGAGCAGTGGCGAGGAAGTTGGCATTT 347
SEMG2_Colobus_guereza           GGGACTTTGACATTATCCCCCACTGAGCAGTGGCGAGGAAGTTGGCATTT 332
SEMG2_Callithrix_jacchus        GGGACTTTGATATTATCCCCCACTGAGCAGGGGTGAGGAAGCTGACATTT 346
SEMG2_Saimiri_boliviensis       GGGACTTTGACATTATCCCCCACTGAGCAGGGGTGAGGAAGTTGACATTT 346
                                ** ******* *****  ************ ** ** ****  * *****

SEMG2_Human                     ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 398
SEMG2_Chimpanzee                ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 398
SEMG2_Bonobo                    ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 398
SEMG2_Gorilla                   ACTAATAAGCTATGAAAGGGCAGTACCTTTTGACATTTCAGCTCCACCCA 399
SEMG2_Orangutan                 ACTAATAAGCTATGAAAGGGCAGTGCCTTTTCACATTTCAGCTCCACCCA 398
SEMG2_Gibbon                    ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 396
SEMG2_Macaque                   ACTAATAAGCTATGAAAGGGGGGAGCCTTTTGACATTTCAGCTCCACCCA 398
SEMG2_Papio_anubis              ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 396
SEMG2_Chlorocebus_aethiops      ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 397
SEMG2_Colobus_guereza           ACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAGCTCCACCCA 382
SEMG2_Callithrix_jacchus        ATTAATAAGCTATGAAAGGGCAGTGCCTTTTGAAATTTCAGCTCCACCCA 396
SEMG2_Saimiri_boliviensis       ATTAATAAGCTATGAAAGGGCAGTGTCTTTTGAAATTTCAGCTCCACCCA 396
                                * ******************  *   ***** * ***************

SEMG2_Human                     TAGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGTTCTC 448
SEMG2_Chimpanzee                TAGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTC 448
SEMG2_Bonobo                    TAGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTC 448
SEMG2_Gorilla                   TAGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTC 449
```

```
SEMG2_Orangutan                 TGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTGAGCTCTC 448
SEMG2_Gibbon                    TGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTC 446
SEMG2_Macaque                   TGGCACACCCACTCAAGGAACATATAAATGA-GAGATCCCCTCCGGTCTC 447
SEMG2_Papio_anubis              TGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCATTCAGTTCTC 446
SEMG2_Chlorocebus_aethiops      TGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCATTCAGTTCTC 447
SEMG2_Colobus_guereza           TGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCACTCAGTTCTC 432
SEMG2_Callithrix_jacchus        TGGTACACCCACTCAAGGAAGATACAAACGAAGATATCCACTCGGCTCTC 446
SEMG2_Saimiri_boliviensis       TGGTAAGCCCACTCAAGGAAGATATAAATGAAGAGAACCACTCGGCTCTC 446
                                * * *  ************* *** *** ** ** * **  *  * ****



SEMG2_Human                     AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 498
SEMG2_Chimpanzee                AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 498
SEMG2_Bonobo                    AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 498
SEMG2_Gorilla                   AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 499
SEMG2_Orangutan                 AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 498
SEMG2_Gibbon                    AGACAAGATTTTTCGAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 496
SEMG2_Macaque                   AGACAAGATTTTTCAAGCAAAATGAAGTCCATCATCCTCTTTGTCCTTTC 497
SEMG2_Papio_anubis              AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 496
SEMG2_Chlorocebus_aethiops      AGACAAGATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 497
SEMG2_Colobus_guereza           AGACAACATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTC 482
SEMG2_Callithrix_jacchus        AGACAAGGTTTTCCAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTTC 496
SEMG2_Saimiri_boliviensis       AGACAAGGTTTTCCAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTTC 496
                                ******  **** * ***** ****** ******** **** ** *****

SEMG2_Human                     CC 500
SEMG2_Chimpanzee                CC 500
SEMG2_Bonobo                    CC 500
SEMG2_Gorilla                   CC 501
SEMG2_Orangutan                 CC 500
SEMG2_Gibbon                    CC 498
SEMG2_Macaque                   CC 499
SEMG2_Papio_anubis              CC 498
SEMG2_Chlorocebus_aethiops      CC 499
SEMG2_Colobus_guereza           CC 484
SEMG2_Callithrix_jacchus        CC 498
SEMG2_Saimiri_boliviensis       CT 498
                                *
```

Ancestral sequences

Ancestral sequences reconstructed in this study

>*SEMG1/SEMG2*_ancestralgene
AAAATAGAATGTGTCTCAAGATCATTTTAAAACAAGAAGAAGTACAGAGTTCTATCTAAAATAGG
GTATTTAAATTATTGCATCATGAAAGGAAACTCACATTTAGAATATAAAGGCATTCTCAGACACC
AATTACTTTTGTAACCTGAAGCTAGTCTCTTTCCTACTCTGGACTGAATTTCTTCTGTAAAATGC
AAGCGATCTGGCATGATGATCTACAAGGACTGATAAAATTTTGCTGGGGCTTCCGGAAGTAAGAA
AAATGCCTTTGACATTATGTCCCCGTGCTAAGTCCCTGGGGACTTTGACATTGTCCCCCACTGAG
CAGGGGTGAGGAAGTTGGCATTTACTGATAAGCTAAGAAAGGGCAGTGCCTTTTGTAATTTCAGC
TCCACCCATGGCACACCCACTCAAGGAAGATATAAATGAAGAGATCCACTCAGCTCTCAGACAAG
GTTTTCCAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTTCCC

>*SEMG1*_haplorrhine_LCA
AAAATAGAATGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAAAATAG
AGTATTTAAATTATTACATCATGAAGGGAAACTCACATTTAGAATATAAAGGCATTCTCAGAAAC
CAATTACTTTTGTAACCTGAAGCTAGTCTCTTTCCTACTTTTGTCTATACTTCCGTAAAATGCAA
GTGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGCTGGGGCTTCCAGAAGAAAGAAAA
TGCCTTTGACATTATGTCGCTGGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTT
GGCATTTACTGATAAGCTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACAC
TCACTCAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGTTTTCCAAGCAAGAT
GAAGCCCATCATCTTCTTCGTACTTTCCC

>*SEMG1*_catarrhine_LCA
AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAAAATAG
AGTATTTAAATTATTACATCATGAAGGGAAACTCACATTTAGAATATAAAGGCATTCTCAGAAAC
CAATTACTTTTGTAGCCTGAAGCTAGTCTCTTTCCTACTTTTGTCTATAATTCCGTAAAATGCAA
GTGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGCTGGGGCTTCCAGAAGAAAGAAAA
TGCCTTTGACATTATGTTGCTGGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTT
GGCATTTACTGATAAGCTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACAC
TCACTCAAGGAAGATATAAATGACAAGGTCCACTCAGCTCTCAGACAAGGTTTTCCAAGCAAGAT
GAAGCCCAACATCATCTTCGTACTTT

>*SEMG1*_hominoid_LCA
AAAATAGAACGTGTCTCAAGATCATTTTTAAAACAAAAGGAAGTATGGAGTTCTATCTAAAATAG
AGTATTTAAATTATTACATCATGAAGGGAAACTCACATTTAGAATATAAAGGCATTCTCAGAAAC
CAATTGCTTTTGTAGCCTGAAGCTAGTCTCTTTCCTACTTTTGTCTATAATTCCGTAAAATGAAA
GTGATCTGGCATGATGATCTACAAGGACTGATAAAAATTTGCTGGGGCTTCCAGAAGAAAGAAAA
TGCCTTTGACATTATGTTGCTGGGGACATTGACTTTGTCCCACACTCAGCAGGGGTGAGGAAGTT
GGCATTTACTGATAAGCTAAGAAAAGGCAGTGCCTTTTGTAATTTAAGCTCCACCCATGGCACAC
TCACTCAAGGAAGATATAAATGACAAGGTCCGCTCAGCTCTCAGACAAGGTTTTCCAAGCAAGAT
GAAGCCCAACATCATCTTTGTACTTT

>*SEMG2*_haplorrhine_LCA
AAAACAGAATGTGTCTCAGGATTATTTTAAAACAAGACGAAGTACAGAGTTATACCTAAAATTGG
GTATTTAAATTATTGCATCAGAAAGGAAACTCACATTTAGAATATGAAGGCATTGTCAGCCACCA
ATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCTGGACTGAATTTCTTCTGTAAAATGCA
AGCGATCTGGCATGATGATATACAAGGACTGATAAAATTTTGCTGGGGATTCTGGAAGTAAAAAA

AATTGCCTTTGACATTATGTCCCCGTGCTAAGTCCCTGGGGACTTTGACATTATCCCCCACTGAG
CAGGGGTGAGGAAGTTGGCATTTACTAATAAGCTATGAAAGGGCAGTGCCTTTTGAAATTTCAGC
TCCACCCATGGCACACCCACTCAAGGAAGATATAAATGAAGAGATCCACTCAGCTCTCAGACAAG
GTTTTCCAAGCAAGATGAAGCCCATCATCTTCTTCGTACTTTCCC

>*SEMG2*_catarrhine_LCA
AAAACAGAATGTGTCTCAGGATTATTTTAAAACAAGACGAAGTACAGAGTTATACCTAAAATTGA
GTATTTAAGTTATTGCATCAGAAAGGAAACTCACATTTAGAATATGAAGGCATTGTCAGCCACCA
ATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCGGACTGAATTTCTTCTGTATAATGCA
AGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGGAAGTAAAAAA
AAATTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTGGGGACTTTGACATTATCCCCCACTGA
GCAGGGGCGAGGAAGTTGGCATTTACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAG
CTCCACCCATGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAA
GATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTCCC

>*SEMG2*_hominoid_LCA
AAAACAGAATGTGTCTCAGGATTATTTTAAAACAAGACGAAGTACAGAGTTATACCTAAAATTGA
GTATTTAAGTTATTGCATCAGAAAGGAAACTCACATTTAGAATATGAAGGCATTGTCAGCCACCA
ATTACTTTTGTAACCTGAAGCTAGTCTCCTTCCTACTCCGGACTGAATTTCTTCTGTATAATGCA
AGCGATCTGGCATGATGATATACAAAGACCGATAAAATTTTGCTGGGGATTCTGGAAGTAAAAAA
AAATTGCCTTTGACATTATGTCCCCATGCTAAGTCCCTGGGGACTTTGACATTATCCCCCACTGA
GCAGGGGCGAGGAAGTTGGCATTTACTAATAAGCTATGAAAGGGCAGTGCCTTTTGACATTTCAG
CTCCACCCATGGCACACCCACTCAAGGAACATATAAATGAAGAGATCCGCTCAGCTCTCAGACAA
GATTTTTCAAGCAAGATGAAGTCCATCATCCTCTTTGTCCTTTCCC